

WIREH

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:31:00 1998: Master time 5.54 Seconds
Tabular output not generated. 221.678 Million cell updates/sec
Title: >US-08-844-215-14
Description: (1-106) from US08844215 pep
Perfect Score: 749
Sequence: 1 AFIQSGILSLSPGEAIL YCCQYGPRTFGGINKVEIK 106

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13899129 residues
Post-processing: Minimum Match 0
Listing first 45 summaries
Database: a-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 29.587 Variance 163.436: scale 0.181

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result	Score	Query	Length	ID	Description	Pred No.
No. <th>Match</th> <th></th> <th></th> <th></th> <th></th> <th></th>	Match					
1	575	90.1	106	P54275	Anti-HIV gp41 immunog	3.03e-41
2	575	90.1	106	W01320	VL of Fab, DL 41 19,	3.03e-41
3	570	89.5	108	P54316	Anti-HIV gp120 immuno	7.26e-41
4	570	89.5	106	W01278	VL region of HIV neut	7.26e-41
5	570	89.5	129	P38572	vk225-JK2	7.26e-41
6	566	88.9	108	W01265	VL region of HIV neut	1.46e-40
7	565	88.9	108	P54307	Anti-HIV gp120 immuno	1.46e-40
8	565	88.9	111	P54377	Anti-HIV gp41 immunog	1.46e-40
9	566	88.9	111	W01327	VL of Fab, GL 41 1, b	1.46e-40
10	563	88.5	107	P54311	Anti-HIV gp120 immuno	2.46e-40
11	563	88.5	107	W01264	VL region of HIV neut	2.46e-40
12	558	87.9	107	P38593	Human lambda light ch	5.89e-40
13	556	87.6	109	P50217	HSV glycoprotein F bi	8.38e-40
14	550	86.8	104	P54317	Anti-HIV gp120 immuno	2.38e-39
15	550	86.8	104	W01276	VL region of HIV neut	2.38e-39
16	548	86.5	129	P41286	P105 rearranged varia	3.37e-39
17	546	86.2	109	P56286	Light chain of Amb al	4.77e-39
18	542	85.7	214	W07615	Ulcerative colitis-as	9.59e-39
19	541	85.6	108	W01289	VL region of HIV neut	1.14e-38
20	541	85.6	134	W11155	Anti-lung tumour anti	1.14e-38

21	628	85.2	129	7	P39673	P105VP-P10576	1.92e-38
22	634	84.6	109	10	P54263	Anti-HIV gp120 immuno	3.69e-38
23	628	83.8	107	10	P54308	Anti-HIV gp120 immuno	1.17e-37
24	628	83.8	107	19	W01266	VL region of HIV neut	1.10e-37
25	626	83.6	108	10	P54255	Anti-HIV gp120 immuno	1.59e-37
26	626	83.6	108	19	W01275	VL region of HIV neut	1.59e-37
27	625	83.4	215	19	W07616	Ulcerative colitis-as	1.85e-37
28	624	83.3	124	22	W24539	Immunoglobulin Fc12	2.20e-37
29	619	82.7	109	9	P50218	HSV glycoprotein F bi	5.26e-37
30	618	82.5	112	10	P54279	Anti-HIV gp41 immuno	5.26e-37
31	618	82.5	112	19	W01324	VL of Fab, SS 41 8, B	5.26e-37
32	616	82.2	104	9	P54315	Anti-HIV gp120 immuno	8.86e-37
33	616	82.2	104	19	W01273	VL region of HIV neut	8.86e-37
34	612	82.2	112	2	P81245	Anti-pseudomonas aer	8.86e-37
35	616	82.2	128	1	P91001	Anti-P. aeruginosa st	8.86e-37
36	612	81.7	105	19	W01272	VL region of HIV neut	1.78e-36
37	612	81.7	105	9	P54314	Anti-HIV gp120 immuno	1.78e-36
38	611	81.6	116	7	P38650	Human V-kappa fragmen	2.11e-36
39	611	81.6	116	20	W03948	DNA fragment vk65.8,	2.11e-36
40	611	81.6	116	11	P54330	Human V-kappa fragme	2.11e-36
41	610	81.4	108	19	W01267	VL region of HIV neut	2.55e-36
42	607	81.0	109	5	P25224	LY region of human th	4.24e-36
43	597	79.7	108	10	P54309	Anti-HIV gp120 immuno	2.41e-35
44	594	79.3	107	19	W01297	VL region of HIV neut	4.96e-35
45	594	79.3	107	19	W01295	VL region of HIV neut	4.06e-35

ALIGNMENTS

RESULT 1
ID R54275 standard: protein: 109 AA.
AC R54275:
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW neutralisation; monoclonal antibody; light chain; variable region;
KW framework region; complementarity determining region.
OS Homo sapiens.
PH Key Location/Qualifiers
FT Region 1...23
FT /Label= FR1
FT Region 24...35
FT /Label= CDR1
FT Region 36...50
FT /Label= FR2
FT Region 51...57
FT /Label= CDR2
FT Region 58...89
FT /Label= FR3
FT Region 90...97
FT /Label= CDR3
FT Region 98...109
FT /Label= FR4
PR W09457922-A.
PD 14-APR-1994.
PE 30-SEP-1993: 509328.
PR 30-SEP-1992: GS-954.48.
PA (SRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
WP1: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immunotherapy
FS Claim 1: Page 215-216, 248pp, English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC diatomic vector to produce a library of fragments. Entry: XLI
CC Blue cells were transfected with the library. Filamentous phage were
CC produced which expressed the VAB regions of their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence P54275 neutralises HIV1
CC gp41.

100

RESOLUTION	10	R54277	standard; protein; l11 AA.
AC	AC	R54277;	
DT	DT	10-NOV-1994	(first entry)
DE	DE	Anti-HIV gp41 immunoglobulin light chain V region clone GL 41 1.	
KW	KW	Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;	
KW	KW	neutralisation; monoclonal antibody; light chain; variable region;	
KW	KW	framework region; complementarity determining region.	
OS	OS	Homo sapiens.	
FT	FT	key	Location/Qualifiers
FT	FT	Region	1..23
FT	FT	/label= FR1	

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FT      Region          CDR1           36...50
FT /Label= FR2
FT      Region          CDR2           51..57
FT /Label= CDR2
FT      Region          CDR3           58..89
FT /Label= FR3
FT      Region          CDR3           90...97
FT /Label= CDR3
FT      Region          CDR3           98...111
FT /Label= FR4
FN WQ940792-2-A.
PD   14 -APR-1994.
PF    30-SEP-1993; U09328.
PR    30-SEP-1992; US-954148.
PI     (SRI ) SCRIPPS RES INST.
PA Barbas CF, Burton DR, Lerner RA;
DP WPI; 94-135516/16
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them. Useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PT Claim 11; Page 217; 248pp; English.
CC lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence R54277 neutralises HIV1
CC gp41.
SQ Sequence            111 AA;

Query Match              88 aa; Score 666; DP 10; Length 111;
Best Local Similarity 86 %*; Pred No 1 4aa-40;
Matches               92; Conservative         10; Mismatches       4; Indels        0; Gaps

Db                2 aeitcpqtisipgeratlscragssvsgylawyqgkqqagorliiygastruidpd 61
QY                 1 AEUTSPGTLISPGERATLSICPASQSUSSYLAWYVGRKPKAPPRTFYDASSRAFSIFD 60
Db                62 rfegsgsgadftlaistrlopedfavyrycggaygshtfrgatkieik 107
```

CY 61 PFSGSGTDTLSISPLPEFAVYVQYVGTPTPTGQTKVEIK 106

RESULT 9
ID W01322 standard: Protein: 111 AA.
AC W01322:
DI 29-JAN-1997 (first entry)
DE VL of Fab, GL 411, binds to HIV gp41.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
MA: HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.

EH Key Location/Qualifiers

FT Region 1..23
FT /label= FR1
FT Region 24..35
FT /label= CDR1
FT Region 36..50
FT /label= FR2
FT Region 51..57
FT /label= CDR2
FT Region 58..89
FT /label= FR3
FT Region 90..97
FT /label= CDR3
FT Region 98..111
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
passive immuno-therapy and detection of HIV infection.
PS Example 3: Fig 19: 36pp; English.
CC The sequences given in W01320-24 represent the light chain variable
regions (VH) of a series of antibody fragments (FAB's) which are
immunoreactive with HIV glycoprotein gp41. This sequence represents
the sequence of the clone, GL 411. These sequences represent light
chains which bind to the heavy light chain clones given in W01315-19. A
monoclonal antibody containing one of these Fab sequences may have the
capacity to reduce HIV infectivity titre in an in vivo virus infectivity
assay by 50% at a concentration of less than 700 ng of antibody/ml.
CC The Mab may be used for determining immunocompetence of a human anti-HIV
antibody and in the detection of HIV infection.
SQ Sequence 111 AA;

Query Match 88.9%; Score 666; DB 19; Length 111;
Best Local Similarity 86.8%; Pred No 1 45e-40;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 2 eltsptlslspertatlsrasqslsnnylawyyqkqgqprlllygsstrgtatpdr 61
|||||
QY 1 AELTSPGTLSPGERATLSRASQSLSSKYLAWYQKQAPRLLFYDASSRATGIPDR 60
|||||

Db 62 rfsqsgsadtltlsrlpepfavvyqcygagshftfgqtkleik 107
|||||

QY 61 #FSGSGSTDTLSISPLPEDEFAVYVQYVGTPTPTGQTKVEIK 106
|||||

RESULT 10

ID R54311 standard: protein: 107 AA.

AC R54311:
DI 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region
OS Homo sapiens.
EH Key Location/Qualifiers

FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
PN W09407925-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
gp120 or gp41 and nucleic acid encoding them, useful for in vivo
or in vitro diagnosis and for passive immuno-therapy
PS Example; Page 180; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
amplification using primers specific for heavy and light chain
variable regions. The amplification products were inserted into a
dicistronic vector to produce a library of fragments. E.coli XL1
Blue cells were transformed with the library. Filamentous phage were
produced which expressed the MAB regions on their surface. Panning
with gp120 and gp41 resulted in the recovery of immunoreactive
clones. The light chain VK region sequence R54311 is from a gp120-
specific clone
SQ Sequence 107 AA;

Query Match 88.5%; Score 663; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.45e-40;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

Db 1 eltsptlslspertatlsrasqslsnnylawyyqkqgqprlllygsstrgtatpdr 60
|||||

QY 2 ELTSPGTLSPGERATLSRASQSLSSKYLAWYQKQAPRLLFYDASSRATGIPDR 61
|||||

Db 61 fsgsgsadtltlsrlpepfavvyqcygagshftfgqtkleik 106
|||||

QY 62 FSGSGSGTDTLSISPLPEDEFAVYVQYVGTPTPTGQTKVEIK 106
|||||

RESULT 11

ID W01269 standard: Protein: 107 AA.

AC W01269:
DI 28-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone B20.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
MA: HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.

EH Key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..33

FT /label= CDR1

FT Region 34..48

FT /label= FR2

FT Region 49..55

FT /label= CDR2

FT Region 56..87

FT /label= FR3

FT Region 88..96

FT /label= CDR3

FT Region 98..107

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FT /label= FR4
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-275852.
PA (SRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DP, Lerner PA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example: Fig 11; 366pp; English.
CC The sequences given in WO1261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection
SQ Sequence 107 AA:

Query Match 88.5%; Score 663; DB 19; Length 107;
Best Local Similarity 85.8%; Pred. No. 2,46e-40;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1,

Db 1 eltspgtllspgeratlscrasqslsnnnylawyqkqgqaprrlllygsstrgtgipdr 60
QY 2 flttspgtllspgeratlscrasqslsnnnylawyqkqgqaprrlllygsstrgtgipdr 61
Db 61 fsgqsgtdftltisrlepafavyqcgqyngsnvytfggatkileik 106
QY 62 fsgsgsgtdftltisrlepafavyqcgqyngsnvytfggatkileik 106

RESULT 12
ID R38593 standard; peptide; 107 AA
AC R38593:
DT 28-OCT-1993 (first entry)
DE Human lambda light chain subgroup 3 (HL3).
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
QS Homo sapiens.
FH Key Location/Qualifiers
FT /note= "residue conserved in less than 50% of the
FT known sequences of HL3"
PN WO9311794-A.
PD 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-808464
PA (XOMA ) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
DR WPI: 93-213827/25.
PT Antibodies prep. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Claim 2: Page 93-94; 160pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (HK1 - R38590, HK3 - NGK, HK2 - GST, HLI - R38591, HL2 -
CC R38592, HL3 - R38593, HL4 - R38594, HK4 - R38595, HL4 - R38596,
CC and HL5 - R38597) and heavy chains (HH3 - R38598, HH1 - R38599 and
CC HH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans.
CC *Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding
CC This ensures that the binding properties of the modified antibody
CC are not diminished.

SQ Sequence 107 AA:

Query Match 87.9%; Score 658; DB 7; Length 107;
Best Local Similarity 90.5%; Pred. No. 5,89e-40;
Matches 95; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

Db 4 ltspgtllspgeratlscrasqslsnnnylawyqkqgqaprrlllygsstrgtgipdr 62
QY 3 ltspgtllspgeratlscrasqslsnnnylawyqkqgqaprrlllygsstrgtgipdr 62
Db 63 sgsqsgtdftltisrlepafavyqcgqyngsnvytfggatkileik 107
QY 63 sgsqsgtdftltisrlepafavyqcgqyngsnvytfggatkileik 106

RESULT 13
ID R50217 standard; Protein: 109 AA.
AC R50217:
DT 31-OCT-1994 (first entry)
DE HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.
KW Complementarity Determination region, CDR3, human, bronchiolitis;
KW monoclonal antibody; epitope; glycoprotein F; influenza virus;
KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;
KW lung; pneumonia.
QS Synthetic.
FH Key Location/Qualifiers
FT /Region= FR1
FT /label= FR1
FT /Region= FR1
FT /label= CDR1
FT /Region= FR2
FT /label= FR2
FT /Region= CDR2
FT /label= CDR2
FT /Region= FR3
FT /label= FR3
FT /Region= CDR3
FT /label= CDR3
FT /Region= FR4
FT /label= FR4
PN WO9406448-A.
PD 31-MAR-1994.
PR 16-SEP-1993; U08796.
PA (SRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DP, Chanock PM, Crowe JE, Murphy BR;
DR WPI: 94-118147/14.
PT Human neutralising monoclonal antibodies to respiratory syncytial
PT virus - for treatment prophylaxis and diagnosis of RSV and other
PT diseases of the respiratory tract
PS Disclosure: Fig 4; 104pp; English.
CC The sequences given in R50215-19 represent the heavy and light chain
CC variable domains of various clones of a human monoclonal antibody
CC which binds to an epitope of glycoprotein F of respiratory syncytial
CC virus (RSV). These antibodies may be used as a reagent for the
CC diagnosis of RSV disease and other viral mucosal diseases, eg.
CC influenza virus, rhinovirus and coronavirus. They are particularly
CC useful in ameliorating RSV when delivered directly to the lungs, and
CC may also be used for treating pneumonia and bronchiolitis.
SQ Sequence 109 AA:

Query Match 87.9%; Score 656; DB 9; Length 109;
Best Local Similarity 86.0%; Pred. No. 8,35e-40;
Matches 92; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltqspgllspgoratlscratqslsnnnylawyqkqgqaprrlllygsstrgtgipdr 61
QY 1 aeltqspgllspgoratlscratqslsnnnylawyqkqgqaprrlllygsstrgtgipdr 60
Db 62 rfsqsgsgtdftltisrlepafavyqcgqyngsnvytfggatkileik 108
QY 61 rfsqsgsgtdftltisrlepafavyqcgqyngsnvytfggatkileik 106

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RESULT 14
ID R54317 standard: protein: 104 AA

AC R54317;
DI 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region s6
KW Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope;
KW neutralisation: monoclonal antibody; kappa light chain;
KW variable region: framework: complementarity determining region.
OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..18

FT /label= FR1

FT Region 19..30

FT /label= CDR1

FT Region 31..45

FT /label= FR2

FT Region 46..52

FT /label= CDR2

FT Region 53..84

FT /label= FR3

FT Region 85..93

FT /label= CDR3

FT Region 94..104

FT /label= FR4

PN W09407922-A.

PD 14-APR-1994.

PF 30-SEP-1993: U09428.

PR 30-SEP-1992: ES-354.48

PA (SCR1) SCRIPPS RES INST

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 94-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with
gp120 or gp41 and nucleic acid encoding them, useful for in vivo
or in vitro diagnosis and for passive immuno-therapy

PS Example: Page 185-187; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
amplification using primers specific for heavy and light chain
variable regions. The amplification products were inserted into a
dicistronic vector to produce a library of fragments. E.coli XL1
Blue cells were transformed with the library. Filamentous phage were
produced which expressed the MAB regions on their surface. Panning
with gp120 and gp41 resulted in the recovery of immunoreactive
clones. The light chain VK region sequence R54317 neutralises HIV1
gp120.

CC Sequence 104 AA;

Query Match 86.8%; Score 650; DB 9; Length 104;

Best Local Similarity 87.4%; Pred. No. 2.38e-39;

Matches 90; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

Db 1 qspqtlsipgeratlsrscasqslsnnylawyqgkpgqaprllygsstratgipdrfsq 60
|||||

QY 5 QSPQTLSIPGERATLSRSPASQSLSSKYLAWYQKPGQAPPLFIYDASSRATGIPDPFSG 64
|||||

Db 61 gsgtdftltisrlepedfavyvccqygnsvytfqgqtkleik 103
|||||

QY 65 SSGSDFTLTISRLEPEDFAVYVCCQYGTTPR-TFGQGTKEIK 106
|||||

RESULT 15

ID W01279 standard: Protein: 104 AA.

AC W01279;

DI 29-JAN-1997 (first entry)

DE VL region of HIV neutralising MAB, clone s6.

KW Heavy chain; light chain; variable region; VH: monoclonal antibody;

KW MAB: HIV; human immunodeficiency virus; glycoprotein: gp120; clone;

KW virus infectivity assay; precursor gp160; immunocompetence, human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..18

FT /label= FR1

FT Region 19..30

FT /label= CDR1

FT Region 31..45

FT /label= FR2

FT Region 46..52

FT /label= CDR2

FT Region 53..84

FT /label= FR3

FT Region 85..93

FT /label= CDR3

FT Region 94..104

FT /label= FR4

PN W09602273-A1.

PD 01-FEB-1996.

PF 11-JUL-1995: U08743.

PR 18-JUL-1994: US-276852.

PA (SCR1) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 96-179601/18.

PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
passive immuno-therapy and detection of HIV infection.

PS Example: Fig 11; 386pp; English.

CC The sequences given in W01261-92 represent the light chain variable
regions (VL) of a series of monoclonal antibodies (MAB's) which are
immunoreactive with HIV glycoprotein gp120 and are capable of
neutralising HIV. This sequence represents the sequence of the JK2
gene clone, s6. A MAB containing this VL sequence has the capacity
to reduce HIV infectivity titre in an in-vivo virus infectivity assay
by 50 % at a concentration of less than 100 ng of anti-gp120, and
binds mature gp120 preferentially over the precursor gp160. The MAB
may be used for determining immunocompetence of a human anti-HIV
antibody and in the detection of HIV infection.

CC Sequence 104 AA;

Query Match 86.8%; Score 650; DB 19; Length 104;

Best Local Similarity 87.4%; Pred. No. 2.38e-39;

Matches 90; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

Db 1 qspqtlsipgeratlsrscasqslsnnylawyqgkpgqaprllygsstratgipdrfsq 60
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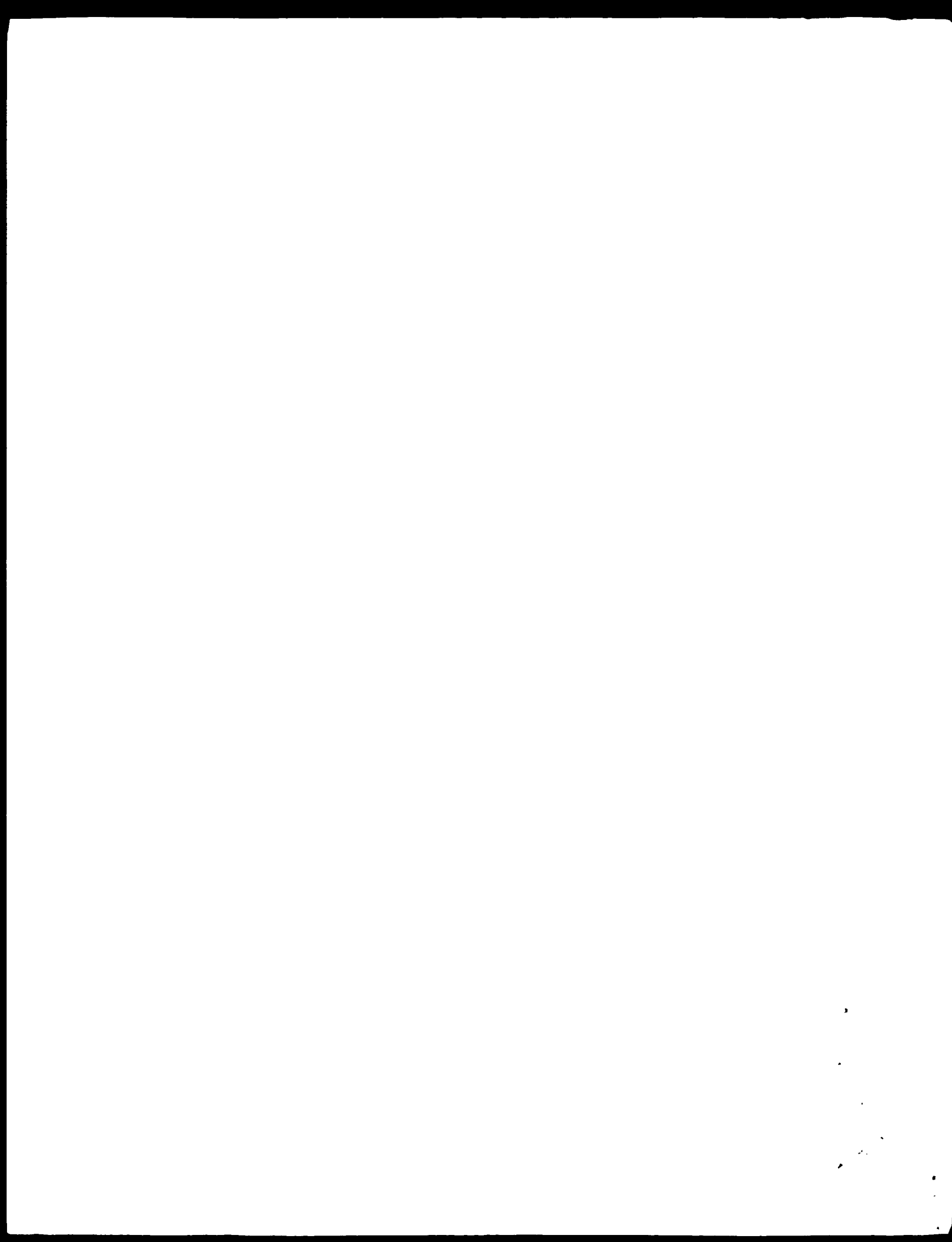
QY 5 QSPQTLSIPGERATLSRSPASQSLSSKYLAWYQKPGQAPPLFIYDASSRATGIPDPFSG 64
|||||

Db 61 gsgtdftltisrlepedfavyvccqygnsvytfqgqtkleik 103
|||||

QY 65 SSGSDFTLTISRLEPEDFAVYVCCQYGTTPR-TFGQGTKEIK 106
|||||

Search completed. Tue Feb 24 07:31:32 1998

Job time : 32 secs.



WIREH (IM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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Mparch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:27:53 1998; MasPar time 7.38 Seconds
Tabular output not generated. 437.627 Million cell updates/sec

Title: >US-08-844-215-13
Description: (1-106) from US08844215 pep
Perfect Score: 728
Sequence: 1 AELTQSPSSLSAFVGDPTVI CQSGVTTPTTFGGGKVEVK 106

Scoring table: PAM 150
Gap 11
Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir33
1:unann1 2:unann2 3:unann3 4:unann4 5:unann5 6:unann6 7:unann7 8:unann8 9:unann9 10:unann10 11:unann11 12:unann12 13:unann13 14:unann14 15:unann15 16:unann16 17:unann17 18:unann18 19:unann19 20:unann20 21:unann21 22:unann22 23:unann23 24:unann24 25:unann25 26:unann26 27:unann27 28:unann28 29:unann29 30:unann30 31:unann31 32:unann32 33:unann33 34:unann34 35:unann35 36:unann36 37:unann37 38:unann38 39:unann39 40:unann40 41:unann41 42:unann42 43:unann43 44:unann44 45:unann45 46:unann46 47:unann47 48:unann48 49:unann49 50:unann50 51:unann51 52:unann52 53:unann53 54:unann54 55:unann55 56:unann56 57:unann57 58:unann58 59:unann59 60:unann60 61:unann61 62:unann62 63:unann63 64:unann64 65:unann65 66:unann66 67:unann67 68:unann68 69:unann69 70:unann70 71:unann71 72:unann72 73:unann73 74:unann74 75:unann75 76:unann76 77:unann77 78:unann78 79:unann79 80:unann80 81:unann81 82:unann82 83:unann83 84:unann84 85:unann85 86:unann86 87:unann87 88:unann88 89:unann89 90:unann90 91:unann91 92:unann92 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#title	Expressed human immunoglobulin chi genes and their hypermutation.
#accession	S40367
##status	preliminary; translation not shown
##molecule_type	mRNA
##residues	1-127 ##label KLE
##cross-references	EMBL:X72477
CLASSIFICATION	#superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 127 #molecular-weight 13919 #checksum 8394
Query Match	89.4%; Score 651; DB 7; Length 127;
Best Local Similarity	88.6%; Pred. No. 1.52e-71;
Matches	93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db	20 qmtqpslsasvdrvtitcrasgsisnylnwqkpgkapklliyaaslsqgvsprf 79
Qy	2 ELTQSPSSLSAFVGPVITITCPASQISPNLNWYQKPKGTAPKVLIIYAASLSQSGVSPRF 61
Db	80 sgsqsgtdftllisslqpedfatycqgsytpwtfgggtkveik 124
Qy	62 SGSGSGTDFLTITSLQPEDFATYCCQSYTTPRTFGGKTVEIK 106
RESULT	3
ENTRY	B49047 #type fragment
TITLE	IgM monoclonal strational autoantibody kappa chain variable (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
ACCESSIONS	B49047
REFERENCE	A49047
#authors	Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
#journal	Eur. J. Immunol. (1992) 22:2231-2236
#title	Human monoclonal strational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autoimmune repertoire.
#cross-references	MUID:92387224
#accession	B49047
##status	preliminary
##molecule_type	nucleic acid
##residues	1-108 ##label VIC
##cross-references	NCBI:113209; NCBI:113209
##experimental_source	thymic B lymphocytes
##note	#sequence extracted from NCBI backbone
CLASSIFICATION	#superfamily immunoglobulin V region: immunoglobulin homology
SUMMARY	#length 108 #checksum 1741
Query Match	88.2%; Score 642; DB 7; Length 108;
Best Local Similarity	88.6%; Pred. No. 2.70e-70;
Matches	93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Db	3 qmtqpslsasvdrvtitcrasgsisnylnwqkpgkapklliyaaslsqgvsprf 62
Qy	2 ELTQSPSSLSAFVGPVITITCPASQISPNLNWYQKPKGTAPKVLIIYAASLSQSGVSPRF 61
Db	63 sgsqsgtdftllisslqpedfatycqgsytpwtfgggtkveik 107
Qy	62 SGSGSGTDFLTITSLQPEDFATYCCQSYTTPRTFGGKTVEIK 106
RESULT	4
ENTRY	S40370 #type complete
TITLE	Ig kappa chain - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	06-Mar-1994 #sequence_revision 26-May-1995 #text_change 16-Aug-1996
ACCESSIONS	S40370
REFERENCE	S40312
#authors	Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
#submission	submitted to the EMBL Data Library, June 1992
#description	Lack of promiscuity in autoantigen-specific H and L chain combinations as revealed by human H and L chain "roulette"
#title	Expressed human immunoglobulin chi genes and their hypermutation.
#accession	S40367
##status	preliminary; translation not shown
##molecule_type	mRNA
##residues	1-127 ##label KLE
##cross-references	EMBL:X72477
CLASSIFICATION	#superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 127 #molecular-weight 13919 #checksum 8394
Query Match	89.4%; Score 651; DB 7; Length 127;
Best Local Similarity	88.6%; Pred. No. 1.52e-71;
Matches	93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db	20 qmtqpslsasvdrvtitcrasgsisnylnwqkpgkapklliyaaslsqgvsprf 79
Qy	2 ELTQSPSSLSAFVGPVITITCPASQISPNLNWYQKPKGTAPKVLIIYAASLSQSGVSPRF 61
Db	80 sgsqsgtdftllisslqpedfatycqgsytpwtfgggtkveik 124
Qy	62 SGSGSGTDFLTITSLQPEDFATYCCQSYTTPRTFGGKTVEIK 106
RESULT	5
ENTRY	S47182 #type complete
TITLE	Ig kappa chain - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
ACCESSIONS	S47182
REFERENCE	S47181
#authors	McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
#submission	submitted to the EMBL Data Library, June 1994
#description	Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patients with Hashimoto's thyroiditis.
#accession	S47182
##status	preliminary
##molecule_type	mRNA
##residues	1-108 ##label MCI
##cross-references	EMBL:X79786
CLASSIFICATION	#superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 108 #molecular-weight 11655 #checksum 2422
Query Match	87.8%; Score 639; DB 7; Length 108;
Best Local Similarity	87.7%; Pred. No. 7.05e-70;
Matches	93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Db	2 teltqpslsasvdrvtitcrasgsisnylnwqkpgkapklliyaaslsqgvsprf 61
Qy	1 ARLTQSPSSLSAFVGPVITITCPASQISPNLNWYQKPKGTAPKVLIIYAASLSQSGVSPR 60
Db	62 fsgsgsgtdftllisslqpedfatycqgsytpwtfgggtkveik 107
Qy	61 FSGSGSGTDFLTITSLQPEDFATYCCQSYTTPRTFGGKTVEIK 106
RESULT	6
ENTRY	S31998 #type fragment
TITLE	Ig kappa chain - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 16-Aug-1996
ACCESSIONS	S31998
REFERENCE	S31977
#authors	Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
#submission	submitted to the EMBL Data Library, June 1992
#description	Lack of promiscuity in autoantigen-specific H and L chain combinations as revealed by human H and L chain "roulette"


```

#accession S31598
#status Preliminary
#molecule_type mRNA
#residues 1-109 ##label POR
##cross-references EMBL:Z15081
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6177

Query Match 87.8%; Score 639; DB 7; Length 109;
Best Local Similarity 87.5%; Pred. No. 7.05e-70;
Matches 91; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 4 mtqspsslsasvdrvtitcrasgsisaylnwygkpkpapklliyasaslsqgsprfs 63
QY 3 LTQSPSSLSAFVSDPVTITCPASGSISPNLNWYQKRPSTAPKVLIIYAASSLSQGVSPSPFS 52

Db 64 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 63 SSGSGSIDFIIITISLQPEFAIYYQGSYIIPRIFGQTKVEIK 106

RESULT 7
ENTRY K1HCHU #type complete
TITLE Ig kappa chain V-1 region (Hau) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
ACCESSIONS S02574; A01868
REFERENCE #authors Steiner, V.; Chang, J.Y.
#journal FEBS Lett (1987) 222:6-10
#title Chemical modification of the carboxyl groups of protein
#cross-references MUID:98005152
#accession S02574
##status preliminary
##molecule_type protein
##residues 1-109 ##label STE
REFERENCE A01868
#authors Watanabe, S.; Hilschmann, N.
#journal Hoppe-Seyler's Z. Physiol. Chem. (1970) 351:1291-1295
#title The primary structure of a monoclonal kappa-type
#cross-references MUID:71032830
#accession A01868
##molecule_type protein
##residues 1-108 ##label WAT
#note This is a Bence Jones protein.
COMMENT GENETICS
#gene GDB:IGKV1
COMPLEX
#cross-references GDB:136264
an immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds; in some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
FEATURE
SUMMARY #length 109 #molecular_weight 11772 #checksum 7448

Query Match 85.9%; Score 632; DB 2; Length 109;
Best Local Similarity 84.8%; Pred. No. 6.61e-69;
Matches 89; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Db 3 qmtqspsslsasvdrvtitcrasgsisaylnwygkpkpapklliyasaslsqgsprfs 62
QY 2 ELTQSPSSLSAFVSDPVTITCPASGSISPNLNWYQKRPSTAPKVLIIYAASSLSQGVSPSPFS 61

#accession S31598
#status Preliminary
#molecule_type mRNA
#residues 1-109 ##label POR
##cross-references EMBL:Z15081
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6177

Query Match 85.9%; Score 625; DB 7; Length 109;
Best Local Similarity 82.7%; Pred. No. 6.19e-68;
Matches 86; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 4 mtqspsslsasvdrvtitcrasgsisaylnwygkpkpapklliyasaslsqgsprfs 63
QY 3 LTQSPSSLSAFVSDPVTITCPASGSISPNLNWYQKRPSTAPKVLIIYAASSLSQGVSPSPFS 52
Dt 64 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 63 SSGSGSIDFIIITISLQPEFAIYYQGSYIIPRIFGQTKVEIK 106

RESULT 8
ENTRY S44122 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-1995
ACCESSIONS S44122
REFERENCE #authors Hawkins, P.E.; Zhu, P.; Czecka, M.; Winter, G.; Hamblin,
I.J.; Stevenson, F.K.
#submission submitted to the EMBL Data Library, March 1994
#description Idiotype vaccination against human B-cell lymphoma: rescue
of variable region gene sequences from biopsy material for
assembly as single chain fv "personal" vaccine.
#accession S44122
##status preliminary
##molecule_type DNA
##residues 1-108 ##label HAW
##cross-references EMBL:Z31390
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 108 #molecular_weight 11750 #checksum 3040

Query Match 86.4%; Score 629; DB 7; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.72e-68;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Db 3 qmtqspsslsasvdrvtitcrasgsisaylnwygkpkpapklliyasaslsqgsprfs 62
QY 2 ELTQSPSSLSAFVSDPVTITCPASGSISPNLNWYQKRPSTAPKVLIIYAASSLSQGVSPSPFS 61

Db 63 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 62 SSGSGSIDFIIITISLQPEFAIYYQGSYIIPRIFGQTKVEIK 106

RESULT 9
ENTRY S31978 #type fragment
TITLE Ig kappa chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
ACCESSIONS S31978
REFERENCE S31977
#authors Portolano, S.; Chazembault, G.D.; Hutchison, S.J.; McLachlan,
S.M.; Rapoport, B.
#submission submitted to the EMBL Data Library, June 1992
#description Lack of promiscuity in autoantigen-specific H and L chain
combinations as revealed by human H and L chain "doublets".
#accession S31978
##status preliminary
##molecule_type mRNA
##residues 1-109 ##label POR
##cross-references EMBL:Z15074
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6130

Query Match 85.9%; Score 625; DB 7; Length 109;
Best Local Similarity 82.7%; Pred. No. 6.19e-68;
Matches 86; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 4 mtqspsslsasvdrvtitcrasgsisaylnwygkpkpapklliyasaslsqgsprfs 63
QY 3 LTQSPSSLSAFVSDPVTITCPASGSISPNLNWYQKRPSTAPKVLIIYAASSLSQGVSPSPFS 62
Dt 64 gsgsgtdftltisslqpedfatyyccgysdtpwtfqggtkveik 107
QY 63 SSGSGSIDFIIITISLQPEFAIYYQGSYIIPRIFGQTKVEIK 106

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```

QY 63 GSGSGDTFTLTITSLQPEDFATYYCQSQSYTTPRTFGQGTKEVK 106

RESULT 10
ENTRY
TITLE Ig kappa chain - human
ORGANISM Homo sapiens
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS S40317
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Eur. J. Immunol. (1993) 23:3248-3271
#journal Expressed human immunoglobulin chi genes and their
#title hypermutation.
#accession S40317
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-129 #label KLE
#cross-references EMBL:X72427
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 129 #molecular-weight 13997 #checksum 8930

Query Match 85.9%; Score 625; DB 7; Length 129;
Best Local Similarity 83.8%; Pred. No. 6.19e-68; Indels 0; Gaps 0;
Matches 88; Conservative 10; Mismatches 7;

Db 24 qmtzpslsasvdrvtitcrasqstgtylnwvqqkpkapkllygasslqsgvpsrf 83
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGDRTVITCPASQSI SRNLNMYQKPGTAPKVLIIYAASSLQSGVPSRF 61

Db 84 sgsgsgtftltisslqpedfatyyccqtystptfgggtkveik 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SSGSGDTFTLTITSLQPEDFATYYCQSQSYTTPRTFGQGTKEVK 106

RESULT 11
ENTRY
TITLE Ig kappa chain V-I region (Ou) - human
ORGANISM Homo sapiens
DATE 06-Sep-1996
ACCESSIONS A01872
REFERENCE Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
#authors Science (1970) 169:56-59
#journal Macroglobulin structure: variable sequence of light and heavy
#title chains.
#cross-references MUID:70201507
#accession A01872
#molecule_type protein
#residues 1-108 #label KOH
#note the sequence of the C region, which has the Inv (3)
marker, is also given
COMMENT This chain was isolated from a Waldenstrom's macroglobulin
GENETICS
#gene GDB:IGKV1
#cross-references GDB:136264
COMPLEX
#identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily immunoglobulin V region: immunoglobulin homology
heterotetramer
FEATURE
#disulfide_bonds #status predicted
23-88 #length 108 #molecular-weight 11777 #checksum 3565

Query Match 85.4%; Score 622; DB 2; Length 108;
Best Local Similarity 68.6%; Pred. No. 1.61e-67;
Matches 72; Conservative 28; Mismatches 5; Indels 0; Gaps 0;

Db 3 qmtzpslsasvdrvtitcrasqstgtylnwvqqkpkapkllygasslqsgvpsrf 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGDRTVITCPASQSI SRNLNMYQKPGTAPKVLIIYAASSLQSGVPSRF 61

Db 63 sgsgsgtftltisslqpedfatyycczssysstptfggtzlik 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SSGSGDTFTLTITSLQPEDFATYYCQSQSYTTPRTFGQGTKEVK 106

RESULT 12
ENTRY
TITLE Ig kappa chain - human (fragment)
ORGANISM Homo sapiens
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
ACCESSIONS S31981
REFERENCE Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan,
#authors S.M.; Rapoport, B.
#submission submitted to the EMBL Data Library, June 1992
#description Lack of promiscuity in autoantigen-specific H and L chain
combinations as revealed by human H and L chain "roulette".
#accession S31981
#status preliminary
#molecule_type mRNA
#residues 1-109 #label POR
#cross-references EMBL:Z15077
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 4724

Query Match 85.2%; Score 620; DB 7; Length 109;
Best Local Similarity 83.7%; Pred. No. 3.05e-67;
Matches 87; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Db 4 mtzpslsasvdrvtitcrasqstgtylnwvqqkpkapkllygasslqsgvpsrf 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 LTQSPSSLSAFVGDRTVITCPASQSI SRNLNMYQKPGTAPKVLIIYAASSLQSGVPSRF 62

Db 64 sgsgsgtftltisslqpedfatyyccqsyystptfgggtkveik 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 GSGSGDTFTLTITSLQPEDFATYYCQSQSYTTPRTFGQGTKEVK 106

RESULT 13
ENTRY
TITLE Ig kappa chain V-I region (Dee) - human
ORGANISM Homo sapiens
DATE 06-Sep-1996
ACCESSIONS A01865
REFERENCE Milstein, C.P.; Deverson, E.V.
#authors Biochem. J. (1971) 123:945-958
#journal The amino acid sequence of a human kappa light chain.
#title #cross-references MUID:72053133
#accession A01865
#molecule_type protein
#residues 1-108 #label MIL
#note the C region of this chain as the Inv (3) marker
GENETICS
#gene GDB:IGKV1
#cross-references GDB:136264
COMPLEX
#identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily immunoglobulin V region: immunoglobulin homology
heterotetramer
FEATURE
#disulfide_bonds #status predicted
23-88

```

```

SUMMARY      *length 108 *molecular-weight 11661 *checksum 1858
Query Match      84.6% Score 617 DB 2 Length 108
Best Local Similarity 83.7% Pred. No. 7 95e-67;
Matches 87; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Db 3 zmtqpsstlsasvdrvtlcrasgsvnykylwvqkpgkpkapvllfaaslsrsvpsrf 62
Cy 2 ELIQSPSSLSAFVSGVRVITTCFASQGISPNLNWYQKPKGIAPKVLIVAASSLQSGVPSRF 61

Db 63 qsgsgtdfltltslqpedfaayfcqysvswptfgqtkveir 107
Cy 62 GSGSGTDFLTITSLQPEDFAIYCCQSYTTPRFGGKVEVK 105

RESULT 14
ENTRY      JL0139      *type fragment
TITLE      Ig kappa chain V region (AND) - human (fragment)
ALTERNATE_NAMES amyloid protein
ORGANISM   *formal_name Homo sapiens *common_name man
DATE       31-Dec-1991 *sequence_revision 31-Dec-1991 *text_change
16-Aug-1996

ACCESSIONS JL0139
REFERENCE   JL0139
  *authors   Liepinieks, J. J.; Dwyer, F. E.; Benson, M. D.
  *journal   Mol. Immunol. (1990) 27:481-485
  *title     Amino acid sequence of a kappa I primary (AL) amyloid protein
              (AND).
  *cross-references MUID:90340314
  *accession JL0139
  *molecule_type protein
  *residues 1-107
  *label LIE
  *experimental_source spleen
  *note      this protein is isolated from amyloid fibrils
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin

1-23      *region framework 1\
24-34      *region complementarity-determining 1\
35-49      *region framework 2\
50-56      *region complementarity-determining 2\
57-88      *region framework 3\
89-97      *region complementarity-determining 3\
98-107     *region framework 4\

SUMMARY      *length 107 *checksum 5932
Query Match      84.6% Score 616; DB 7; Length 107;
Best Local Similarity 80.0% Pred. No. 1.09e-56;
Matches 84; Conservative 17; Mismatches 4; Indels 0; Gaps 0;

Db 3 qmtqpsstlsasvdrvtlcrasgsvnykylwvqkpgkpkapvllfaaslsrsvpsrf 62
Cy 2 ELIQSPSSLSAFVSGVRVITTCFASQGISPNLNWYQKPKGIAPKVLIVAASSLQSGVPSRF 61

Db 63 qsgsgtdfltltslqpedfaayfcqysvswptfgqtkveir 107
Cy 62 GSGSGTDFLTITSLQPEDFAIYCCQSYTTPRFGGKVEVK 105

RESULT 15
ENTRY      S46372      *type complete
TITLE      IG light chain variable region (VJ) - human
ORGANISM   *formal_name Homo sapiens *common_name man
DATE       07-May-1995 *sequence_revision 21-Jul-1995 *text_change
16-Aug-1996

ACCESSIONS S46372
REFERENCE   S46369
  *authors   Bensimon, C.; Chastagner, P.; Zouali, M.
  *journal   EMBO J. (1994) 13:2951-2962
  *title     Human lupus anti-DNA autoantibodies undergo essentially
              primary V(chi) gene rearrangements.
  *accession S46372
  *status    preliminary

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**molecule_type mRNA
**residues 1-128 **label BEN
**cross-references EMBL 227173
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      immunoglobulin
SUMMARY      *length 128 *molecular-weight 13987 *checksum 7251

Query Match      84.5% Score 615; DB 7; Length 128;
Best Local Similarity 83.7% Pred. No. 1.51e-56;
Matches 87; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Db 24 ltqpsstlsasvdrvtlcrasgsvnykylwvqkpgkpkapvllfaaslsrsvpsrf 63
Cy 3 LTQSPSSLSAFVSGVRVITTCFASQGISPNLNWYQKPKGIAPKVLIVAASSLQSGVPSRF 62

Db 84 qsgsgtdfltltslqpedfaayfcqysvswptfgqtkveir 127
Cy 63 GSGSGTDFLTITSLQPEDFAIYCCQSYTTPRFGGKVEVK 106

Search completed: Tue Feb 24 07:28:23 1998
Job time : 30 secs.

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100

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:27:18 1998; Master time 4.94 Seconds
Tabular output not generated.
454,834 Million cell updates/sec

Title: >US-08-844-215-13
Description: (1-106) from US08844215.pep
Perfect Score: 728
Sequence: 1 AELTQSPSSLSAFVGPVTI CQSQSYTPRTFGQTKVEVK 106
Scoring table: PAM 150
Gap 11
Searched: 59021 seqs. 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 40.195; Variance 69.494; scale 0.578

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES							
Result No.	Score	Query Match	Length	DR	ID	Description	Pred. No.
1	632	86.8	108	5	KV1H_HUMAN	IG KAPPA CHAIN V-I RE	4.76e-119
2	522	85.4	108	5	KV1N_HUMAN	IG KAPPA CHAIN V-I RE	1.09e-116
3	617	84.8	108	5	KV1E_HUMAN	IG KAPPA CHAIN V-I RE	1.64e-115
4	610	83.8	108	5	KV1W_HUMAN	IG KAPPA CHAIN V-I RE	7.29e-114
5	506	83.2	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	6.37e-113
6	601	82.6	108	5	KV1G_HUMAN	IG KAPPA CHAIN V-I RE	9.56e-112
7	585	80.4	107	5	KV1D_HUMAN	IG KAPPA CHAIN V-I RE	5.49e-108
8	581	79.8	108	5	KV1F_HUMAN	IG KAPPA CHAIN V-I RE	4.77e-107
9	575	79.0	108	5	KV1S_HUMAN	IG KAPPA CHAIN V-I RE	1.22e-105
10	570	78.3	108	5	KV1X_HUMAN	IG KAPPA CHAIN V-I RE	1.81e-104
11	569	78.2	108	5	KV1T_HUMAN	IG KAPPA CHAIN V-I RE	3.10e-104
12	568	78.0	108	5	KV1B_HUMAN	IG KAPPA CHAIN V-I RE	5.32e-104
13	568	78.0	108	5	KV1V_HUMAN	IG KAPPA CHAIN V-I RE	9.12e-104
14	567	77.9	108	5	KV1U_HUMAN	IG KAPPA CHAIN V-I RE	1.35e-102
15	562	77.2	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	1.35e-102
16	562	77.2	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	1.35e-102
17	560	76.0	108	5	KV1A_HUMAN	IG KAPPA CHAIN V-I RE	3.97e-102
18	559	76.8	108	5	KV1M_HUMAN	IG KAPPA CHAIN V-I RE	6.80e-102
19	553	76.0	108	5	KV1C_HUMAN	IG KAPPA CHAIN V-I RE	1.72e-100
20	552	75.8	108	5	KV1L_HUMAN	IG KAPPA CHAIN V-I RE	2.95e-100
21	550	75.5	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	8.65e-100
22	545	75.0	108	5	KV1P_HUMAN	IG KAPPA CHAIN V-I RE	7.44e-99

23	538	73.9	108	5	KV5M_MOUSE	IG KAPPA CHAIN V-V RE	5.48e-97
24	537	73.8	129	5	KV1L_HUMAN	IG KAPPA CHAIN V-V RE	5.38e-97
25	533	73.2	117	5	KV1I_HUMAN	IG KAPPA CHAIN V-V RE	8.44e-96
26	532	73.1	108	5	KV5J_MOUSE	IG KAPPA CHAIN V-V RE	1.37e-95
27	526	72.3	117	5	KV1I_HUMAN	IG KAPPA CHAIN V-V RE	3.44e-94
28	525	72.1	108	5	KV5K_MOUSE	IG KAPPA CHAIN V-V RE	5.87e-94
29	522	71.7	108	5	KV5L_MOUSE	IG KAPPA CHAIN V-V RE	2.93e-93
30	522	71.7	108	5	KV5O_MOUSE	IG KAPPA CHAIN V-V RE	2.94e-93
31	522	71.7	109	5	KV3B_HUMAN	IG KAPPA CHAIN V-III	2.94e-93
32	521	71.6	129	5	KV3L_HUMAN	IG KAPPA CHAIN V-III	5.01e-93
33	521	71.6	129	5	KV3M_HUMAN	IG KAPPA CHAIN V-III	5.01e-93
34	520	71.4	109	5	KV3E_HUMAN	IG KAPPA CHAIN V-III	8.57e-94
35	519	71.3	108	5	KV5N_MOUSE	IG KAPPA CHAIN V-V RE	1.46e-92
36	519	71.3	109	5	KV3D_HUMAN	IG KAPPA CHAIN V-III	1.46e-92
37	509	69.9	108	5	KV4F_HUMAN	IG KAPPA CHAIN V-III	3.09e-90
38	508	69.8	109	5	KV4G_MOUSE	IG KAPPA CHAIN V-V RE	5.24e-90
39	507	69.6	108	5	KV5P_MOUSE	IG KAPPA CHAIN V-V RE	9.01e-90
40	506	69.5	108	5	KV5Q_MOUSE	IG KAPPA CHAIN V-V RE	1.54e-89
41	496	68.1	108	5	KV3A_HUMAN	IG KAPPA CHAIN V-III	3.21e-87
42	494	67.9	149	5	KV5A_MOUSE	IG KAPPA CHAIN V-III	9.33e-87
43	488	67.0	108	5	KV5S_MOUSE	IG KAPPA CHAIN V-V RE	2.29e-85
44	486	66.8	108	5	KV5U_MOUSE	IG KAPPA CHAIN V-V RE	6.64e-85
45	485	66.6	128	5	KV3K_HUMAN	IG KAPPA CHAIN V-III	1.13e-84

ALIGNMENTS

RESULT 1
ID KV1H_HUMAN STANDARD: PRT: 108 AA.
AC P01600;
DI 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-I REGION (HAU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
OC EUTHERIA, PRIMATES.
RN [1]
RP SEQUENCE: 71032830.
RX MEDLINE: 71032830.
RA WATANABE S, HILSCHMANN N; CHEM 351-1201-1205(1970).
PL HOPPE-SEYLER S Z PHYSIOL
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIP: A01868; K1HUHU.
DR BSSP: P01607; 1FVC.
KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NONTER 108 108
SQ SEQUENCE 108 AA: 11671 MW: 68426E86 CPG32:
Query Match 86.9%; Score 632; DR 5; Length 108;
Best Local Similarity 84.8%; Pred. No. 4.76e-119;
Matches 89; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
Db 3 qmtqspsslsasvgrdvrticrassissyswvqgkfkfkapqlyiaasalspsrpf: 12
QY 3 ELTQSPSSLSAFVGPVTIIGFASLSISFN.NWY..YFVSIAHVVLYAAASLSLSGVFSRF 61
Db 63 svsgsttdtllissiqgedfatycqqyitpssfqqtveik 107
QY 62 SCGSGIDFILTITSLQPEDFATYCCQSYTPRTFGQTKVEVK 106
RESULT 2
ID KV1N_HUMAN STANDARD: PRT: 108 AA.

AC P01605;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (OU).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE: 70201507.
 RA KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
 RL SCIENCE 163:56-59(1970).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
 CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 DP PIP: A01872; KIHOU.
 DR HSP: P01607; 2FCW.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 45 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DOMAIN 108 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 4809785 CRC32;
 Query Match 85.4%; Score 622; DB 5; Length 108.
 Best Local Similarity 68.6%; Pred No. 1 09e-116; Indels 0; Gaps 0;
 Matches 72; Conservative 28; Mismatches 5;
 Db 3 qmtzspsslsasvdrvtitorasqsyvnywqgkpkapxlliyaasslqsgvtsrf 62
 QY 2 ELTQSPSSLSAFVGDRTTICPASQISPNLNWYCKPKGTAPKVLIIYAASSLQSGVSPF 61
 Db 63 sgsqsgtbflltisslpczbfatyycczasyssptfgzgrlzik 107
 QY 62 SGSGSGTDFLTITSLQPEDFATYYCCQSYTTPFTFGGKTKEVK 106
 RESULT 3
 ID KVIH_HUMAN STANDARD: PRT: 108 AA.
 AC P01597;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (DEE).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE: 72051133
 RA MILSTEIN C.P., DEVERSON E.V.;
 RL BIOCHEM. J. 123:945-958(1971).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DP PIP: A01865; KIHOU.
 DR HSP: P01607; 1FVC.
 KW IMMUNOGLOBULIN V REGION
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; 1D844F3 CRC32;
 Query Match 84.8%; Score 617; DB 5; Length 108;
 Matches 72; Conservative 28; Mismatches 5; Indels 0; Gaps 0;

Best Local Similarity 83.7%; Pred No. 1 64e-115; Indels 0; Gaps 0;
 Matches 87; Conservative 10; Mismatches 7;
 Db 3 zmtzspsslsasvdrvtitorasqsyvnywqgkpkapxlliyaasslqsgvtsrf 62
 QY 2 ELTQSPSSLSAFVGDRTTICPASQISPNLNWYCKPKGTAPKVLIIYAASSLQSGVSPF 61
 Db 63 sgsqsgtbflltisslpczbfatyycczasyssptfgzgrlzik 106
 QY 62 SGSGSGTDFLTITSLQPEDFATYYCCQSYTTPFTFGGKTKEVK 105
 RESULT 4
 ID KVIH_HUMAN STANDARD: PRT: 129 AA.
 AC P04431;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE: 85014148.
 RA KLOBECK H.G., COMBETATO G., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
 DR EMBL: X09965; G296644; ALT_TERM
 DR PIR: A01883; KIHOU.
 DP HSP: P01607; 2FCW.
 KW IMMUNOGLOBULIN V REGION; SIGNAL
 FT SIGNAL 1 22
 FT CHAIN 23 129
 FT DOMAIN 23 45
 FT DOMAIN 46 56
 FT DOMAIN 57 71
 FT DOMAIN 72 78
 FT DOMAIN 79 110
 FT DOMAIN 111 119
 FT DOMAIN 120 129
 FT DISULFID 45 110
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14069 MW; 99935172 CRC32;
 Query Match 83.8%; Score 610; DB 5; Length 129;
 Best Local Similarity 84.8%; Pred No. 7 29e-114; Indels 0; Gaps 0;
 Matches 89; Conservative 8; Mismatches 8;
 Db 25 qmtzspsslsasvdrvtitorasqsyvnywqgkpkapxlliyaasslqsgvtsrf 84
 QY 2 ELTQSPSSLSAFVGDRTTICPASQISPNLNWYCKPKGTAPKVLIIYAASSLQSGVSPF 61
 Db 85 sgsqsgtbflltisslpczbfatyycczasyssptfgzgrlzik 129
 QY 62 SGSGSGTDFLTITSLQPEDFATYYCCQSYTTPFTFGGKTKEVK 106
 RESULT 5
 ID KVIH_HUMAN STANDARD: PRT: 108 AA.
 AC P01610;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (WEA).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 RN [1]
 RX MEDLINE: 83273707.
 RA GONI F., FRANGIONE B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).
 CC -1- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST

CC 3.4-PURIFIED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR: A01876; K1H06.

DR HSP: P01607; 2FCW.

KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.

FT DOMAIN 1 23 FRAMEWORK 1

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1

FT DOMAIN 35 49 FRAMEWORK 2

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2

FT DOMAIN 57 88 FRAMEWORK 3

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3

FT DOMAIN 98 107 FRAMEWORK 4

FT DISULFID 23 88 BY SIMILARITY

FT NON_TER 108 108

SQ SEQUENCE 108 AA: 11840 MW: 88AD251 CPG32:

Query Match 83.2% Score 606; DB 5; Length 108;

Best Local Similarity 82.1%; Pred. No. 6.37e-113;

Matches 87; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

Db 3 qmtqpslsasvqdrvticrasqinditwqgkpkapkeliycaatslqsgvpsrf 62

QY 2 ELIQSPSSLSAFAVGDVITCPASQISPNLNWYQQKPGTAPKVLIIYAASSLSQSGVPSRF 61

Db 63 ssgsgstftltisslqpedfatyyclq-yssfptfsggtkvek 107

QY 62 SGSGSGTFTLTITSLQPEDFAIYYCQSYIT-PTFSGGKVEVK 106

RESULT 5

ID KVIF_HUMAN STANDARD: PRT: 108 AA:

AC P01599:

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-I REGION (GAL)

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:

OC EUTHERIA: PRIMATES:

RN [1]

RP SEQUENCE:

RX MEDLINE: 75059122.

RA LAURE C J, WATANABE S, HILSCHMANN N

RL HOPPE-SEYLER S Z, PHYSIOL CHEM 354:1503-1504 (1973)

CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.

DR PIR: A01847; K1H06L

DR HSP: P01607; 1DFB

KW IMMUNOGLOBULIN V REGION:

FT DOMAIN 1 23 FRAMEWORK 1

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1

FT DOMAIN 35 49 FRAMEWORK 2

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2

FT DOMAIN 57 88 FRAMEWORK 3

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3

FT DOMAIN 98 107 FRAMEWORK 4

FT DISULFID 23 88 BY SIMILARITY

FT NON_TER 108 108

SQ SEQUENCE 108 AA: CCAEAA2 CPG32:

Query Match 82.6% Score 601; DB 5; Length 108;

Best Local Similarity 79.0%; Pred. No. 9.56e-112;

Matches 83; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 3 qmtqpslsasvqdrvticrasqinditwqgkpkapkeliycaatslqsgvpsrf 62

QY 2 ELIQSPSSLSAFAVGDVITCPASQISPNLNWYQQKPGTAPKVLIIYAASSLSQSGVPSRF 61

Db 63 ssgsgstftltisslqpedfatyyclqsgvpsrfsggtkvek 107

QY 62 SGSGSGTFTLTITSLQPEDFAIYYCQSYIT-PTFSGGKVEVK 106

RESULT 7

ID KVIF_HUMAN STANDARD: PRT: 107 AA:

AC P01596:

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-I REGION (CAP)

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:

OC EUTHERIA: PRIMATES

RN [1]

RP SEQUENCE:

RX MEDLINE: 75075135.

RA MILSTEIN C P, DEVERSON E V

PL EUR J BIOCHEM 49:377-391 (1974)

CC -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR: A01864; K1H0AP

DR HSP: P01607; 1DFB

KW IMMUNOGLOBULIN V REGION: GLYCOPROTEIN.

FT CARBOHYD 28 107

FT NON_TER 107 107

SQ SEQUENCE 107 AA: 11703 MW: 94BF9FD CPG32:

Query Match 80.4% Score 585; DB 5; Length 107;

Best Local Similarity 77.1%; Pred. No. 5.49e-108;

Matches 81; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

Db 3 qmtqpslsasvqdrvticrasqinditwqgkpkapkeliykssslqsgvpsrf 62

QY 2 ELIQSPSSLSAFAVGDVITCPASQISPNLNWYQQKPGTAPKVLIIYAASSLSQSGVPSRF 61

Db 63 ssgsgstftltisslqpedfatyyclq-yssfptfsggtkvek 106

QY 62 SGSGSGTFTLTITSLQPEDFAIYYCQSYIT-PTFSGGKVEVK 106

RESULT 8

ID KVIF_HUMAN STANDARD: PRT: 108 AA:

AC P01598:

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-I REGION (EU)

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:

OC EUTHERIA: PRIMATES

RN [1]

RP SEQUENCE:

RX MEDLINE: 71064023.

RA GOTTLIEB P D, CUNNINGHAM P A, PUTISHAUSER H, EDELMAN G M

RL BIOCHEMISTRY 9:3155-3161 (1970).

RN [2]

RP DISULFIDE BOND

RX MEDLINE: 71064027.

RA GALL W E, EDELMAN G M

RL BIOCHEMISTRY 9:3188-3196 (1970).

CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR: A01866; K1H0EU

DR HSP: P01607; 1DFB

KW IMMUNOGLOBULIN V REGION:

FT DOMAIN 1 23 FRAMEWORK 1

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1

FT DOMAIN 35 49 FRAMEWORK 2

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2

FT DOMAIN 57 88 FRAMEWORK 3

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3

FT DOMAIN 98 107 FRAMEWORK 4

FT DISULFID 23 88

FT NON_TER 108 108

SQ SEQUENCE 108 AA: 9AF455E5 CPG32:

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Query Match      79.8%; Score 581; DB 5; Length 108;
Best Local Similarity 77.1%; Pred. No. 4.77e-107;
Matches      81; Conservative      13; Mismatches 11; Indels      0; Gaps      0;

Db      3 qmtqspstlsasvgrdvltitcrasgsintwlawyqkqkpkapklilykasslengvpsrf 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      2 ELTQSPSSLSAFVGRVITTCPASQISPNLNWYQKPKGTAPKVLIIYAASSLSQGVPSRF 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db      63 isgsgstetfltlisslqddfatyvcqgynsdskmfaggtkvdk 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGSGSGTDFLTITSLQPEDFAIYVQCSYTTPTPTFGQTKVEVK 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT      9
ID      KV1S.HUMAN      STANDARD;      PRT;      108 AA.
AC      P01611;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE      IG KAPPA CHAIN V-I REGION (WES).
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PRIMATES.
RN      [1]
RP      SEQUENCE.
FX      MEDLINE; 81092279
RL      KRATZIN H., YANG C., KRUSCHE J.U., HILSCHMANN N.;
      HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 361:1591-1598(1980).
CC      -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC      -1- THIS IS A BENCE-JONES PROTEIN
DR      PIR: A01869; KIHUKA.
DR      HSSP: P01607; 1DFB.
KW      IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT      DOMAIN      1      23      FRAMEWORK 1.
FT      DOMAIN      24      34      COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN      35      49      FRAMEWORK 2.
FT      DOMAIN      50      56      COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN      57      88      FRAMEWORK 3.
FT      DOMAIN      89      97      COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN      98      107      FRAMEWORK 4.
FT      DISULFID      23      88      BY SIMILARITY.
FT      NON_TER      108
SQ      SEQUENCE      108 AA; 11608 MW; C68080FD CPG32;

Query Match      79.0%; Score 575; DB 5; Length 108;
Best Local Similarity 75.2%; Pred. No. 1.22e-105;
Matches      79; Conservative      16; Mismatches 10; Indels      0; Gaps      0;

Db      3 qmtqspssasvgrdvltitcrasqdishlawyqkqkpkapklilykasslengvpsrf 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      2 ELTQSPSSLSAFVGRVITTCPASQISPNLNWYQKPKGTAPKVLIIYAASSLSQGVPSRF 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db      63 ssgsgstetfltlisslqddfatyvcqgahsvptlfgggttdvik 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGSGSGTDFLTITSLQPEDFAIYVQCSYTTPTPTFGQTKVEVK 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT      10
ID      KV1K.HUMAN      STANDARD;      PRT;      108 AA.
AC      P01603;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE      IG KAPPA CHAIN V-I REGION (KA)
OS      HOMO SAPIENS (HUMAN)
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PRIMATES.
RN      [1]
RP      SEQUENCE.
FX      MEDLINE; 76199985
RL      SWINODA T.;
      J. BIOCHEM. 77:1277-1296(1975)
CC      -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER

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-1- THIS IS A BENCE-JONES PROTEIN.
CC      PIR: A01869; KIHUKA.
DR      HSSP: P01607; 1LGM.
KW      IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT      DOMAIN      1      23      FRAMEWORK 1.
FT      DOMAIN      24      34      COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN      35      49      FRAMEWORK 2.
FT      DOMAIN      50      56      COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN      57      88      FRAMEWORK 3.
FT      DOMAIN      89      97      COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN      98      107      FRAMEWORK 4.
FT      DISULFID      23      88      BY SIMILARITY.
FT      NON_TER      108
SQ      SEQUENCE      108 AA; 11900 MW; 41BC730E CPG32;

Query Match      78.3%; Score 570; DB 5; Length 108;
Best Local Similarity 71.4%; Pred. No. 1.81e-104;
Matches      75; Conservative      18; Mismatches 12; Indels      0; Gaps      0;

Db      3 qmtqspstlsasvgrdvltitcrasqstvlslwlyqkqkpkapklilykasslengvpsrf 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      2 ELTQSPSSLSAFVGRVITTCPASQISPNLNWYQKPKGTAPKVLIIYAASSLSQGVPSRF 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db      63 ssgsgstetfltlissvzpbzbfatyvcqzyldlprtfgggtkvdk 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGSGSGTDFLTITSLQPEDFAIYVQCSYTTPTPTFGQTKVEVK 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT      11
ID      KV1T.HUMAN      STANDARD;      PRT;      109 AA.
AC      P01612;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE      IG KAPPA CHAIN V-I REGION (MEV).
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PRIMATES.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE; 83081018.
RX      EULITZ M., LINKE R.P.;
      HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 363:1347-1359(1982).
CC      -1- ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.
CC      -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR      PIR: A01879; KIHUKV
DR      HSSP: P01607; 2FGW
KW      IMMUNOGLOBULIN V REGION.
FT      DOMAIN      1      23      FRAMEWORK 1.
FT      DOMAIN      24      34      COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN      35      49      FRAMEWORK 2.
FT      DOMAIN      50      56      COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN      57      88      FRAMEWORK 3.
FT      DOMAIN      89      98      COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN      99      108      FRAMEWORK 4.
FT      DISULFID      23      88      BY SIMILARITY.
FT      NON_TER      109
SQ      SEQUENCE      109 AA; D724EC01 CPG32;

Query Match      78.2%; Score 569; DB 5; Length 109;
Best Local Similarity 76.4%; Pred. No. 3.10e-104;
Matches      81; Conservative      11; Mismatches 13; Indels      1; Gaps      1;

Db      3 qmtqspsslsasvgrdvltitcrasqssvdlwlyqkqkpkapklilykasslengvpsrf 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      2 ELTQSPSSLSAFVGRVITTCPASQISPNLNWYQKPKGTAPKVLIIYAASSLSQGVPSRF 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db      63 ssgsgstetfltlisslqddfatyvcqgysynpntvfgggttdvik 108
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGSGSGTDFLTITSLQPEDFAIYVQCSYTTPTPTFGQTKVEVK 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT      12

```



```

ID KV18_HUMAN STANDARD: PRI: 108 AA.
AC P01594:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (AU)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUETHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 72189444.
RA SCHIEHL H., HILSCHMANN N.,
RL HOPPE-SEYLER S Z. PHYSIOL. CHEM 353:345-370(1972)
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE: 77022433.
RA FEHLMAYER H., SCHIFFER M., EPP O., COLMAN P M., LATTMAN E E.,
RA SCHWAGER P., STEIGEMANN W., SCHRAMM H J.,
RL BIOPHYS. STRUCT. MECH. 1:139-146(1975)
CC -!- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR
CC REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF
CC THE KAPPA CHAIN PEI
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01862; K1H0U.
DR HSSP: P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3
FT DOMAIN 89 97 FRAMEWORK 4
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11939 MW: 8455AF00 CRC32:

Query Match 78.0%; Score 568; DB 5; Length 108;
Best Local Similarity 77.4%; Pred. No. 5,32e-104;
Matches 82; Conservative 13; Mismatches 9; Indels 2; Gaps 2.

Db 3 qmtqpsalsasvdrvtitcrasqdisdylnwvqqkpkapklitydasnlesgvsrf 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGVDPVITTPASQISPNLNWYQKPGTAPKVLIIYAASSLSGVSPF 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 sgsgsgahtftisslqpedatyyccqdydl-pwtfgqgkveik 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGIDFTLTITSLQPEDFAIYQQQ-SYIPIPIFGQGTKEVK 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ID KV18_HUMAN STANDARD: PRI: 129 AA.
AC P04432:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN SPECIESOR V-I REGION (DAUDI)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUETHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85014148.
RA KLOECK H G. COMBRIATO G., ZACHAU H G.,
RL NUCLEIC ACIDS RES. 12:5995-7006(1984).
DR EMBL: X02134; G185822;
DR EMBL: X00965; G296685; A17_TERM.
DR PIR: A01884; K1H0U.
DR HSSP: P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 22

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FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (DAUDI).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 115 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14235 MW: 05B40B5E CRC32:

Query Match 78.0%; Score 568; DB 5; Length 129;
Best Local Similarity 74.3%; Pred. No. 5,32e-104;
Matches 78; Conservative 15; Mismatches 12; Indels 0; Gaps 0.

Db 25 qmtqpsalsasvdrvtitcrasqdisdylnwvqqkpkapklitydasnlesgvsrf 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGVDPVITTPASQISPNLNWYQKPGTAPKVLIIYAASSLSGVSPF 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 sgsgsgahtftisslqpedatyyccqdylnwvqqkpkapklitydasnlesgvsrf 129
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGIDFTLTITSLQPEDFAIYQQQ-SYIPIPIFGQGTKEVK 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ID KV18_HUMAN STANDARD: PRI: 108 AA.
AC P04430:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (PAN)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUETHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 86174817.
RA DWULET F E., O'CONNOR T P., BENSON M D.,
RL MOL. IMMUNOL. 23:73-78(1986).
DR PIR: A01878; K1H0U.
DR HSSP: P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION: AMYLOID.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 0D44DA0A CRC32:

Query Match 77.9%; Score 567; DB 5; Length 108;
Best Local Similarity 77.1%; Pred. No. 9,12e-104;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0.

Db 3 qmtqpsalsasvdrvtitcrasqdisdylnwvqqkpkapklitydasnlesgvsrf 82
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 ELTQSPSSLSAFVGVDPVITTPASQISPNLNWYQKPGTAPKVLIIYAASSLSGVSPF 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 sgsgsgahtftisslqpedatyyccqdylnwvqqkpkapklitydasnlesgvsrf 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGIDFTLTITSLQPEDFAIYQQQ-SYIPIPIFGQGTKEVK 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ID KV18_HUMAN STANDARD: PRI: 108 AA.
AC P03362:
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-I REGION (WAT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTERATA: TETRAPODA; MAMMALIA;
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE: 95086080.
RA HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,
RA SOLOMON A., STEVENS F.J., SCHIFFER M.;
RL BIOCHEMISTRY 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE: 81267384.
RA STEVENS F.J., WESTHOIM F.A., PANAGIOTOPoulos N., SCHIFFER M.,
RA POPP P.A., SOLOMON A.;
RL J. MOL. BIOL. 147:185-193(1981).
CC -!- THIS IS A RENCE-JONES PROTEIN.
DR PDB: 1WTL: 01-NOV-94.
KW IMMUNOGLOBULIN V REGION: RENCE-JONES PROTEIN; 3D-STRUCTURE.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN PEF 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11737 MW: 41A2388C CRC32;

Query Match 77.2%; Score 562; DB 5; Length 108;
Best Local Similarity 76.4%; Pred. No. 1.35e-102;
Matches 81; Conservative 14; Mismatches 9; Indels 2; Gaps 2;

Db 3 qmtqspsslsasvgrdvtitcrasgditnyvnmfgrpggqpkvliygasiletgypsr 62
QY 2 ELTQSPSSLSAFVGRVITTCRASQISISRNLNWYQQRPSTAPKVLIIYAASSLSQSGVPSRF 61

Db 63 sgsqsgtdfttisslqpdiatyyccq-ydtlpltfgggktvdik 107
QY 62 SSGSGGTDFTLTITSLOPDEDFATYYCQOQSYTT-PRTFQGGTKVEVK 106

Search completed: Tue Feb 24 07:27:34 1998
Job time : 16 secs.

```

W O E R E L I
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.
MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:55:23 1998; MasPar time 4.27 Seconds
Tabular output not generated. 126.565 Million cell updates/sec

Title: >US-08-844-215-13
Description: (1-106) from US08844215.pep
Perfect Score: 728
Sequence: 1 AELTQSPSSLSAFVGPVTI... CQSYTTPFGGKVEVK 106
Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:pcr90 9:pcr91
10:pcr92 11:pcr93 12:pcr94 13:pcr95 14:pcr96
Statistics: Mean 27.078; Variance 147.594; scale 0.183
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	659	90.5	107	13	PCT-US95-0 Sequence 105, Applicat	1.45e-41	
2	659	90.5	107	7	US-08-276- Sequence 105, Applicat	1.45e-41	
3	651	89.4	107	7	US-08-276- Sequence 104, Applicat	5.98e-41	
4	651	89.4	107	13	PCT-US95-0 Sequence 104, Applicat	5.98e-41	
5	635	87.2	108	13	PCT-US95-0 Sequence 109, Applicat	1.02e-39	
6	635	87.2	108	7	US-08-276- Sequence 103, Applicat	2.96e-39	
7	629	86.4	108	7	US-08-276- Sequence 102, Applicat	2.96e-39	
8	629	86.4	108	13	PCT-US95-0 Sequence 106, Applicat	4.21e-39	
9	627	86.1	104	7	US-08-276- Sequence 106, Applicat	4.21e-39	
10	627	86.1	104	7	US-08-276- Sequence 66, Applicat	6.01e-39	
11	625	85.9	107	13	PCT-US95-1 Sequence 66, Applicat	6.01e-39	
12	625	85.9	111	7	US-08-276- Sequence 150, Applicat	6.01e-39	
13	625	85.9	111	13	PCT-US95-0 Sequence 150, Applicat	6.01e-39	
14	625	85.9	111	13	PCT-US95-0 Sequence 18, Applicat	1.46e-38	
15	620	85.2	107	13	PCT-US95-1 Sequence 68, Applicat	1.46e-38	
16	620	85.2	104	7	US-08-300- Sequence 68, Applicat	1.46e-38	
17	620	85.2	104	13	PCT-US95-1 Sequence 68, Applicat	1.46e-38	
18	613	84.2	107	13	PCT-US95-0 Sequence 84, Applicat	5.03e-38	
19	613	84.2	107	7	US-08-276- Sequence 84, Applicat	5.03e-38	
20	611	83.9	107	13	PCT-US95-0 Sequence 103, Applicat	7.17e-38	
21	611	83.9	107	7	US-08-276- Sequence 103, Applicat	7.17e-38	
22	607	83.4	107	7	US-08-276- Sequence 82, Applicat	1.45e-37	

23	607	83.4	107	13	PCT-US95-0 Sequence 82, Applicati	1.45e-37
24	607	83.4	109	11	PCT-US93-0 Sequence 1, Applicatio	1.45e-37
25	607	83.4	214	11	PCT-US93-0 Sequence 40, Applicati	1.45e-37
26	607	83.4	233	11	PCT-US93-0 Sequence 25, Applicati	1.45e-37
27	606	83.2	214	11	PCT-US93-0 Sequence 39, Applicati	1.74e-37
28	605	83.1	109	11	PCT-US93-0 Sequence 3, Applicatio	2.07e-37
29	604	83.0	107	11	PCT-US95-1 Sequence 17, Applicati	2.47e-37
30	601	82.6	107	13	PCT-US95-1 Sequence 67, Applicati	4.21e-37
31	601	82.6	107	7	US-08-300- Sequence 67, Applicati	4.21e-37
32	601	82.6	110	7	US-08-300- Sequence 70, Applicati	4.21e-37
33	601	82.6	110	13	PCT-US95-1 Sequence 70, Applicati	4.21e-37
34	598	82.1	237	9	PCT-US91-0 Sequence 26, Applicati	7.15e-37
35	589	80.9	108	7	US-08-478- Sequence 84, Applicati	3.51e-36
36	588	80.8	106	7	US-08-276- Sequence 83, Applicati	4.19e-36
37	588	80.8	106	13	PCT-US95-0 Sequence 83, Applicati	4.19e-36
38	581	79.8	107	7	US-08-477- Sequence 2, Applicatio	1.44e-35
39	581	79.8	107	7	US-07-942- Sequence 12, Applicati	1.44e-35
40	581	79.8	107	6	US-08-477- Sequence 17, Applicati	1.44e-35
41	581	79.8	107	6	US-07-634- Sequence 102, Applicat	1.44e-35
42	581	79.8	107	6	US-07-634- Sequence 17, Applicati	1.44e-35
43	581	79.8	107	6	US-07-634- Sequence 2, Applicatio	1.44e-35
44	581	79.8	107	6	US-07-634- Sequence 70, Applicati	1.44e-35
45	581	79.8	107	6	US-08-477- Sequence 70, Applicati	1.44e-35

ALIGNMENTS

RESULT 1
ID PCT-US95-08743-105 STANDARD: PRT: 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 105, Application PC/TUS9508743.
XX
Sequence 105, Application PC/TUS9508743
CC
GENERAL INFORMATION:
CC
APPLICANT:
CC
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC
NUMBER OF SEQUENCES: 170
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: Floppy disk
CC
COMPUTER: IBM PC compatible
CC
OPERATING SYSTEM: PC-DOS/MS-DOS
CC
SOFTWARE: PatentIn Release #1.0 Version #1 25 (FPO)
CC
CURRENT APPLICATION DATA
CC
APPLICATION NUMBER: PCT/US95/08743
CC
FILING DATE: 11-JUL-1995
CC
PRIOR APPLICATION DATA:
CC
PRIOR APPLICATION NUMBER: US 08/276,852
CC
FILING DATE: 18-JUL-1994
CC
INFORMATION FOR SEQ ID NO: 105:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 107 amino acids
CC
TYPE: amino acid
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: protein
CC
SEQUENCE 107 AA: 11573 MW: 66905 CN:
SQ
Query Match 90.5%; Score 659; DB 13; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.45e-41;
Matches 95, Conservative 6, Mismatches 4, Indels 0, Gaps 0;
Db 1 EUTQSPSSLSAFVGPVTIIPASUSISSYLNWYQKPKAPKLLIYAASLSQGVPSRF 60
QY 2 EUTQSPSSLSAFVGPVTIIPASUSISSYLNWYQKPKAPKLLIYAASLSQGVPSRF 61
Db 61 SSGSGTDTLLTISLQPDFAFYCCQSYSTPQTFGGGKVEVK 105
QY 62 SSGSGTDTLLTISLQPDFAFYCCQSYSTPQTFGGGKVEVK 106

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XX      xxxxxx
XX      01-JAN-1900
XX
XX      Sequence 104, Application US/08276852.
XX
XX      Sequence 104, Application US/08276852
XX      Patent No. 5652138
XX      GENERAL INFORMATION:
XX      APPLICANT: Burton, Dennis P
XX      APPLICANT: Barbas, Carlos F
XX      APPLICANT: Lerher, Richard A
XX      TITLE OF INVENTION: HUMAN IMMUTALIZING MONOCLONAL ANTIBODIES
XX      TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX      NUMBER OF SEQUENCES: 170
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: The Scripps Research Institute, Office of
XX      ADDRESSEE: Patent Counsel
XX      STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
XX      STREET: Mail Drop TPC8
XX      CITY: La Jolla
XX      STATE: CA
XX      COUNTRY: USA
XX      ZIP: 92037
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
XX      COMPUTER: IBM PC compatible
XX      OPERATING SYSTEM: PC-DOS/MS-DOS
XX      SOFTWARE: Patent In Release #1 0, Version #1 25
XX      CURRENT APPLICATION DATA:
XX      APPLICATION NUMBER: US/08/276,852
XX      FILING DATE: 18-JUL-1994
XX      CLASSIFICATION: 514
XX      PRIOR APPLICATION DATA:
XX      APPLICATION NUMBER: US 08/178,302
XX      FILING DATE: 30-SEP-1993
XX      PRIOR APPLICATION DATA:
XX      APPLICATION NUMBER: US 07/954,148
XX      FILING DATE: 30-SEP-1992
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Fitting, Thomas
XX      REGISTRATION NUMBER: 34,163
XX      REFERENCE/DOCKET NUMBER: SCR1452P
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 619-554-2937
XX      TELEFAX: 619-554-6312
XX      INFORMATION FOR SEQ ID NO: 104:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 107 amino acids
XX      TYPE: amino acid
XX      TOPOLOGY: linear
XX      MOLECULE TYPE: protein
XX      SEQUENCE 107 AA; 11608 MW; 68127 CN;
XX
XX      Query Match 89.4%; Score 651; DR 7; Length 107;
XX      Best Local Similarity 90.5%; Pred. No. 5,98e-41;
XX      Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps
XX
Db      1 ELTQSPSSISASVGKPVITITPASQSSISYLNWYQKPGKAPKLLIYAASSLQSGVPSF 60
QY      2 ELTQSPSSISASVGKPVITITPASQSSISYLNWYQKPGTAPKVLIIYAASSLQSGVPSF 61
Db      61 SGSGSGTDTLTLSLQPPEDPATYVQOOSYSTPTVFGQTKETK 105
QY      62 SGSGSGTDTLTLTLSLQPPEDPATYVQOOSYSTPTVFGQTKVEVY 106
XX
XX      RESULT 4
XX      ID PCT-US95-08743-104 STANDARD: PPT: 107 AA.
XX      xxxxxx
XX

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Query Match 87.2%; Score 635; DB 7; Length 108;
 Best Local Similarity 84.9%; Pred. No. 1.02e-39;
 Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDPTITTCRASQTSINVLNWYQKPKAPKLLIYGASNLQSGVPSRF 60
 QY 2 ELTQSPSSLSAFVGDPTITTCRASQTSINVLNWYQKPKAPKLLIYAASSIQSGVPSRF 61

Db 61 SGSGSGDTFTLTISSLOPEDFATYCCQSYNTPTWTFGGQTKVEIK 106
 QY 62 SGSGSGDTFTLTISSLOPEDFATYCCQSYTTP-RTFGGQTKVEIK 106

RESULT 7
 ID US-08-276-852-102 STANDARD: PRT: 108 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 102, Application US/08276852.
 XX CC Sequence 102, Application US/08276852.
 XX CC Patent No. 5652138
 XX CC GENERAL INFORMATION:
 XX CC APPLICANT: Burton, Dennis R
 XX CC APPLICANT: Barbas, Carlos F
 XX CC APPLICANT: Lerner, Richard A
 XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 XX CC NUMBER OF SEQUENCES: 170
 XX CC CORRESPONDENCE ADDRESS:
 XX CC ADDRESSEE: the Scripps Research Institute, Office of
 XX CC ADDRESSEE: Patent Counsel
 XX CC STREET: 10655 NO. 5652138th Torrey Pines Road, Suite 220.
 XX CC CITY: Mail Drop TPC8
 XX CC STATE: La Jolla
 XX CC COUNTRY: CA
 XX CC ZIP: 92037
 XX CC COMPUTER READABLE FORM:
 XX CC MEDIUM TYPE: Floppy disk
 XX CC COMPUTER: IBM PC compatible
 XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
 XX CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 XX CC CURRENT APPLICATION NUMBER: US/08/276,852
 XX CC FILING DATE: 18-JUL-1994
 XX CC CLASSIFICATION: 514
 XX CC PRIOR APPLICATION DATA:
 XX CC APPLICATION NUMBER: US 08/178,302
 XX CC FILING DATE: 30-SEP-1993
 XX CC PRIOR APPLICATION DATA:
 XX CC APPLICATION NUMBER: US 07/954,148
 XX CC FILING DATE: 30-SEP-1992
 XX CC ATTORNEY/AGENT INFORMATION:
 XX CC NAME: Fitting, Thomas
 XX CC REGISTRATION NUMBER: 34,163
 XX CC REFERENCE/DOCKET NUMBER: SCPI452P
 XX CC TELECOMMUNICATION INFORMATION:
 XX CC TELEPHONE: 619-554-2937
 XX CC TELEFAX: 619-554-6312
 XX CC INFORMATION FOR SEQ ID NO: 102:
 XX CC SEQUENCE CHARACTERISTICS:
 XX CC LENGTH: 108 amino acids
 XX CC TYPE: amino acid
 XX CC TOPOLOGY: linear
 XX CC MOLECULE TYPE: protein
 XX CC SEQUENCE 108 AA; 11664 MW; 68213 CN;

Query Match 86.4%; Score 629; DB 7; Length 108;
 Best Local Similarity 86.8%; Pred. No. 2.96e-39;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDPTITTCRASQTSINVLNWYQKPKAPKLLIYAASSIQSGVPSRF 60
 QY 2 ELTQSPSSLSAFVGDPTITTCRASQTSINVLNWYQKPKAPKLLIYAASSIQSGVPSRF 61

Db 61 SGSGSGDTFTLTISSLOPEDFATYCCQSYNTPTWTFGGQTKVEIK 106
 QY 62 SGSGSGDTFTLTISSLOPEDFATYCCQSYTTP-RTFGGQTKVEIK 106

RESULT 8
 ID PCT-US95-08743-102 STANDARD: PRT: 108 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 102, Application PC/TUS9508743.
 XX CC Sequence 102, Application PC/TUS9508743
 XX CC GENERAL INFORMATION:
 XX CC APPLICANT:
 XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 XX CC NUMBER OF SEQUENCES: 170
 XX CC COMPUTER READABLE FORM:
 XX CC MEDIUM TYPE: Floppy disk
 XX CC COMPUTER: IBM PC compatible
 XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
 XX CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 XX CC CURRENT APPLICATION DATA:
 XX CC APPLICATION NUMBER: PCT/US95/08743
 XX CC FILING DATE: 11-JUL-1995
 XX CC PRIOR APPLICATION DATA:
 XX CC APPLICATION NUMBER: US 08/276,852
 XX CC FILING DATE: 18-JUL-1994
 XX CC INFORMATION FOR SEQ ID NO: 102:
 XX CC SEQUENCE CHARACTERISTICS:
 XX CC LENGTH: 108 amino acids
 XX CC TYPE: amino acid
 XX CC TOPOLOGY: linear
 XX CC MOLECULE TYPE: protein
 XX CC SEQUENCE 108 AA; 11664 MW; 68213 CN;

Query Match 86.4%; Score 629; DB 13; Length 108;
 Best Local Similarity 86.8%; Pred. No. 2.96e-39;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 ELTQSPSSLSASVGDPTITTCRASQTSINVLNWYQKPKAPKLLIYAASSIQSGVPSRF 60
 QY 2 ELTQSPSSLSAFVGDPTITTCRASQTSINVLNWYQKPKAPKLLIYAASSIQSGVPSRF 61

Db 61 SGSGSGDTFTLTISSLOPEDFATYCCQSYNTPTWTFGGQTKVEIK 106
 QY 62 SGSGSGDTFTLTISSLOPEDFATYCCQSYTTP-RTFGGQTKVEIK 106

RESULT 9
 ID PCT-US95-08743-106 STANDARD: PRT: 104 AA
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 106, Application PC/TUS9508743.
 XX CC Sequence 106, Application PC/TUS9508743
 XX CC GENERAL INFORMATION:
 XX CC APPLICANT:
 XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 XX CC NUMBER OF SEQUENCES: 170
 XX CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 106:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 104 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 104 AA: 11248 MW: 63942 CN:
SQ
Query Match 86.1%; Score 627; DB 13; Length 104;
Best Local Similarity 88.2%; Pred No 4.21e-39;
Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db 1 QSPSSLSASVGRVTITCRASQTSISYLNWYQKPKAPKLLIYAASSLSQGVSPFSGG 60
QY 5 QSPSSLSAFVGRVTITCRASQTSISYLNWYQKPKAPKLLIYAASSLSQGVSPFSGS 64
Db 61 GSGDTFTLIISLQPEDFATYVCOOSYSTPTFTGQGTKEIK 102
QY 65 GSGDTFTLIISLQPEDFATYVCOOSYSTPTFTGQGTKEIK 106
RESULT 10
ID US-08-276-852-106 STANDARD: PRT: 104 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 106, Application US/08276852.
CC Sequence 106, Application US/08276852
CC Patent No. 3652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC STREET: 10666 No. 565798th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SC1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 106:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 104 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 104 AA: 11248 MW: 63942 CN:
SQ
Query Match 86.1%; Score 627; DB 7; Length 104;
Best Local Similarity 89.2%; Pred No 4.21e-39;
Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db 1 QSPSSLSASVGRVTITCRASQTSISYLNWYQKPKAPKLLIYAASSLSQGVSPFSGG 60
QY 5 QSPSSLSAFVGRVTITCRASQTSISYLNWYQKPKAPKLLIYAASSLSQGVSPFSGS 64
Db 61 GSGDTFTLIISLQPEDFATYVCOOSYSTPTFTGQGTKEIK 102
QY 65 GSGDTFTLIISLQPEDFATYVCOOSYSTPTFTGQGTKEIK 106
RESULT 11
ID US-08-300-386A-66 STANDARD: PRT: 107 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 66, Application US/08300386A.
CC Sequence 66, Application US/08300386A
CC Patent No. 5667988
CC GENERAL INFORMATION:
CC APPLICANT: Barbas, Carlos F, III
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGH
T CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10666 No. 565798th Torrey Pines Road, IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/300,386A
CC FILING DATE: 02-SEP-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/836,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:

```
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 66:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11611 MW: 68881 CN;

Query Match 85.9%; Score 625; DB 7; Length 107;
Best Local Similarity 85.7%; Pred. No. 6,01e-39;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Db 1 EMTQSPSSLSASVGRVITTCRASQISISYINWYQKPKAPKLLIYAASTLQSGVPSRF 60
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 2 ELTQSPSSLSAFVGDVITTCRASQISIRNLNMYQKPKGTAPKVLIIYAASSLQSGVPSRF 61
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 SGSGSGTDFLTITSLQPEDFATYYCQOSYSTPTFTFCPTKVDIK 105
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 SGSGSGTDFLTITSLQPEDFATYYCQOSYSTPTFTFGGKTVEVK 106
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ID PCT-US95-11235-66 STANDARD; PRT: 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 66, Application PC/TUS9511235.
XX
CC Sequence 66, Application PC/TUS9511235
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLORULIN LIGH
T CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10666 North Torrey Pines Road, TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11235
CC FILING DATE: 01-SEP-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/300,386
CC FILING DATE: 02-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/826,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148

CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 66:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11611 MW: 68881 CN;

Query Match 85.9%; Score 625; DB 13; Length 107;
Best Local Similarity 85.7%; Pred. No. 6,01e-39;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

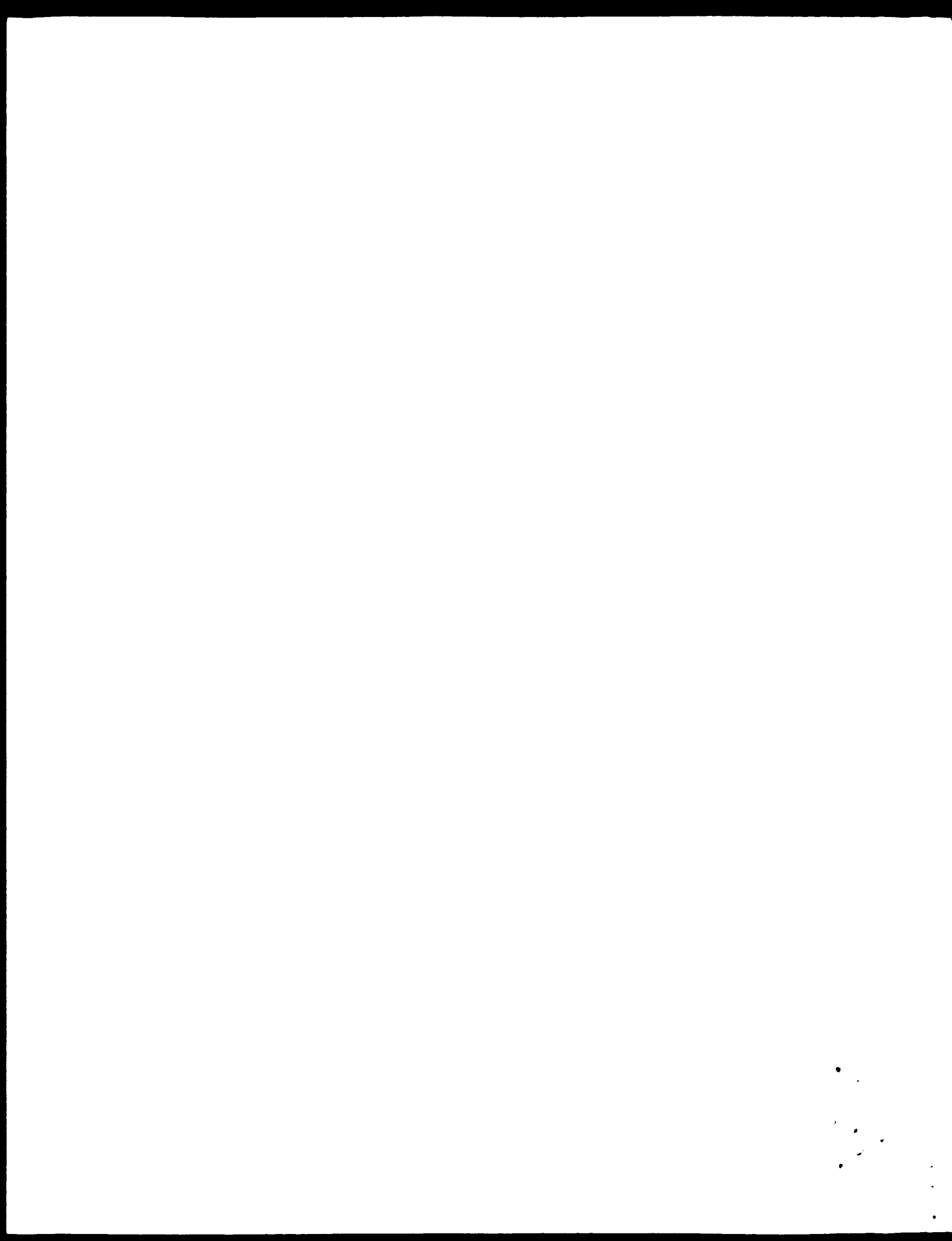
Db 1 EMTQSPSSLSASVGRVITTCRASQISISYINWYQKPKAPKLLIYAASTLQSGVPSRF 60
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 2 ELTQSPSSLSAFVGDVITTCRASQISIRNLNMYQKPKGTAPKVLIIYAASSLQSGVPSRF 61
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 SGSGSGTDFLTITSLQPEDFATYYCQOSYSTPTFTFCPTKVDIK 105
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 SGSGSGTDFLTITSLQPEDFATYYCQOSYSTPTFTFGGKTVEVK 106
   I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ID US-08-276-852-150 STANDARD; PRT: 111 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 150, Application US/08276852.
XX
CC Sequence 150, Application: US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
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CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34, 163
 CC REFERENCE/DOCKET NUMBER: SCPI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 150:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 111 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 111 AA: 12087 MW: 69654 CN:
 Query Match 85.9%; Score 625; DB 7; Length 111;
 Best Local Similarity 93.0%; Pred. No. 6,01e-39;
 Matches 88; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Db 2 AELTQSPSSLSASVGDVPTITCPGSGIGRFFNWNWYQKPGKAPNLLIYAADILQSGVSP 61
 QY 1 AELTQSPSSLSAFVGDVPTITCRASQISRNLMWYQKPGTAPKVLIIYAASLSQGVSP 60
 Db 62 FSGSGSGTDTLLTISLQPEDFATYYCQGSYSTPTFGGTPLDIK 107
 QY 61 FSGSGSGTDTLLTISLQPEDFATYYCQGSYSTPTFGGTPKVEK 106
 RESULT 14
 ID PCT-US95-08743-150 STANDARD: PRT: 111 AA.
 XX xxxxxx
 DT 01-JAN-1990
 DE Sequence 150, Application PC/TUS9508743.
 CC Sequence 150, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 19-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 150:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 111 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 111 AA: 12087 MW: 69654 CN:
 Query Match 85.9%; Score 625; DB 13; Length 111;
 Best Local Similarity 83.0%; Pred. No. 6,01e-39;
 Matches 88; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Db 2 AELTQSPSSLSASVGDVPTITCPGSGIGRFFNWNWYQKPGKAPNLLIYAADILQSGVSP 61
 QY 1 AELTQSPSSLSAFVGDVPTITCRASQISRNLMWYQKPGTAPKVLIIYAASLSQGVSP 60
 Db 62 FSGSGSGTDTLLTISLQPEDFATYYCQGSYSTPTFGGTPLDIK 107

QY 61 FSGSGSGTDTLLTISLQPEDFATYYCQGSYSTPTFGGTPKVEK 106
 RESULT 15
 ID PCT-US93-07832-18 STANDARD: PRT: 107 AA.
 XX xxxxxx
 DT 01-JAN-1990
 DE Sequence 18, Application PC/TUS9307832.
 CC Sequence 18, Application PC/TUS9307832
 CC GENERAL INFORMATION:
 CC APPLICANT: Genentech, Inc
 CC TITLE OF INVENTION: Immunoglobulin Variants
 CC NUMBER OF SEQUENCES: 40
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc
 CC STREET: 460 Point San Bruno Blvd
 CC CITY: South San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94080
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: patin (Genentech)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/07832
 CC FILING DATE: 19930820
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 07/715272
 CC FILING DATE: 14-JUN-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/05126
 CC FILING DATE: 15-JUN-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 07/934373
 CC FILING DATE: 21-AUG-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME:
 CC REGISTRATION NUMBER:
 CC REFERENCE/DOCKET NUMBER: 709P2PCT
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE:
 CC TELEFAX: 415/952-9881
 CC TELEFAX: 910/371-7168
 CC INFORMATION FOR SEQ ID NO: 18:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC SEQUENCE 107 AA: 11623 MW: 67250 CN:
 Query Match 85.2%; Score 620; DB 11; Length 107;
 Best Local Similarity 84.8%; Pred. No. 1,46e-38;
 Matches 89; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
 Db 3 QMIQSPSSLSASVGDVPTITCPASQISRNLMWYQKPGKAPKLLIYAASLSQGVSP 62
 QY 2 ELTQSPSSLSAFVGDVPTITCPASQISRNLMWYQKPGTAPKVLIIYAASLSQGVSP 61
 Db 63 SSGSGTDTLLTISLQPEDFATYYCQGSYNLPLWTFGGGTPKVEK 107
 QY 62 SSGSGTDTLLTISLQPEDFATYYCQGSYSTPTFGGTPKVEK 106
 Search completed: Tue Feb 24 07:55:30 1998
 Job time : 7 secs.



DR N-PSDB: T75423.
 PT Anticancer human monoclonal antibody variable region sequences - and
 PS Related DNA and RNA
 PS Claim 9: Page 11: 14pp; Japanese.
 CC The present sequence is a human anti-tumour antigen
 CC monoclonal antibody (MAB) light chain variable region, useful in
 CC medicine, pharmacology and biochemistry. The isotype of a MAB
 CC secreted by the human/human hybridoma HT was determined to be mu
 CC and kappa. Human MAB was purified, and the antigen recognised by
 CC human MAB CLN⁺-IgM identified by western blotting.
 SQ Sequence 132 AA;

Query Match 90.4%; Score 658; DB 22; Length 132;
 Best Local Similarity 89.5%; Pred. No. 2,13e-38;
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 Db 25 qntqpsalsasvdrvtitorasqssissynwvqgkpgkapklliyaasslsgvpsrf 84
 QY 2 ELTQSPSSLSAFVGRVITITCPASQSSISPNLNWVQKPGTAPKVI IYAASSLSQGVPSRF 61
 Db 85 ssgsgstfttisslqpedfatyyqgqssystptfaggtkveik 129
 QY 62 SSGSGSIUFIITISLQPEFAIYVQWQSYTIIPFQSGIKVEVK 106

RESULT 5
 ID R54260 standard: Protein: 107 AA.

DE Anti-HIV gp120 immunoglobulin light chain variable region b22.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation: monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.

EH Key Location/Qualifiers

FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..67
 FT /label= FR3
 FT Region 68..95
 FT /label= CDR3
 FT Region 96..107
 FT /label= FR4
 PN W09407822-A
 PD 14-APR-1994.
 PR 30-SEP-1993: m09328
 PA (SCPI) SCRIPPS RES INST.
 PI Barbas CF., Burton DR., Lerner RA.
 PI WPI: 94-14515/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 5: Page 183: 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC diclontic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54260 neutralises HIV1
 SQ Sequence 107 AA;

Query Match 89.4%; Score 651; DB 10; Length 107;
 Best Local Similarity 90.5%; Pred. No. 6.90e-38;
 Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

RESULT 7
 ID W15524 standard: Protein: 108 AA.

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Db 1 eltqpsalsasvdrvtitorasqssissynwvqgkpgkapklliyaasslsgvpsrf 60
 QY 2 ELTQSPSSLSAFVGRVITITCPASQSSISPNLNWVQKPGTAPKVI IYAASSLSQGVPSRF 61
 Db 61 ssgsgstfttisslqpedfatyyqgqssystptfaggtkveik 105
 QY 62 SSGSGSIUFIITISLQPEFAIYVQWQSYTIIPFQSGIKVEVK 106

RESULT 6

ID W01283 standard: Protein: 107 AA.

DE 29-JAN-1997 (first entry)
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp120; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Region 1..21
 FT /label= FR1
 FT Region 22..32
 FT /label= CDR1
 FT Region 33..47
 FT /label= FR2
 FT Region 48..54
 FT /label= CDR2
 FT Region 55..86
 FT /label= FR3
 FT Region 87..95
 FT /label= CDR3
 FT Region 96..107
 FT /label= FR4
 PN W0950273-A1.
 PD 01-FEB-1996.
 PR 11-JUL-1995: U08743.
 PR 18-JUL-1994: US-276852.
 PA (SCPI) SCRIPPS RES INST.
 PI Barbas CF., Burton DR., Lerner RA.
 PI WPI: 96-179601/18
 PT Monoclonal antibody binding to VL42 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example: Fig 11: 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the J2
 CC gene clones, b22 and B35. A MAB containing this VL sequence has the
 CC capacity to reduce HIV infectivity titre in an in vivo virus
 CC infectivity assay by 50 % at a concentration of less than 700 ng
 CC of antibody/ml, and binds mature gp120 preferentially over the
 CC precursor gp160. The MAB may be used for determining immunocompetence
 CC of a human anti-HIV antibody and in the detection of HIV infection.
 SQ Sequence 107 AA;

Query Match 89.4%; Score 651; DB 19; Length 107;

Best Local Similarity 90.5%; Pred. No. 6.90e-38;

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Db 1 eltqpsalsasvdrvtitorasqssissynwvqgkpgkapklliyaasslsgvpsrf 60
 QY 2 ELTQSPSSLSAFVGRVITITCPASQSSISPNLNWVQKPGTAPKVI IYAASSLSQGVPSRF 61
 Db 61 ssgsgstfttisslqpedfatyyqgqssystptfaggtkveik 105
 QY 62 SSGSGSIUFIITISLQPEFAIYVQWQSYTIIPFQSGIKVEVK 106

RESULT 7

ID W15524 standard: Protein: 108 AA.

AC W1524;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-2 scFv antibody 6-H1 VL domain.
 KW Transforming growth factor beta-2, TGF-beta-2, human,
 KW antibody engineering; scFv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis,
 KW post myocardial infarction, post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection, therapy; chain shuffling.
 OS Chimeric Homo sapiens;
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 89..97
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN GB2305921-A
 PD 23-APR-1997
 PF 07-OCT-1996; 020920.
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DR WPI. 97-215360/20.
 DR N-PSDB; T60371.
 DT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease
 PS Claim 5; Fig 2b(1); 184pp; English.
 CC This polypeptide sequence comprises the VL domain of human scFv
 CC antibody 2A-H1 (also known as 6H1), which is specific for
 CC transforming growth factor (TGF) beta-2. It is encoded by a gene
 CC (T60371) obtd. from a light chain shuffle repertoire of a peripheral
 CC blood lymphocyte library. The antigen-binding domains of human
 CC antibodies (see W1522-40) to TGF beta-1 and/or beta-2 can be used
 CC to counter the adverse effects of TGF beta, such as (i) promotion
 CC of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis,
 CC arterial injury, proliferative retinopathy, retinal detachment,
 CC adult respiratory distress syndrome, liver cirrhosis, post
 CC myocardial infarction, post-angioplasty restenosis, scleroderma,
 CC vascular disorders, cataract, glaucoma, or esp. neural scarring and
 CC glomerulonephritis, also (not claimed) osteoporosis), or (ii)
 CC immune and inflammatory diseases (e.g. rheumatoid arthritis,
 CC macrophage deficiency diseases or macrophage pathogen infection).
 CC Nucleic acids encoding human antibody VH and VL can be used for
 CC prodn. of recombinant antigen-binding domains. These are highly
 CC specific, have low dissociation constants (pref. less than 5 nM)
 CC and low IC50s for neutralisation.
 SQ Sequence 108 AA;
 Query Match 87.9%; Score 640; DB 23; Length 108;
 Best Local Similarity 84.6%; Pred No 4 37e-37;
 Matches 88; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Db 4 mtospslsasvdrvtitcrasqisnlyawqqkpkapkllykastlesgvsrfs 63
 QY 3 LTQSPSSLSAFVGDVRTITCPASQSISRNLNMYQKPTAPKVLIIAASSLQSGVPSF 62
 Db 64 gsgsgtftltisslqpedfatyyccqsystrptfsggktkvdik 107
 QY 63 GSGSGTDFLTITSLQPEDFATYYCQSQSYTTPRTFGGCTKVEVK 106

RESULT 8
 ID W01288 standard; Protein: 108 AA.
 AC W01288;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone B8.
 KW Heavy chain, light chain, variable region, VH, monoclonal antibody,
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..32
 FT /label= CDR1
 FT Region 33..47
 FT /label= FR2
 FT Region 48..54
 FT /label= CDR2
 FT Region 55..86
 FT /label= FR3
 FT Region 87..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PP 18-JUL-1994; HS-276852
 PA (SCRI) SCRIpps RES INST
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 DT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK1
 CC gene clone, B8. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;
 Query Match 87.2%; Score 635; DB 19; Length 108;
 Best Local Similarity 84.9%; Pred No 1.01e-36;
 Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;
 Db 1 eitqspsslsasvdrvtitcrasqisnlyawqqkpkapkllykastlesgvsrfs 60
 QY 2 ELTQSPSSLSAFVGDVRTITCPASQSISRNLNMYQKPTAPKVLIIAASSLQSGVPSF 61
 Db 61 gsgsgtftltisslqpedfatyyccqsystrptfsggktkveik 106
 QY 62 GSGSGTDFLTITSLQPEDFATYYCQSQSYTTP-PTFGGCTKVEVK 106
 RESULT 9
 ID R54320 standard; protein: 108 AA
 AC R54320;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region B8.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1

FT /Region 22...33
 FT /label= CDR1
 FT /Region 34...48
 FT /label= FR2
 FT /Region 49...55
 FT /label= CDR2
 FT /Region 56...87
 FT /label= FR3
 FT /Region 88...96
 FT /label= CDR3
 FT /Region 97...108
 FT /label= FR4
 PN W09407922-A.
 PD 14-APR-1994.

PF 30-SEP-1993: U09328.

PR 30-SEP-1992: US-954148.

PA (SCFI) SCFIPPS PES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 94-135515/16.

PT New human monoclonal antibodies neutralising HIV - react with

PI gp120 or gp41 and nucleic acid encoding them. Useful for in vivo

PT or in vitro diagnosis and for passive immuno-therapy

PS Example: Page 192-193; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC amplification using primers specific for heavy and light chain

CC variable regions. The amplification products were inserted into a

CC dicistronic vector to produce a library of fragments. E.coli XL1

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAB regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence R54320 neutralises HIV1

CC gp120.

SQ Sequence 108 AA;

Query Match 87.2%; Score 635; DB 9; Length 108;

Best Local Similarity 84.9%; Pred. No. 1.01e-36;

Matches 90; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 1 elqtspsslsasvdrvtitcrasqslslnwvqgkpkapkllygaaslgqvpsrf 50

QY 2 ELTQSPSSLSAFVSDRVITTCRASQSLSRNLNWKYQKPGTAPKVIYAASLSLQGVPSRF 51

Db 61 sgsqsgtdftltslqpedfatycqgsyntppwtfggatkveik 106

QY 62 SGSGSGTDFTLTITSLOPEDFATYCOOSYITP-RFGQGTKEVK 106

RESULT 10

ID R54258 standard; protein: 108 AA.

AC R54258;

DE 10-NOV-1994 (first entry)

KW Anti-HIV gp120 immunoglobulin light chain variable region b8.

KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KW neutralisation; monoclonal antibody; kappa light chain;

KW variable region; framework; complementarity determining region.

OS Homo sapiens.

FH Key Location/Qualifiers

FT /Region 1...21

FT /label= FR1

FT /Region 22...33

FT /label= CDR1

FT /Region 34...48

FT /label= FR2

FT /Region 49...55

FT /label= CDR2

FT /Region 56...87

FT /label= FR3

FT /Region 88...96

FT /label= CDR3

FT /Region 97...108

FT /label= FR4

PN W09407922-A.

PD 14-APR-1994.

PF 30-SEP-1993: U09328.

PR 30-SEP-1992: US-954148.

PA (SCFI) SCFIPPS PES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 94-135515/16.

PT New human monoclonal antibodies neutralising HIV - react with

PI gp120 or gp41 and nucleic acid encoding them. Useful for in vivo

PT or in vitro diagnosis and for passive immuno-therapy

PS Claim 5; Page 188; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC amplification using primers specific for heavy and light chain

CC variable regions. The amplification products were inserted into a

CC dicistronic vector to produce a library of fragments. E.coli XL1

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAB regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence R54258 neutralises HIV1

CC gp120.

SQ Sequence 108 AA;

Query Match 86.4%; Score 629; DB 10; Length 108;

Best Local Similarity 86.8%; Pred. No. 2.76e-36;

Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 elqtspsslsasvdrvtitcrasqslslnwvqgkpkapkllygaaslgqvpsrf 50

QY 2 ELTQSPSSLSAFVSDRVITTCRASQSLSRNLNWKYQKPGTAPKVIYAASLSLQGVPSRF 51

Db 61 sgsqsgtdftltslqpedfatycqgsyntppwtfggatkveik 106

QY 62 SGSGSGTDFTLTITSLOPEDFATYCOOSYITP-RFGQGTKEVK 106

RESULT 11

ID W01281 standard; protein: 108 AA.

AC W01281;

DE 29-JAN-1997 (first entry)

KW VL region of HIV neutralising MAB, clone b8.

KW Heavy chain; light chain; variable region; VH: monoclonal antibody;

KW MAB; HIV: human immunodeficiency virus; glycoprotein; gp120; clone;

KW virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

FH Key Location/Qualifiers

FT /Region 1...21

FT /label= FR1

FT /Region 22...32

FT /label= CDR1

FT /Region 33...47

FT /label= FR2

FT /Region 48...54

FT /label= CDR2

FT /Region 55...86

FT /label= FR3

FT /Region 87...96

FT /label= CDR3

FT /Region 97...108

FT /label= FR4

PN W09502273-A1.

PD 01-FEB-1996.

PF 11-JUL-1995: U08743.

PR 18-JUL-1994: US-278852.

PA (SCFI) SCFIPPS PES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 96-179601/18.

PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in

PT passive immunotherapy and detection of HIV infection.

PS Example; Fig 11; 366pp; English.

CC The sequences given in W01261-92 represent the light chain variable

CC regions (VL) of a series of monoclonal antibodies (MAB's) which are

CC immunoreactive with HIV glycoprotein gp120 and are capable of

CC neutralising HIV. This sequence represents the sequence of the Jk4

CC gene clone, b8. A MAB containing this VL sequence has the capacity

CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 86.4%; Score 629; DB 19; Length 108;
 Best Local Similarity 86.8%; Pred. No. 2.76e-36;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 eltcqpsllsasvqdrvtitcrasqtsisynlnwygqkpgkapklliyaasslgrvpsrf 60

QY 2 ELTCQPSLLSAFVGDVDTITCRASQTSISRNLNWYQKPGTAPKVLIIYAASSLQSGVPSRF 61

Db 61 sgsgsgtdftlittslqpdedfatyyccqsyssipptlftgggtkveik 106

QY 62 SGSGSGTDFTLTITSLQPEDFATYYCQOSYTPR-TFGQGTKEVK 106

RESULT 12
 ID P54318 standard; protein: 104 AA

AC R54318;

DE 10-NOV-1994 (first entry)

DE Anti-HIV gp120 immunoglobulin light chain variable region s4.

KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KW neutralisation; monoclonal antibody; kappa light chain;

KW variable region; framework; complementarity determining region.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..18

FT /label= FR1

FT Region 19..29

FT /label= CDR1

FT Region 30..44

FT /label= FR2

FT Region 45..51

FT /label= CDR2

FT Region 52..83

FT /label= FR3

FT Region 84..92

FT /label= CDR3

FT Region 93..104

FT /label= FR4

PN W09407922-A.

PD 14-APR-1994.

PF 30-SEP-1993; U09328.

PR 30-SEP-1992; US-954148.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 94-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example: Page 190-191; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E coli XL1

CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54318 neutralises HIV1
 CC gp120

SQ Sequence 104 AA;

Query Match 86.1%; Score 627; DB 9; Length 104;

Best Local Similarity 88.2%; Pred No 3.86e-36;

Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 qspsslsasvqdrvtitcrasqtsisynlnwygqkpgkapklliyaasslgrvpsrfsg 60

QY 5 QSPSSLSAFVGDVDTITCRASQTSISPNLNWYQKPGTAPKVLIIYAASSLQSGVPSRFSG 64

Db 61 gsgrtdftlittslqpdedfatyyccqsyssipptfqqgtkleik 102

QY 65 GSSTDFTLTITSLQPEDFATYYCQOSYTPRTFGQGTKEVK 106

RESULT 13

ID W01285 standard; Protein: 104 AA.

AC W01285;

DT 29-JAN-1997 (first entry)

DE VL region of HIV neutralising MAB, clone s4.

KW Heavy chain; light chain; variable region; VH, monoclonal antibody;

KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KW virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..18

FT /label= FR1

FT Region 19..29

FT /label= CDR1

FT Region 30..44

FT /label= FR2

FT Region 45..51

FT /label= CDR2

FT Region 52..83

FT /label= FR3

FT Region 84..92

FT /label= CDR3

FT Region 93..104

FT /label= FR4

PN W09602273-A1.

PD 01-FEB-1996.

PF 11-JUL-1995; U08743.

PR 18-JUL-1994; US-275352.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 96-179601/18.

PT Monoclonal antibody; binding to VL/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example: Fig 11; 366pp; English

CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, s4. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.

SQ Sequence 104 AA;

Query Match 86.1%; Score 627; DB 19; Length 104;

Best Local Similarity 88.2%; Pred. No. 3.86e-36;

Matches 90; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 qspsslsasvqdrvtitcrasqtsisynlnwygqkpgkapklliyaasslgrvpsrfsg 60

QY 5 QSPSSLSAFVGDVDTITCRASQTSISPNLNWYQKPGTAPKVLIIYAASSLQSGVPSRFSG 64

Db 61 gsgrtdftlittslqpdedfatyyccqsyssipptfqqgtkleik 102

QY 65 GSSTDFTLTITSLQPEDFATYYCQOSYTPRTFGQGTKEVK 106

RESULT 14

ID W15539 standard; Protein: 108 AA.

AC W15539;

DT 27-NOV-1997 (first entry)

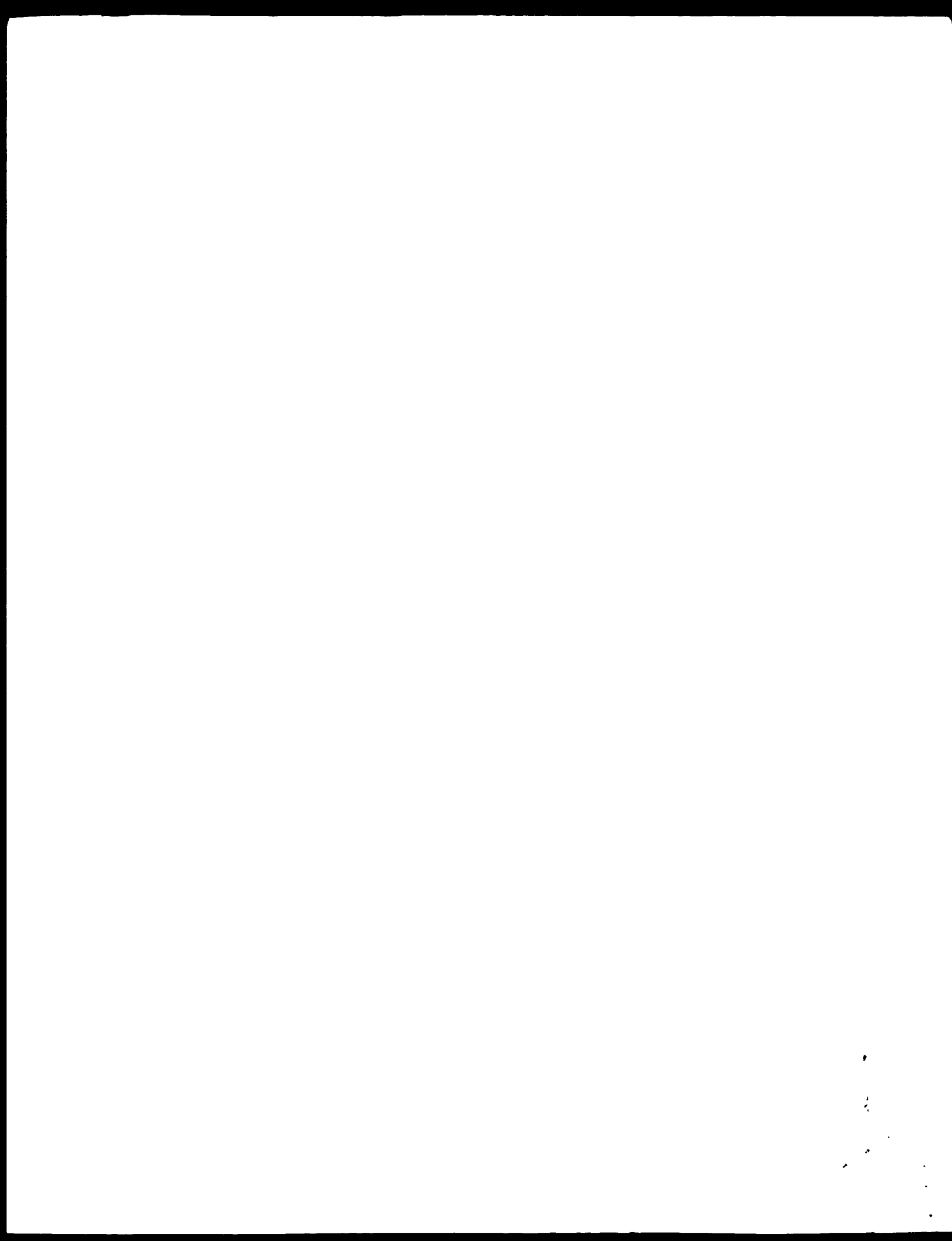
DE Anti-TGF beta-1 scFv antibody 31G9 VL domain.

KW Transforming growth factor beta-1; TGF-beta-1; human;

KW antibody engineering; scFv; phage display; lung fibrosis.

KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy
 OS Homo sapiens.
 PN GB2105421-A
 PD 23-APR-1997
 PF 07-OCT-1996; 020920
 PR 19-JAN-1996; GB-001081
 PR 06-OCT-1995; GB-020486
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 PF WPI: 97-215365/20
 DR N-PSDB: T60385.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease
 PS Claim 15: Fig 1a(iii): 184pp: English
 CC This polypeptide sequence comprises the VL domain of human scFv
 CC antibody 31G9, which is specific for transforming growth factor
 CC (TGF) beta-1. Antigen-binding domains of human antibodies (see
 CC W1522240) to TGF beta-1 and/or beta-2 can be used to counter the
 CC adverse effects of TGF beta, such as (i) promotion of fibrosis (in
 CC dermal, ocular or keloid scarring, lung fibrosis, arterial injury,
 CC proliferative retinopathy, retinal detachment, adult respiratory
 CC distress syndrome, liver cirrhosis, post myocardial infarction,
 CC post-angioplasty restenosis, scleroderma, vascular disorders,
 CC cataract, glaucoma, or esp. neural scarring and glomerulonephritis,
 CC also (not claimed) osteoporosis), or (ii) immune and inflammatory
 CC diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases
 CC or macrophage pathogen infection). Nucleic acids encoding human
 CC antibody VH and VL can be used for prodn. of recombinant antigen-
 CC binding domains. These are highly specific, have low dissociation
 CC constants (pref. less than 5 nM) and low IC50s for neutralisation
 SQ Sequence 108 AA:
 Query Match 86.0%; Score 626; DB 23; Length 108.
 Best Local Similarity 84.6%; Pred NO 4 56e-36;
 Matches 88; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Db 4 mtqspstiasvgdrvtitcrasqgisswlawyqkqkgrapkvllykastlesvpsrfs 63
 QY 3 LTQSPSSLSAFVGDRTITICRASQSISRNUNWYQKPKTAPKVLIIYAASSIQSGVSPFS 62
 Db 64 qsgstgdtftltisslqpedfatyyccqgsystptwfgggtkleik 107
 QY 63 GSGSGTDFLTIIISLQPELFATYYCQGSYTPRTFGGQTKVEVK 106
 RESULT 15
 ID W19894 standard; Protein: 108 AA.
 AC W19894;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VL variant T0608 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 CH Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Region 24...34
 FT /label- CDR1
 FT /note- "complementarity determining region 1"
 FT Region 50...59
 FT /label- CDR2
 FT /note- "complementarity determining region 2"
 FT Region 89...97

FT /label- CDR3
 FT /note- "complementarity determining region 3"
 PN W09720932-A1.
 PD 12-JUN-1997
 PF 09-DEC-1996; G03043.
 PR 11-OCT-1996; GB-021295.
 PR 07-DEC-1996; GB-025004
 PR 23-MAY-1996; GB-010824.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 PI WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells used for diagnosing
 PT cancer
 PS Claim 4: Fig 4: 128pp: English.
 CC This polypeptide sequence comprises the light chain variable region
 CC (VL), T0608, obtained by light chain shuffling of the VL CDR3 of
 CC human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19885). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1 x 10⁻⁸ M. is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. An example of a claimed pairing
 CC is T0608 VL with CEA6 VH. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing
 CC cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 108 AA:
 Query Match 86.0%; Score 626; DB 23; Length 108.
 Best Local Similarity 84.6%; Pred. No. 4 56e-36;
 Matches 88; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 Db 4 mtqspstiasvgdrvtitcrasqgisswlawyqkqkgrapkvllykastlesvpsrfs 63
 QY 3 LTQSPSSLSAFVGDRTITICRASQSISRNUNWYQKPKTAPKVLIIYAASSIQSGVSPFS 62
 Db 64 qsgstgdtftltisslqpedfatyyccqgsystptwfgggtkleik 107
 QY 63 GSGSGTDFLTIIISLQPELFATYYCQGSYTPRTFGGQTKVEVK 106
 Search completed: Tue Feb 24 07:29:15 1998
 Job time : 33 secs.



Handwriting practice lines for the letter 'L'. The first row shows the letter 'L' on a set of three horizontal lines (top, middle, bottom). The second row shows the letter 'L' on a set of three horizontal lines, with a dashed line indicating the stroke path. The third row shows the letter 'L' on a set of three horizontal lines, with a dashed line indicating the stroke path. The fourth row shows the letter 'L' on a set of three horizontal lines, with a dashed line indicating the stroke path. The fifth row shows the letter 'L' on a set of three horizontal lines, with a dashed line indicating the stroke path. The sixth row shows the letter 'L' on a set of three horizontal lines, with a dashed line indicating the stroke path.

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mpsrch_pp protein - protein database search, using Smith-Waterman algorithm:

Run on: Tue Feb 24 07:25:45 1998; Maspar time 7.39 Seconds
441.114 Million cell updates/sec
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Perfect Score: 759
Sequence: 1 AELTOSPGTILSLVGEPTAT

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Scoring table:  PAM 150
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Searched:      9501 seqs, 30469580 residues
Post-processing: Minimum Match 0%
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8:unacn4 9:unacn5 10:unacn6 11:unacn7 12:unacn8
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18:unacnrev
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	688	89.5	109	7	H30601		Ig kappa chain V-III	1 87a-63
2	687	88.3	104	7	F44151		Ig kappa chain V req	2 45a-63
3	686	89.2	114	7	S46375		Ig kappa chain V-Jr	3 320b-63
4	685	89.1	107	7	PH0965		Ig kappa chain V req	4 18a-63
5	681	88.6	109	7	A30608		Ig kappa chain V-III	1 22a-62
6	679	88.3	109	7	B30601		Ig kappa chain V-III	2 09a-62
7	676	87.9	108	7	G30608		Ig kappa chain V-III	4 56b-62
8	676	87.9	109	7	G30601		Ig kappa chain V-III	4 56b-62
9	676	87.9	129	2	K3HHR		Ig kappa chain precu	4 66a-62
10	675	87.8	109	7	G30601		Ig kappa chain V-III	6 08a-62
11	675	87.8	129	7	S46369		IG light chain varia	6 08b-62
12	675	87.8	134	7	S4654		Ig kappa chain V req	4 08a-62
13	673	87.5	129	2	K3HURA		Ig kappa chain precu	1 04a-61
14	672	87.4	104	7	G30607		Ig kappa chain V-III	1 36a-61
15	672	87.4	109	2	K3HURL		Ig kappa chain V-III	1 36b-61
16	671	87.3	109	7	PH0963		Ig kappa chain V req	1 77a-61
17	671	87.3	129	7	S20536		Ig kappa chain V req	1 77b-61
18	669	87.0	109	7	F30507		Ig kappa chain V-III	3 03b-61
19	669	87.0	104	2	K3HHR		Ig kappa chain V-III	4 03a-61
20	666	86.6	104	7	H44151		Ig kappa chain V req	6 76b-61

ALIGNMENTS

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RESULT 1
ENTRY
  #type fragment
  Ig kappa chain V-lII region (Gar and Flo) - human (fragment)
ORGANISM
  #formal_name Homo sapiens #common_name man
  #date 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
  16-Aug-1996
ACCESSIONS
  H30601: E30601
REFERENCE
  A30601
  #authors Goni, F. R., Chen, F. P., McGinnis, D., Arjonilla, M.L.,
    Fernandez, J., Carson, D., Solomon, A., Mendez, E.,
    Frangione, B.
  #journal J. Immunol. (1989) 142:3158-3163
  #title Structural and idiotypic characterization of the L chains of
    human IgM autoantibodies with different specificities.
  #cross-references MIMD:89215279
  #accession H30601
  #status preliminary
  #molecule_type protein
  #residues 1-109 #label GON1
  #accession E30601
  #status preliminary
  #molecule_type protein
  #residues 1-109 #label GON2
  #classification #superfamily immunoglobulin V region: immunoglobulin heterodimer;
  #keywords heterotrimer; Immunoglobulin
  #summary #length 109 #checksum 5951

  Query Match 89.5%; Score 688; DB 7; Length 109;
  Best Local Similarity 89.5%; Pred. No. 1.87e-63;
  Matches 94; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

4 ltspgtslspgeratiscrasqsvssylawvqgkpgqaplllyvassratcpdrt 63
|||||
3 ltspgtslspgeratiscrasqsvssylawvqgkpgqaplllyvassratcpdrt 62
|||||
64 sgsgsgdftllstlcpedfawvqgqygssvffgagivvleik 108
|||||
63 sgsgsgdftllstlcpedfawvqgqygssvffgagivvleik 107
|||||

RESULT 2
ENTRY
  #type fragment
  Ig kappa chain V region (JM-01) - human (fragment)
ORGANISM
  #formal_name Homo sapiens #common_name man

```

```

DATE          27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
ACCESSIONS    16-Aug-1996
REFERENCE      F44151
#authors       Zebadee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.;
               Graff, P.; DeGraw, J.; Pyati, J.; LaPolla, R.; Burton,
               D.R.; Lerner, R.A.; Thornton, G.B.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title         Human combinatorial antibody libraries to hepatitis B surface
               antigen.
#accession     F44151
#status        preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues      1-109 ##label ZEB
#note          nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 5518

Query Match      89.3%; Score 687; DB 7; Length 109;
Best Local Similarity 86.9%; Pred. No. 2.45e-63;
Matches 93; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Db 1 aeltspgtlslspgeratlscrasqsvfnsylawqkpgqaprrliygassratgipd 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1 AELTSPGTLSSLVGERATLSCRASQNIYSGLWYQKPGQPPPLLIYGASNPATGIPD 60

Db 61 rfsgsgtdftltisrlepedfavyycqygsspstfgggtkveik 107
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 RFSGSGTDFTLTISRLESEDFAVYICQYQYSPPTFGQGTKEIK 107

RESULT 3
ENTRY   S46375      #type fragment
TITLE   Ig kappa chain V-J region (T33-5) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change
        16-Aug-1996
ACCESSIONS S46375; S38648
REFERENCE   S46369;
#authors    Bensimon, C.; Chastagner, P.; Zouali, M.
#journal    EMBO J. (1994) 13:2951-2962
#title      Human lupus anti-DNA autoantibodies undergo essentially
               primary V(chi) gene rearrangements.
#accession  S46375
#molecule_type mRNA
#residues   1-114 ##label BEN
#cross-references EMBL:Z27176
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
SUMMARY      #length 114 #checksum 6780

Query Match      89.2%; Score 686; DB 7; Length 114;
Best Local Similarity 90.6%; Pred. No. 3.20e-63;
Matches 96; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Db 8 ltspgtlslspgeratlscrasqsvfnsylawqkpgqaprrliygassratgipdrf 67
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 3 LTSPGTLSSLVGERATLSCRASQNIYSGLWYQKPGQPPPLLIYGASNPATGIPDRF 62

Db 68 ssgsgtdftltisrlepedfavyycqygssppytfgggtkveik 113
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 63 SGSGSGTDFTLTISRLESEDFAVYICQYQYGS-PPYTFGQGTKEIK 107

RESULT 4
ENTRY   PH0965      #type fragment
TITLE   Ig kappa chain V region (G6+ CLL-BRA) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
        16-Aug-1996
ACCESSIONS PH0965
REFERENCE   PH0945;

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#authors       Martin, T.; Duffy, S.F.; Carson, P.A.; Kipps, T.J
#journal       J. Exp. Med. (1992) 175:983-991
#title         Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession     PH0965
#status        nucleic acid sequence not shown
#molecule_type DNA
#residues      1-107 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        #region framework 1\
               22-32
               #region complementarity-determining 1\
               33-48
               #region framework 2\
               49-54
               #region complementarity-determining 2\
               55-87
               #region framework 3\
               88-95
               #region complementarity-determining 3
SUMMARY        #length 107 #checksum 7830

Query Match      89.1%; Score 685; DB 7; Length 107;
Best Local Similarity 89.3%; Pred. No. 4.18e-63;
Matches 94; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 2 ltspgtlslspgeratlscrasqsvfnsylawqkpgqaprrliygassratgipdrf 61
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 3 LTSPGTLSSLVGERATLSCRASQNIYSGLWYQKPGQPPPLLIYGASNPATGIPDRF 62

Db 62 ssgsgtdftltisrlepedfavyycqygssrytfgggtkveik 106
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 63 SGSGSGTDFTLTISRLESEDFAVYICQYQYSPPTFGQGTKEIK 107

RESULT 5
ENTRY   A30608      #type fragment
TITLE   Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
        16-Aug-1996
ACCESSIONS A30608
REFERENCE   A30601;
#authors    Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
               Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal    J. Immunol. (1989) 142:3158-3163
#title      Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession  A30608
#status      preliminary
#molecule_type protein
#residues    1-209 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
SUMMARY      #length 109 #checksum 6031

Query Match      88.6%; Score 681; DB 7; Length 109;
Best Local Similarity 88.6%; Pred. No. 1.22e-62;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscrasqsvfnsylawqkpgqaprrliygassratgipdrf 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 3 LTSPGTLSSLVGERATLSCRASQNIYSGLWYQKPGQPPPLLIYGASNPATGIPDRF 62

Db 64 ssgsgtdftltisrlepedfavyycqygsspytfgggtkveik 108
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 63 SGSGSGTDFTLTISRLESEDFAVYICQYQYSPPTFGQGTKEIK 107

RESULT 6
ENTRY   B30601      #type fragment
TITLE   Ig kappa chain V-III region (Glo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change

```

```

16-Aug-1996
ACCESSIONS B30601
REFERENCE A30601
#authors Gonf, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession C30601
##status preliminary
##molecule_type protein
##residues 1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
#length 109 #checksum 5911
SUMMARY
Query Match 88.3%; Score 679; DB 7; Length 109;
Best Local Similarity 89.5%; Pred No 2,00e-62;
Matches 94; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
Db 4 ltqspgtlslpgeratiscrasqsvssylawyqkpgqaprllygassratgipdrf 63
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
QY 3 LTQSPGTLSSVGERATLSCRASQSVSSYLGWYQKPGQAPRLLYGASNPATGIPDRF 62
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
Db 64 ssgsgtdftltisrlepedfavyycqygsspltfaggtkveik 108
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109
QY 63 SSGSGTDFTLTISLESEDFAVYCYQYGGSPPIFGGKVEIK 107
||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109 ||||| 1-109

RESULT 7
ENTRY Q30508 #type fragment
TITLE Ig kappa chain V-III region (Pie) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS C30608
REFERENCE A30608
#authors Gonf, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession C30608
##status preliminary
##molecule_type protein
##residues 1-108 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
#length 108 #checksum 1607
SUMMARY
Query Match 87.9%; Score 676; DB 7; Length 108;
Best Local Similarity 88.6%; Pred. No. 4.56e-62;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Db 4 ltqspgtlslpgeratiscrasqsvssylawyqkpgqaprllygassratgipdrf 63
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
QY 3 LTQSPGTLSSVGERATLSCRASQSVSSYLGWYQKPGQAPRLLYGASNPATGIPDRF 62
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
Db 64 ssgsgtdftltisrlepedfavyycqygsspltfaggtkveik 108
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
QY 63 SSGSGTDFTLTISLESEDFAVYCYQYGGSPPIFGGKVEIK 107
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108

RESULT 8
ENTRY Q30601
TITLE Ig kappa chain V-III region (Pay) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 26-Jun-1989 #sequence_revision 26-Jun-1989 #text_change
16-Aug-1996
SUMMARY
Query Match 87.9%; Score 676; DB 7; Length 108;
Best Local Similarity 88.6%; Pred. No. 4.56e-62;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Db 4 ltqspgtlslpgeratiscrasqsvssylawyqkpgqaprllygassratgipdrf 63
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
QY 3 LTQSPGTLSSVGERATLSCRASQSVSSYLGWYQKPGQAPRLLYGASNPATGIPDRF 62
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
Db 64 ssgsgtdftltisrlepedfavyycqygsspltfaggtkveik 108
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108
QY 63 SSGSGTDFTLTISLESEDFAVYCYQYGGSPPIFGGKVEIK 107
||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108 ||||| 1-108

RESULT 9
ENTRY K3H0H1 #type complete
TITLE Ig kappa chain precursor V-III region (Hic) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
30-May-1997
ACCESSIONS PL0021
REFERENCE PL0021
#authors Kipps, T.J.; Tomhave, F.; Chen, P.P.; Carson, D.A.;
J. Exp. Med. (1988) 167:840-852
#journal J. Exp. Med. (1988) 167:840-852
#title Autobody-associated kappa light chain variable region
gene expressed in chronic lymphocytic leukemia with little
or no somatic mutation: implications for etiology and
immunotherapy.
#cross-references MUID:86171307
#accession PL0021
##molecule_type mRNA
##residues 1-129 ##label KIP
COMMENT The protein is one of the surface immunoglobulin M autoantibodies
expressed in patients with chronic lymphocytic leukemia.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:136266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS autobody; chronic lymphocytic leukemia; heterotetramer;
immunoglobulin
FEATURE
1-20 #domain signal sequence #status predicted #label K3H
21-129 #product Ig kappa chain V-III region (Hic) #status
predicted #label MATN
#region V segment\
21-117 #region complementarity-determining 1\
44-55 #region complementarity-determining 2\
71-77 #region complementarity-determining 3\
110-117 #region J segment (CKI)\
118-129 #disulfide_bonds #status predicted
43-109 #length 129 #molecular_weight 14070 #checksum #174
SUMMARY

```



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CLASSIFICATION  #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS        antibody, chronic lymphocytic leukemia, heterotetramer,
                 immunoglobulin
FEATURE
1-20            #domain signal sequence #status predicted #label S15\
21-129          #product Ig kappa chain V-III region (Hah) #status
                 predicted #label MAT\
21-117          #region V segment\
44-55           #region complementarity-determining 1\
71-77           #region complementarity-determining 2\
110-117         #region complementarity-determining 3\
118-129         #region J segment (JK1)\
43-109          #disulfide bonds #status predicted
SUMMARY         #length 129 #molecular-weight 14073 #checksum 7361
Query Match     87.5% Score 673; DB 2; Length 129;
Best Local Similarity 88.6% Pred. No. 1.04e-61;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Db 24 ltspqtlslspgeratlscrasqssvslawyygkpgqgprlliygassratgipdrf 83
Qy 3 LTSPGTLSSVGERATLSCPASQNIYSGYLGWYQKPKGPPPLLIYGASNPATGIPDPF 62
Db 84 sasgsatdftltisrlepedfavyycqygtsprtfggatkveik 128
Qy 53 SGSGSGTDFTLISRLSESEFVAVYCYQYGVSPPYIFGQIKVEIK 107

RESULT 14
ENTRY        G30607      #type fragment
TITLE        Ig kappa chain V-III region (Kas) - human (fragment)
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1995
ACCESSIONS   G30607
REFERENCE    A30601
#authors     Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
             Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
             Frangione, B.
#journal:    J Immunol (1994) 142:3159-3163
#title       Structural and idiotypic characterization of the L chains of
             human IgM autoantibodies with different specificities.
#cross-references MIM:89215279
#accession   G30607
#status      Preliminary
#molecule_type protein
#residues    1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer: immunoglobulin
SUMMARY       #length 109 #checksum 4998
Query Match    87.4% Score 672; DB 7; Length 109;
Best Local Similarity 87.6% Pred. No. 1.36e-61;
Matches 92; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Db 4 ltspqtlslspgeratlscrasqssvslawyygkpgqgprlliygassratgipdrf 63
Qy 3 LTSPGTLSSVGERATLSCPASQNIYSGYLGWYQKPKGPPPLLIYGASNPATGIPDPF 62
Db 64 sasgsatdftltisrlepedfavyycqygssptfggatkveik 108
Qy 53 SGSGSGTDFTLISRLSESEFVAVYCYQYGVSPPYIFGQIKVEIK 107

RESULT 15
ENTRY        K3HJWL      #type complete
TITLE        Ig kappa chain V-III region (Wol) - human
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change
06-Sep-1995
ACCESSIONS   A01895
REFERENCE    A00450

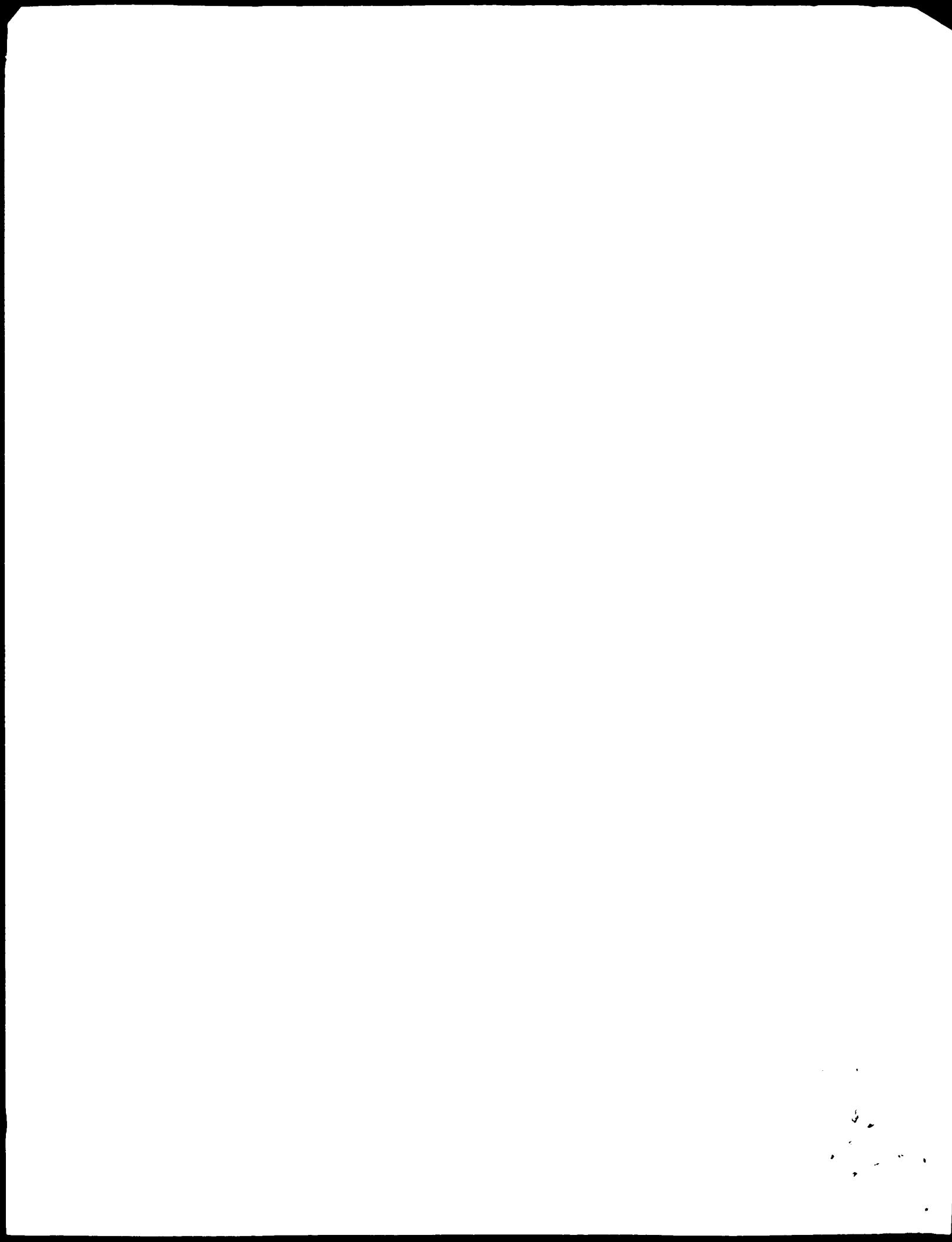
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#authors       Andrews, D.W.; Capra, J.D.
#journal       Biochemistry (1994) 20:5916-5922
#title         Amino acid sequence of the variable regions of light chains
                 from two idiotypically cross-reactive human IgM
                 anti-gamma-globulins of the Wa group.
#cross-references MIM:82046598
#accession     A01896
#molecule_type protein
#residues      1-109 #label AND
COMMENT        This chain was isolated from an IgM with anti-gamma globulin
                 activity.
GENETICS
#gene          GDB:IGKV3
#cross-references GDB:136266
COMPLEX        An immunoglobulin heterotetramer subunit consists of two
                 identical light (kappa or lambda) and two identical heavy
                 (alpha, delta, epsilon, gamma, or mu) chains usually
                 stabilized by interchain disulfide bonds. In some cases,
                 such as IgA and IgM, the subunits associate into larger
                 oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS       heterotetramer
FEATURE        23-89
SUMMARY        #disulfide_bonds #status predicted
                 #length 109 #molecular-weight 11746 #checksum 5360
Query Match    87.4% Score 672; DB 2; Length 109;
Best Local Similarity 90.5% Pred. No. 1.36e-61;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Db 4 ltspqtlslspgeratlscrasqssvslawyygkpgqgprlliygassratgipdrf 63
Qy 3 LTSPGTLSSVGERATLSCPASQNIYSGYLGWYQKPKGPPPLLIYGASNPATGIPDPF 62
Db 64 sasgsatdftltisrlepedfavyycqygslgrtfggatkveik 108
Qy 53 SGSGSGTDFTLISRLSESEFVAVYCYQYGVSPPYIFGQIKVEIK 107

Search completed, Tue Feb 24 07:26:07 1998
Tot time: 22 secs

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Db	13	acgacgctctccagcaccctgtctctgtctccagcgaaagaaacacacacctctctccagcag	72
QY	7	AGCGAGTCTCCAGCGAGCCCTGCTCTCTAGGGGAAAAGAGGATCTCTCTCTCTCTAGG	56
Db	73	gccactcagactgttagcagcaactactttagctcgtaccagcacaacacctggccaggct	132
QY	67	GCCAGTCAGAGTGTTAGCAGCAATTACTTAGTCTGTGTATCCAGCAAGATCTGGTCACT	126
Db	133	cccaagctcctcactctatgctacatccataaagdtcatcttgagcatccacagacaggttcact	192
QY	127	CCGAGGCTCCATCTATGTGTGATCCAGAGGGGCACTTGGCATCCAGACAGGTTTCAGT	186
Db	193	ggcagtgggtctggacagacttccactccaccatcagcagactggagctctgaagatttt	252
QY	187	GGCAGCTGGGCTGTGGAAAGACTTCATCTCCACATCACTCAATCTAGATTTT	246
Db	253	gcagtgattactctcagcaggtttctgtaactcacagtgaggagcttcggccaaggagccaag	312
QY	247	GAGTGTATTAATCTGTCAAGTTTATGTAACTTAAGTTGAGGTTCTGACCAAGGCAAG	306
Db	313	gttgaatatcaaa	324
QY	307	GTGGAGATCAAA	318

RESULT	3	
ID	Q42707	standard; DNA: 390 BP.
AC	Q42707;	
DT	01-NOV-1993	(first entry)
DE	F105Vk-F105Jk.	
KW	Monoclonal antibody; MAb; envelope: glycoprotein; gp120; HIV: AIDS;	
KW	CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light	
KW	chain; epitope; immune deficiency; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	sig_peptide	1..60
FT	/*tag= a	
FT	mat_protein	61..390
FT	/*tag= b	
FT	misc_RNA	1..351
FT	/*tag= c	
FT	/label= F105Vk	
FT	misc_RNA	352..390
FT	/*tag= d	
FT	/label= F105Jk	
FT	misc_RNA	130 165
FT	/*tag= e	
FT	/label= CDR1	
FT	misc_RNA	211..231
FT	/*tag= f	
FT	/label= CDR2	
FT	misc_RNA	328..354
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PN	W09312332-A.	PN
PD	24-JUN-1993.	PD
PP	10-DEC-1992: 510928	PP
PR	10-DEC-1991: US-804652.	PR
PA	(DAND) DANA FAPER CANCER INST INC.	PA
PA	(NEWSE-) NEW ENGLAND DEACONESS HOSPITAL CORP.	PA
PI	Hasetline WA, Marasco WA, Posner MR, Sodroski JG;	PI
DR	WPI: 93-214174/76.	DR
PT	P-PSDB: R36672.	PT
PT	DNA segments encoding monoclonal antibody - which binds to gp120	PT
PT	and neutralises HIV, for treating AIDS, and for diagnosing and	PT
PT	monitoring HIV infection	PT
PS	Disclosure; Page 73-74: 109pp; English.	PS
CC	The nucleotide sequence of F105 Vk (Q42707 - sequence differs from	CC
CC	other F105 Vk sequences given elsewhere in the specification) was	CC
CC	compared with germline gene HumVk.2.5 (Q42706), showing 97.7%	CC
CC	similarity. By nucleotide sequence analysis, F105 appears to	CC
CC	be derived from a member of the Vk II; subgroup gene family.	CC
SC	Sequence 390 BP; 86 A; 115 C; 102 G; 87 T.	SC


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FT misc_RNA 265..291
FT /tag= k
FT /label= CDR1
FT /note= "complementarity determining region 3"
FT misc_RNA 292..324
FT /tag= 1
FT /label= FR4
FT /note= "framework region 4"
PN W09607754-A1.
PD 14-MAR-1995.
PF 01-SEP-1995; U11235.
PR 02-SEP-1994; US-300386.
PA (SCPI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA.
DR WPI: 96-171625/17.
DR Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
PT gene CDR - useful for prodn. of Ig heavy and light chain
PT combinatorial antibody libraries
PS Example 1; Page 84; 125pp; English.
CC T15202 and T15203 are the heavy and light chain variable domains of
CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a pComb3
CC based expression vector. The heavy and light chain variable domains
CC are used in an example to demonstrate the prodn. of antibodies for
CC an antibody library using mutagenic primers. Mutagenic primers of the
CC invention have sequences at their 3' and 5' ends both capable of
CC binding different framework regions linked by a sequence 5 to 50
CC nucleotides long. Different immunoglobulins produced using the
CC primers may be used to produce antibody libraries having diverse
CC novel immunospecificities and affinities. By using mutagenic ONS an
CC extremely large population of different randomised binding sites can
CC be created and use of the universal light chain increases the number
CC of combinations which yield functional heterodimeric antibodies.
CC Sequence 646 BP; 162 A; 187 G; 170 G; 127 T;
SQ
Query Match 82.7%; Score 263; DB 25; Length 642;
Best Local Similarity 91.5%; Pred. No. 1.49e-157; Indels 3; Gaps 1;
Matches 290; Conservative 0; Mismatches 17;
Db 1 gagctccagcagctctccagcagcctctcttcttctccaggggaaagagcctctctcc 60
QY 1 GAGCTCAGCAGCTCTCCAGCAGCCTCTCTTCTTCTCCAGGGGAAAGAGCCTCTCTCC 60
Db 61 tcacagggcagtcacagcagtgtagcagggcctacttaccctgggtaccagagagagcctggc 120
QY 61 TCACAGGGCAGTCACAGCAGTGAGCAGGGCCTACTTACCCTGGGTACCAGAGAGAGCCTGGC 120
Db 121 cagggtcccccagggctcctcattatggtacatccacagcagggccactggcactccagacagg 180
QY 121 CAGGGTCCCCAGGGCTCCTCATATGGTACATCCACAGCAGGGCCACTGGCCTCAGACAGG 180
Db 181 tccagtgagcagtggtctgggacagagccttccactctccaccatcagcagcagcagcctgaa 240
QY 181 TTCAGTGAGCAGTGGTCTGGGACAGAGCCTTCCACTCTCCACCATCAGCAGCAGCAGCCTGAA 240
Db 241 gattttcagctctactactctcagcagctatggtgggcacagctggg---tttcgggcaagg 247
QY 241 GATTTTCAGCTCTACTACTCTCAGCAGCTATGGTGGGCACAGCTGGG---TTTCGGGCAAGG 247
Db 298 accaaggtgggaactcaaa 315
QY 301 ACCAAGGTGGGAGATCAAA 318
RESULT 9
ID Q70487 standard; cDNA; 646 BP.
AC Q70487;
DI 04-APR-1995 (first entry)
DE Anti-tetanus toxoid light chain cDNA from vector, pC3AP313.
KW Polymerase chain reaction; primer; mutagenesis; PCR; amplification;
KW diversity; antibody; complementarity determining region; CDR;
KW framework; constant; light, heavy, phage, immunoglobulin; library; ss.
OS Synthetic.
PN W09418219-A.
PD 18-AUG-1994.
PF 02-FEB-1994; U01234.
PR 02-FEB-1993; US-012566.
PR 28-DEC-1993; US-174674.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA.
DR WPI: 94-279673/34.
PT Oligo-nucleotides - used as PCR primers for producing increased

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FT      misc_RNA      211..231
FT      /*tag= f
FT      /label= CDR2
FT      misc_RNA      328..354
FT      /*tag= g
FT      /label= CDR3
FT      W09312232-A.  PN
FT      24-JUN-1993.  PD
FT      10-DEC-1992:  PF
FT      10-DEC-1991:  PR
FT      (DAND ) DANA FARBER CANCER INST INC.
FT      (NEWELL) NEW ENGLAND DEACONESS HOSPITAL CORP.
FT      Haseltine WA, Marasco WA, Posner MP, Sodroski JG:
FT      WPI: 93-214174/26.
FT      p-PSDB: R38672.
FT      DR
FT      DNA segments encoding monoclonal antibody - which binds to gp120
FT      and neutralises HIV, for treating AIDS, and for diagnosing and
FT      monitoring HIV infection
FT      PS Disclosure: Page 73-74: 109pp; English.
FT      The nucleotide sequence of F105 VK (Q42707 - sequence differs from
FT      other F105 VK sequences given elsewhere in the specification) was
FT      compared with germ-line gene Hurr:k225 (Q42706), showing 97 %
FT      similarity. By nucleotide sequence analysis, F105 appears to
FT      be derived from a member of the VK III subgroup gene family.
FT      Sequence 390 BP, 88 A, 115 C, 99 G, 88 T.
FT      SQ

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[illegible]

Key	Location/Qualifiers
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FT mat_protein	61..390
FT /*tag= b	
FT misc_RNA	1..351
FT /*tag= c	
FT /label= vk325	
FT misc_RNA	352..390
FT /*tag= d	
FT /label= Jk2	
FT misc_PNA	130 165
FT /*tag= e	
FT /label= CDRI	

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FS	CIS	16..650
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FT	Inton	..63..350
FT	*tag= b	
FT	Misc signal	653..659
FT	*tag= C	
FT	label= Splicing-signal	
FT	Misc signal	672..680

PD 13-AUG-1996. 574748.
PF 29-AUG-1996: 574748.
PP 29-AUG-1996: 574748.
PP 31-AUG-1996: 574748.
PP 17-DEC-1991: 574748.
PP 18-MAR-1992: 574748.
PP 23-JUN-1992: 574748.
PP 16-DEC-1992: 574748.
PA (GENP-) GENPHARM INT INC
PI Kay RM, Longberg N;
DR WPI: 96-383736/38.
DR P-PSDB: W03948.
PT Prodn. of heterologous human immunoglobulin(s) - by immunising
PT transgenic mice
PS Example 21; Fig 43; 94pp; English.
CC The present sequence is the variable kappa chain gene segment
CC containing human DNA fragment, vk65.8, which was co-injected along
CC with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half
CC day mouse embryo pronuclei, to generate an unrearranged light chain
CC minilocus transgene. The resulting transgenic mice can be used for
CC the production of heterologous (i.e. human) antibodies against
CC specific antigens, this comprises immunising a mouse with a
CC preselected antigen and collecting antigen binding heterologous
CC human gamma immunoglobulins.
SQ Sequence 900 BP. 220 A; 241 C; 201 G; 238 T;
Query Match 82.4%; Score 262; DB 27; Length 900;
Best Local Similarity 97.8%; Pred. No. 7.19e-157;
Matches 268; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 375 acgagtcctccagcaccctgtttgtctccaggggaagagccacctctcctgcagg 434
Qy 7 ACCGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAGAGACCCCTCTCTCGAGG 66
Db 435 gccagtcagagtttagcagcactacttagcctggtaccacagaaacctggccagct 494
Qy 67 GCCAGTCAGAGTGTAGCAGCAATTAATTAAGCTGGTACCCAGCAGACCTGGCCAGGCT 126
Db 495 ccagagctctctatagtcagcagcagcagcagcagcagcagcagcagcagcagc 554
Qy 127 CCACAGGCTCTCTATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 186
Db 555 gccagtggtgtctggcagacacttccactctccacatcagcagcagcagcagcagc 614
Qy 187 GCCAGTGGGTCCTGGGACAGATTCATCTCTCACCATCAGCAGACTGGACGCTTAT 246
Db 615 gccagtggtgtctggcagacacttccactctccacatcagcagcagcagcagcagc 648
Qy 247 GCAGTGTATTACTGTAGCTTTATGTTAAGTAACTCAC 280
RESULT 14
ID Q29766 standard, cDNA, 324 BP.
AC Q29766; (first entry)
DE Gene for Lv region of human rheumatoid factor antibody.
KW Light chain; variable region; YES8C; arthritis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 25 288
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FT misc.feature 12..24
FT /*tag= b
FT /*note= "leader sequence"
FT misc.feature 72..102
FT /*tag= c
FT /*note= "encodes CDR1"
FT misc.feature 150..168
FT /*tag= d
FT /*note= "encodes CDR2"
FT misc.feature 277..285
FT /*tag= e
FT /*note= "encodes CDR3"

PN J04267889-A.
PD 24-SEP-1992.
PF 22-FEB-1991: 048704.
PP 22-FEB-1991: 048704.
PA (EZAK/) EZAKI K.
PA (NISP) NISSHI PHARM CO LTD.
DR WPI: 92-368404/45.
DR P-PSDB: R25324
PT Monoclonal human rheumatoid factor - obt'd. by prodn. and
PT secretion of hybridoma obt'd. from cell fusion of human bone
PT marrow derived lymphocyte and P3U1 mouse myeloma cell
PS Disclosure: Page 5; 7pp; Japanese.
CC The sequence shown: encodes the variable region of the light chain of
CC a human monoclonal antibody rheumatoid factor YES8C. The gene may
CC be isolated from the bone marrow soln. of a rheumatoid arthritis
CC patient and used to produce hybridomas, allowing prodn. of the
CC rheumatoid arthritis factor at constant quality in large quantities.
CC See also Q29767
SQ Sequence 324 BP. 72 A; 92 C; 80 G; 80 T;
Query Match 81.1%; Score 258; DB 5; Length 324;
Best Local Similarity 97.1%; Pred. No. 3.92e-154;
Matches 266; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 49 acgagtcctccagcaccctgtttgtctccaggggaagagccacctctcctgcagg 108
Qy 7 ACCGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAGAGACCCCTCTCTCGAGG 66
Db 109 gccagtcagagtttagcagcagcagcagcagcagcagcagcagcagcagcagc 168
Qy 67 GCCAGTCAGAGTGTAGCAGCAATTAATTAAGCTGGTACCCAGCAGACCTGGCCAGGCT 126
Db 169 ccagagctctctatagtcagcagcagcagcagcagcagcagcagcagcagcagc 228
Qy 127 CCACAGGCTCTCTATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 186
Db 229 gccagtggtgtctggcagacacttccactctccacatcagcagcagcagcagcagc 288
Qy 187 GCCAGTGGGTCCTGGGACAGATTCATCTCTCACCATCAGCAGACTGGACGCTTAT 246
Db 289 gccagtggtgtctggcagacacttccactctccacatcagcagcagcagcagcagc 322
Qy 247 GCAGTGTATTACTGTAGCTTTATGTTAAGTAACTCAC 280
RESULT 15
ID T33664 standard; cDNA; 402 BP.
AC T33664;
DT 10-JUN-1997 (revised)
DT 14-MAY-1997 (first entry)
DE Anti-lung tumour antigen monoclonal antibody light chain cDNA.
KW Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;
KW Epstein-Barr virus; TB945; human; B cell; screen; antigen;
KW carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
KW cell; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..402
FT /*tag= a
FT W09628473-A1
PD 19-SEP-1996.
PP 18-MAR-1996: U03661.
PP 16-MAR-1995: US-405034.
PA (MEDE/) MEDENICA R D.
PI Mukerjee S;
DR WPI: 96-433764/43.
DR P-PSDB: W11155
PT Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
PT Epstein-Barr virus transfection of human lung cancer patient
PT B-cells, useful in conjunction with other agents for lysis of
PT tumours
PS Claim 12; Pages 24-25; 46pp; English.
CC The present sequence encodes the light chain from the monoclonal



WATERMAN (TM)

Release 2.10 John F. Collins, BioComputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.
Mpsrch_nna n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:00:26 1998; MaxPar time 417.56 Seconds
Tabular output not generated.
Title: >US-08-844-215-15
Description: (1-318); from US08944215.seq
Perfect score: 318
N.A. Sequence: 1 GAGGTCAGGAGTTCAGG
Comp: CAGGAGGCGGACAGAGGTTC

Scoring table: TABLE default
Gap 5
Nmatch STD : Dbase 0; Query 0
Searched: 430261 seqs, 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1:BC1 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HUM1
9:HUM2 10:HUM3 11:INV1 12:INV2 13:OPG 14:MAM 15:VPI
16:PLN 17:POD1 18:POD2 19:POD3 20:SYN 21:UNC 22:VIP
genbank101
23:BC11 24:BC12 25:BC13 26:BC14 27:BC15 28:BC16 29:BC17
30:BC18 31:BC19 32:BC20 33:BC21 34:BC22 35:BC23
36:GEN1 37:GEN2 38:GEN3 39:GEN4 40:GEN5 41:GEN6 42:HTG1
43:HTG2 44:HTG3 45:HTG4 46:HTG5 47:INV1 48:INV2 49:INV3
50:INV4 51:INV5 52:INV6 53:INV7 54:INV8 55:INV9 56:INV10
57:INV11 58:INV12 59:MAM1 60:MAM2 61:MAM3 62:VPI1
63:VPI2 64:VPI3 65:VPI4 66:VPI5 67:VPI6 68:VPI7 69:VPI8
70:VPI9 71:VPI10 72:VPI11 73:VPI12 74:VPI13 75:VPI14 76:VPI15
77:VPI16 78:VPI17 79:VPI18 80:VPI19 81:VPI20 82:VPI21 83:VPI22
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96:VPI35 97:VPI36 98:VPI37 99:VPI38 100:VPI39 101:VPI40
102:VPI41 103:VPI42 104:VPI43 105:VPI44 106:VPI45 107:VPI46
108:VPI47 109:VPI48 110:VPI49 111:VPI50 112:VPI51 113:VPI52
114:VPI53
genbank101
115:VPI54 116:VPI55 117:VPI56 118:VPI57 119:VPI58 120:VPI59
121:VPI60 122:VPI61 123:VPI62 124:VPI63 125:VPI64
genbank-new7
126:BC1 127:GEN 128:HTG1 129:HTG2 130:INV 131:MAM
132:VPI 133:PHG 134:PLN1 135:PLN2 136:PLN3 137:PLN4
138:POD 139:SYN 140:UNA 141:VPI
Database: u-emb15_101
142:part1 143:part2

Statistics: Mean 9.967; Variance 4.684; scale 2 128
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	296	93.1	320	96	HUMIGKAC	Human Ig rearranged k	2,170-23
2	296	93.1	324	91	HSIGVKAC	H sapiens mRNA for Ig	2,170-24
3	295	92.8	402	91	HSIGVKIC	Human mRNA for Ig k	1,700-229
4	294	92.5	447	99	HUMIGHHA	Human Ig rearranged g	1,330-228
5	292	91.8	402	91	HSIGKVAH	Human mRNA for Ig k	9,190-227
6	291	91.5	324	99	HUMIKVCH	Human mRNA for Ig k	9,190-227
7	290	91.2	324	95	HSIGKVEH	Human rearranged k	5,030-225
8	290	91.2	324	99	HUMIKVCH	Human immunoglobulin	5,030-225
9	290	91.2	329	91	HSIGKVEH	H sapiens (BPM16K) m	5,030-225
10	290	91.2	330	93	HSIGKVEH	H sapiens immunoglobulin	5,030-225
11	290	91.2	334	99	HUMIGKAC	Human Ig rearranged k	5,030-225
12	290	91.2	402	99	HUMIGKAC	Human Ig active kappa	5,030-225
13	289	90.9	312	91	HSIGKVEH	H sapiens (BPM16K) m	3,930-224
14	289	90.9	318	91	HSIGKVEH	H sapiens (BPM16K) m	3,930-224
15	288	90.6	339	99	HUMIGKAC	Human active kappa	3,080-223
16	286	89.9	318	99	HUMIGKAC	Human antipeptidelet m	1,890-221
17	286	89.9	320	99	HUMIGKAC	Human Ig rearranged k	1,890-221
18	286	89.9	324	91	HSIGKVEH	H sapiens mRNA for Ig	1,890-221
19	286	89.9	324	94	HSIGKVEH	Human clone 3754 Ig k	1,890-221
20	286	89.9	420	91	HSIGKVEH	H sapiens rearranged k	1,890-221
21	284	89.3	300	99	HUMIGKAC	Human sapiens (clone 1)	1,150-219
22	284	89.3	324	99	HUMIGKAC	Human Ig rearranged k	1,150-219
23	284	89.3	324	99	HUMIGKAC	Human sapiens immunoglobulin	1,150-219
24	284	89.3	327	96	HSIGKVEH	H sapiens mRNA for m	1,150-219
25	282	88.7	300	99	HUMIGKAC	Human sapiens (clone 1)	7,050-218
26	282	88.7	300	99	HUMIGKAC	Human sapiens (clone 1)	7,050-218
27	282	88.7	324	94	HSIGKVEH	Human clone 2951 Ig k	7,050-218
28	282	88.7	333	91	HSIGKVEH	H sapiens rearranged k	7,050-218
29	282	88.7	333	91	HSIGKVEH	H sapiens rearranged k	7,050-218
30	282	88.7	337	96	HSIGKVEH	Human Ig rearranged k	7,050-218
31	280	88.1	327	99	HUMIGKAC	Human immunoglobulin	4,310-216
32	280	88.1	327	99	HUMIGKAC	Human anti-glycoprotein	4,310-216
33	279	87.7	321	91	HSIGKVEH	H sapiens mRNA for Ig	3,960-215
34	278	87.4	327	99	HUMIGKAC	Human Ig rearranged k	3,960-215
35	278	87.4	327	99	HUMIGKAC	Human Ig rearranged k	2,630-214
36	278	87.4	351	91	HSIGKVEH	H sapiens rearranged k	2,630-214
37	278	87.4	351	91	HSIGKVEH	H sapiens rearranged k	2,630-214
38	278	87.4	402	93	HSIGKVEH	H sapiens rearranged k	2,630-214
39	276	86.8	300	99	HUMIGKAC	H sapiens (BPM16K) m	1,600-212
40	276	86.8	300	99	HUMIGKAC	H sapiens (BPM16K) m	1,600-212
41	276	86.8	327	136	HSIGKVEH	Human clone B5.3 immu	1,600-212
42	276	86.8	327	96	HSIGKVEH	Human clone B5.3 immu	1,600-212
43	276	86.8	327	96	HSIGKVEH	Human clone B5.3 immu	1,600-212
44	276	86.8	327	99	HUMIGKAC	Human Ig rearranged k	1,600-212
45	276	86.8	327	102	S4624P	Human Ig rearranged k	1,600-212

ALIGNMENTS

RESULT 1 HUMIGKAC 320 bp DNA PPI 04-JAN-1995
LOCUS Human Ig rearranged kappa chain V-JI-region gene, partial cds.
DEFINITION M28166
ACCESSION G185906
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain; immunoglobulin-kappa.
SOURCE Human lymphocyte DNA, from patient FCB with small lymphocytic lymphoma
ORGANISM Homo sapiens
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 320)
AUTHORS Pratt, L.F., Passaniti, L., Larrick, J., Robbins, B., Banks, P.M. and Kipps, T.J.
TITLE Ig V-region gene expression in small lymphocytic lymphoma with little or no somatic hypermutation

J Immunol 143 (2): 699-705 (1989)
 MEDLINE 89292697
 COMMENT Draft entry and printed sequence for [1] kindly submitted by L.F. Pratt, 20-SRP-J699
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 Best Local Similarity 97.4%; Pred. No. 2.17e-230;
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 QY 7 ACACAGCTCTCCAGGACCCCTGCTCTGTCTCCAGGGGAAGAGCCACCCTCTCTCAGG 66
 Db 67 gccagtcagagtgtagcagcagctactagcctgggtaccagcagaaacctggccagct 126
 QY 67 GCCAGTCAGAGTGTTAGCAGCAATTAATCTAGCTGTGTACACAGAGACCTGGGCGAGGCT 126
 Db 127 ccagagctctcatctatgtgctccagcagggccactggcctccagcagagcttcag 186
 QY 127 CCAGAGCTCTCATCTATGCTGCTATGCTCCAGCAGGGGCACTGGCATCTCCAGAGCTTCAGT 186
 Db 187 ggcagtggtctgggacagactctactctcaccatcagcagactggagcctgaagatttt 246
 QY 187 GGCAGTGGGCTGGGACAGACTTCACTCTCAACATACAGACTGGAGCTTGAAGATTTT 246
 Db 247 gcagttattctgcagcagtatgttagctcagctcagctgagcttcagccagagaccag 306
 QY 247 GCAGTGTATTACTGTCAGCTTTATGTAACTCACTGAGCTTGGAGCTTGGGAGGACCAAG 306
 Db 307 gtggagatcaaa 318
 QY 307 GTGGAGATCAAA 318
 RESULT 2
 LOCUS HSIGKV3C3 324 bp RNA PPI 30-MAP-1995
 DEFINITION H.sapiens mRNA for Ig kappa light chain variable region (V-J). Subgroup III (clone C3).
 ACCESSION X73863
 NID g516187
 KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup III; human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 324)
 REFERENCE Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B., Colls, J.C., Pegg, C.A.S., Rees-Smith, B. and Burton, D.P., 1995. Probing the human anti-thyroid peroxidase repertoire of a Hashimoto's thyroiditis patient using combinatorial phage display libraries.
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 324)
 AUTHORS Hexham, J.
 DIRECT SUBMISSION
 TITLE Submitted (25-JUN-1995); J. Hexham, Univ. of Sheffield, Dept. of Mol. Biology and Biotechnology, P.O. Box 594, Firth Court, Western Bank, Sheffield S10 2UH, UK
 JOURNAL
 REFERENCE 3 (bases 1 to 324)
 AUTHORS Hexham, J.M., Furmaniak, J., Pegg, C., Burton, D.P. and Smith, B.P.
 TITLE Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach
 JOURNAL Autoimmunity 12 (2), 135-141 (1992)
 MEDLINE 92314301
 REFERENCE 4 (bases 1 to 324)
 AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B., Colls, J.C., Pegg, C., Rees-Smith, B. and Burton, D.P.
 TITLE Cloning and characterisation of TPO autoantibodies using combinatorial phage display libraries
 JOURNAL Autoimmunity 17 (3), 167-179 (1994)
 MEDLINE 95035699
 FEATURES Location/Qualifiers
 source 1..324
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 /cell_type="thyroid lymphocyte"
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 Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Db 1 gagctccagcagctccagcagccctctctctctccaggggaagagccaccctctcc 60
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 Db 51 tgcaggggcagctcagctgtagcagcagctacttagctggtaccagcagaaacctggc 120
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 QY 121 CAGGCTCCAGGCT 180
 Db 181 ttcagtgagcagtggtctggagcagactctactctcaccatcagcagactgagactcaa 240
 QY 181 TTCAGTGAGCTGGGTCTGGGACAGACTTCACTCTCACTAGGAGAGGCTATGTCAGAG 240
 Db 241 gatcttcagctgattactgtcagcagctatggtggtccagcagggcagctccagcagag 300
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 QY 301 ACCAAGGTGGAGATCAAA 318
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 DEFINITION Human mRNA for Ig kappa L-chain variable region (Hunk-HIC).
 ACCESSION X06764 Y00648
 NID g33324
 KEYWORDS Ig kappa light chain; Ig light chain; immunoglobulin; variable region.
 SOURCE human.
 ORGANISM Homo sapiens

LOCUS HSICKVAH 402 bp PNA PRI 30-MAP-1995
 DEFINITION Human mRNA for Ig kappa L-chain variable region (HumkvHAH).
 ACCESSION X05763 Y00648
 NID Q33290
 KEYWORDS Ig kappa light chain; Ig light chain; immunoglobulin; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata.
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 402)
 Kipps, T.J.
 Direct Submission
 Submitted (08-FEB-1988) Kipps T.J., Scripps Clinic and Research Foundation, 10666 North Torrey Pines Road, La Jolla, California 92037
 REFERENCE 2 (bases 1 to 402)
 Kipps, T.J., Tomhave, E., Chen, P.P., and Carson, D.A.
 Antibody-Associated k Light Chain Variable Region Gene Expressed in Chronic Lymphocytic Leukemia with Little or No Somatic Mutation
 J. Exp. Med. 167 (1988) In press
 COMMENT see M15038 for corresponding genomic sequence.
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 49..402
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 Db 73 acgagctccaggaccctctgttctccaggaggaaagagccacctctctgcagg 132
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 Qy 67 GCGAGTCAGAGTGTACACCAATTACTTAGCTGTGTACACGACGAGCTGGCCAGGCT 126
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 Qy 127 CCGAGGCTCTCATCTATGTTGTATGTCAGGAGGAGGCTATGGATCCAGAGGTTAGT 186
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 Qy 187 GCGAGTCGGGCTGGGACACACTTCATCTCTACGATCAGCAGACTGGAGCTTGAAGATTT 245
 Db 313 gcaagtgattactgtagcagagtagtgtagctaccctggaagcagagcagagcagag 372
 Qy 247 GCACTGTATTACTTACCTTTATGCTTAACCTACCTTGGAGCTTGGGCAAGGACCAAG 306
 Db 373 gtggaatcaaa 384
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Qy 307 GTGAGATCAAA 318
 RESULT 6 HUMKVHVS 324 bp mRNA PRI 02-MAY-1996
 LOCUS Homo sapiens Ig kappa chain mRNA, V-region, partial cds.
 DEFINITION L37307
 ACCESSION
 NID Q845529
 KEYWORDS immunoglobulin light chain; kappa immunoglobulin, variable region.
 SOURCE Homo sapiens (clone: pAC41) cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 324)
 Ohlin, M., Sundqvist, V.A., Mach, M., Wahren, B. and Borrebaeck, C.A.
 Fine specificity of the human immune response to the major
 neutralization epitopes expressed on cytomegalovirus gp58/116 (gB),
 as determined with human monoclonal antibodies
 J. Virol. 67 (2): 703-710 (1993)
 REFERENCE 2 (bases 1 to 324)
 Ohlin, M., Wahren, B., Mach, M. and Borrebaeck, C.A.
 Light chain shuffling of a high affinity antibody results in a
 drift in epitope recognition
 Mol. Immunol. 33 (1): 47-56 (1996)
 JOURNAL 96174997
 MEDLINE Location/Qualifiers
 FEATURES
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 BASE COUNT 76 a 94 c 89 g 65 t
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 Matches 304; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Db 8 agatgacccagctccagagccctgtcttctgtctcaggaggaaagagccacctctcct 67
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 Qy 62 GCAGGCCAGTCAGAGCTCTTAGCAGCAATTAAGTTAGCTGTGTACGACGAGACTGGCC 121
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 Qy 122 AGGCTCCCGAGGCTCTCAICATCAIGTISGATCCAGAGAGGATCCAGATAGGT 181
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 Qy 182 TCAGTGGAGTGGTCTGGACACACTTCATCTCTCATTATCAGTAGACTGGAGCTTGAAG 241

Db 248 atttaccactattactacagagtagtactacacagggagacatttggcccaaggaa 307
 QY 242 atttaccactattactacagagtagtactacacagggagacatttggcccaaggaa 301
 Db 308 ccaagtagatgacaaa 324
 QY 302 ccaagtagatgacaaa 318
 RESULT 7 HS076682 324 bp mRNA PP1 18-NOV-1996
 LOCUS Human rearranged IgM light chain V region mRNA, partial cds.
 DEFINITION U76682
 ACCESSION g1673602
 NID
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 324)
 AUTHORS Aguilera, I.
 TITLE V region gene usage by autoreactive MoAbs
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 324)
 AUTHORS Aguilera, I.
 TITLE Direct Submission
 JOURNAL Submitted (30-OCT-1996) Aguilera I., Hospital U. Virgen del Rocío,
 Immunology, Manuel Sirot s/n, Seville, Spain, 41013
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 BASE COUNT 74 a 92 c 89 g 59 t
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 Query Match 91.2% Score 290 DB 95 Length 324
 Best Local Similarity 96.5% Pred. No. 5.03e-225
 Matches 301: Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Db 13 accagatctcagagacacatttctctccagggagaaagacacattctctcagg 72
 QY 7 AGSCATCTCCAGGACACCTGCTTGTCTGTCAGAGGAGGAGGAGGAGGAGG 66
 Db 73 gccatcagagtgtagcagcagctacttgcctgggtaccagcagaaacctggcaggct 132
 QY 67 GCACATCAGAGTGTTAGCAGCAATTAAGTCTGGTACAGAGAGAGAGAGAG 126
 Db 133 ccagagctctcattatggttgcagagggggccactggacatccagacagattcagtt 192
 QY 127 CCAGAGCTCTCATATATGTTGATCAGAGAGAGAGAGAGAGAGAGAGAGAG 186
 Db 193 ggtatgggttggag 262
 QY 187 GCACATGAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
 Db 263 ggaatgtatttctcagcagatattgtagctacattcagcagaggtcagcagag 312
 QY 247 GCAGTGTATTATGTTAGTTATAGTAACATCAGCTTGGAGCTTGGAGGAGAG 306
 Db 313 atcagaatcaaa 324
 QY 307 GTGGAGATCAAA 318

RESULT 8 HUMAB55 325 bp mRNA PRI 04-APR-1997
 LOCUS Human immunoglobulin (HAB55) light chain V region mRNA, partial
 DEFINITION sequence.
 ACCESSION D84139
 NID g1255609
 KEYWORDS immunoglobulin light chain V region,
 SOURCE Homo sapiens B cell hybridoma cell_line:AB55 producing hybridoma
 cell cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryotes; Eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
 REFERENCE 1 (bases 1 to 325)
 AUTHORS Ikematsu, H.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1996) to the DDBJ/EMBL/GenBank databases,
 Hideyuki Ikematsu, Kyushu University, Department of General
 Medicine, 3-1-1 Maidashi, Higashi-Ku, Fukuoka 812, JAPAN
 (E-mail: ikematsu@po.ijnet.or.jp, Tel:092-641-1151,
 Fax:092-691-7974)
 REFERENCE 2 (bases 1 to 322)
 AUTHORS Ikematsu, H.
 TITLE Light chain V region sequence
 JOURNAL Unpublished (1996)
 FEATURES
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 TKVEIK"
 BASE COUNT 76 a 91 c 90 g 58 t
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 Query Match 91.2% Score 290 DB 95 Length 325
 Best Local Similarity 96.5% Pred. No. 5.03e-225
 Matches 301: Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Db 13 accagatctcagagacacatttctctccagggagaaagacacattctctcagg 72
 QY 7 AGSCATCTCCAGGACACCTGCTTGTCTGTCAGAGGAGGAGGAGGAGGAGG 66
 Db 73 gccatcagagtgtagcagcagctacttgcctgggtaccagcagaaacctggcaggct 132
 QY 67 GCACATCAGAGTGTTAGCAGCAATTAAGTCTGGTACAGAGAGAGAGAGAG 126
 Db 133 ccagagctctcattatggttgcagagggggccactggacatccagacagattcagtt 192
 QY 127 CCAGAGCTCTCATATATGTTGATCAGAGAGAGAGAGAGAGAGAGAGAGAG 186
 Db 193 ggtatgggttggag 262
 QY 187 GCACATGAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
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 Db 313 atcagaatcaaa 324
 QY 307 GTGGAGATCAAA 318


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DEFINITION      Human Ig rearranged kappa-chain gene VJ125-Jk1 region, complete
ACCESSION       L32748
NID             4598157
KEYWORDS        kappa-immunoglobulin light chain; joining region;
SOURCE          Homo sapiens adult peripheral blood cDNA to mRNA.
ORGANISM        Homo sapiens
Eukaryotes:    mitochondrial eukaryotes: Metazoa; Chordata;
Vertebrata:    Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE       1 (bases 1 to 364)
AUTHORS         Ichiyoshi, Y. and Casali, P.
TITLE           Analysis of the structural correlates for antibody polyreactivity
                by multiple reassortments of chimeric human immunoglobulin heavy
                and light chain V segments.
JOURNAL         J. Exp. Med. 180 (3), 885-895 (1994)
MEDLINE         94342848
FEATURES        Location/Qualifiers
                 1..364
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Best Local Similarity 96.5%; Pred. No. 5.03e-225;
Matches 301; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 127 CCAAGCTCTCTATATATATATATATATATATATATATATATATATATATATAT 186

Db 233 gccagtcagagttttagagagagagagagagagagagagagagagagagagct 292
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QY 187 GCCAGTCAGAGCTTATAGAGCAATTAATTAATTAATTAATTAATTAATTAATTA 246

Db 293 gccagtcagagttttagagagagagagagagagagagagagagagagagagct 352
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QY 247 GCAGTATATATATATATATATATATATATATATATATATATATATATATATAT 306

Db 353 gtagaaatcaaa 364
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QY 307 GTGGAGATCAAA 318

RESULT 12
LOCUS           HUMIGKAI 402 bp mRNA PRI 15-DEC-1989
DEFINITION      Human Ig active kappa chain mRNA V-region (V-J1-C), clone NOV
ACCESSION       M27025
NID             4185845
KEYWORDS        C-region; V-region; immunoglobulin light chain;
SOURCE          Immunoglobulin-kappa; processed gene.
ORGANISM        Homo sapiens
Eukaryotes:    mitochondrial eukaryotes: Metazoa; Chordata;
Vertebrata:    Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE       1 (bases 1 to 402)
AUTHORS         Kips, J.J., Tomhave, E., Chen, P. and Fox, P. I.
TITLE           Molecular characterization of a major autoantibody-associated
                cross-reactive idiotype in Sjogren's syndrome
JOURNAL         J. Immunol. 142, 4261-4266 (1989)
MEDLINE         89256574
COMMENT         Draft entry and printed copy of sequence kindly submitted by

FEATURES        Location/Qualifiers
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Query Match     91.2% Score 290; DB 99; Length 402;
Best Local Similarity 96.5%; Pred. No. 5.03e-225;
Matches 301; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 73 acgagatctccaggagccctgtctttgtctccaggaggaagagccctctctcagg 132
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Db 193 cccagagctctctatctatggtgacacccagagagagagagagagagagagagct 252
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Db 313 gccagtcagagttttagagagagagagagagagagagagagagagagagagct 372
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Db 373 gtggaaatcaaa 384
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QY 307 GTGGAGATCAAA 318

RESULT 13
LOCUS           HSIGRHE18 312 bp RNA PRI 17-APR-1995
DEFINITION      H. sapiens (PFMP13K) mRNA for immunoglobulin mu chain variable
                region, rheumatoid factor (301bp)
ACCESSION       Z34964
NID             9510841
KEYWORDS        immunoglobulin mu chain variable region; rheumatoid factor;
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryotes:    mitochondrial eukaryotes: Metazoa; Chordata;
Vertebrata:    Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE       1 (bases 1 to 312)
AUTHORS         Thompson, K.M.
TITLE           Direct Submission
JOURNAL         Submitted (27-JUN-1994) Thompson K. M., L.G.R.I., Immunology, Fl.
                Quam, G.L., Oslo, Norway, 0172
REFERENCE       2 (bases 1 to 312)
AUTHORS         Borresen, M., Padden, I., Zdzarsky, E., Forre, O., Natvig, J.B. and
                Thompson, K.M.
TITLE           Control of autoantibody affinity by selection against amino acid
                replacements in the complementarity-determining regions
JOURNAL         Proc. Natl. Acad. Sci. U.S.A. 91 (26), 12617-12621 (1994)
MEDLINE         95108069
COMMENT         Location/Qualifiers

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factor; autoantibody; hybridomas; secreted immunoglobulin"
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BASE COUNT 74 a 90 c 83 g 65 t
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Best Local Similarity 96.8%; Pred No 3 93e-224;
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 1 cagctccagggaccctgtcttctccaggggaaagagccacccctctctcaggggcc 60
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Db 241 gtgtattactgtcagcagtagttagtaactcactcagcagcttcggcagcagcagcagtg 300
QY 250 GTGTATTACTGTGAGCTTTATGTAACCTACGTTGGACGTTTGGCCAGGACCAAGGTG 309
Db 301 gaaatcaaa 309
QY 310 GAGATCAAA 318

RESULT 14
LOCUS HSIGRH20 318 bp RNA PPT 11-APP-1095
DEFINITION H. sapiens (RFMP28K) mRNA for immunoglobulin mu chain variable
region, rheumatoid factor (318bp).
ACCESSION 234966
NID g510845
KEYWORDS immunoglobulin mu chain variable region; rheumatoid factor
SOURCE human
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 318)
AUTHORS Thompson, K.M.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Thompson K. M., I.G.R.I., Immunology, Fr.
Qvams St. 1, Oslo, Norway, 0172
PEREPECE 2 (bases 1 to 318)
AUTHORS Borretzen, M., Randsen, I., Zdarsky, E., Forre, O., Natvig, J.B. and
Thompson, K.M.

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TITLE Control of autoantibody affinity by selection against amino acid
replacements in the complementarity-determining regions
JOURNAL: Proc. Natl. Acad. Sci. U S A 91 (26): 12917-12921 (1994)
MEDLINE 95108069
FEATURES
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kappa chain; variable region; joining region; rheumatoid
factor; autoantibody; hybridomas; secreted immunoglobulin"
/codon_start=1
/product="IgM, variable region, rheumatoid factor,
autoantibody"
/db_xref="PID:g510846"
/translation="QSPGTLSPGERATLSGRASQSVSSSYLAWYQKPGAPRLLI
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KPTV"
BASE COUNT 75 a 91 c 86 g 66 t
ORIGIN
Query Match 90.9%; Score 289; DB 91; Length 319;
Best Local Similarity 96.8%; Pred No 3 93e-224;
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 1 cagctccagggaccctgtcttctccaggggaaagagccacccctctctcaggggcc 60
QY 10 CAGTCTCCAGGACCTGTGCTTTGCTCCAGGGAAAGAGGACCTCTCTCCAGGGCC 69
Db 61 agtcagaggttagcagcagctacttagcctgtgtaccagcagaaacctggccaggtccc 120
QY 70 AGTCAGAGGTTAGCAGCAATTAATAGCTGTGTACCAGCAGAGACTTGGCCAGGCTTCC 129
Db 121 aggtcctcatctatgtgtcaccagcagggccactggccatccacagaggttcagtgcc 180
QY 130 AGGCTCTCATCTATGTTGCTATCCAGCAGGGCCACTGGCATCCACAGAGGTTTCAGTGGC 189
Db 181 agtgggtctgggacagactctcaccatcagcagactgggagcctgaagatttgca 240
QY 190 AGTGGGTCTGGGACAGACTTCACTCTCACTATCAGCAGACTGGAGGCTTGAAGATTTTSCA 249
Db 241 gtgtattactgtcagcagtagttagtaactcactcagcagcttcggcagcagcagcagtg 300
QY 250 GTGTATTACTGTGAGCTTTATGTAACCTACGTTGGACGTTTGGCCAGGACCAAGGTG 309
Db 301 gaaatcaaa 309
QY 310 GAGATCAAA 318

RESULT 15
LOCUS HNMIGKAA 339 bp mRNA PPT 05-JAN-1995
DEFINITION Human Ig active kappa chain V-region gene NG9, V-kappa-3 mRNA,
partial cds.
ACCESSION K01321
NID g185813
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;
immunoglobulin kappa; immunoglobulin-kappa subgroup VK-5.
SOURCE Human NG9/9.1 hybridoma (mouse plasmacytoma fused with human spleen
cells); cDNA to mRNA, clones NG9/V-kappa-3 and NG9/3.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 100 to 339)

```

AUTHORS Bentley,D.L. and Rabbitts,T.H.
TITLE Human V kappa immunoglobulin gene number: implications for the
origin of antibody diversity
JOURNAL Cell 24 (3), 513-523 (1981)
MEDLINE 81234547
REFERENCE 2 (bases 1 to 300)
AUTHORS Bentley,D.L.
TITLE Most kappa immunoglobulin mRNA in human lymphocytes is homologous
to a small family of germ-line V genes
JOURNAL Nature 307 (5945), 77-80 (1984)
MEDLINE 84093600
COMMENT [1] and [2] claim that the majority of kappa mRNA (all V-region
sequences from subgroups 1 and 3) is encoded by approximately 25
germline V-region genes, and that the total number of human V-kappa
genes is about 50 or less. Thus, somatic mutation may be the major
source of human kappa-chain diversity [2]. Compared in [1] and [2]
with the subgroup V-kappa-1 germline V-region gene HK101.

FEATURES
source 1..339 /organism="Homo sapiens"
CDS 1..>339
/note="This CDS feature is included to show the
translation of the corresponding V-region. Presently
translation qualifiers on V-region features are illegal."
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/db_xref="PID:g185814"
/translation="VPSGEIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQOK
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FGQTKVEIR"
V_region 1..339
/partial
/note="Ig kappa light chain V-region mature peptide"
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misc_recomb 300..301
BASE COUNT 79 a 94 c 92 g 74 t
ORIGIN

Query Match 90.6% Score 288; DB 95; Length 339;
Best Local Similarity 96.2% Pred. No. 3,08e-223;
Matches 300; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Db 25 acgagctccagccacccctcttctccagggaagagccacccctctctcagcag 84
QY 7 ACCGAGCTCCAGGACCCCTCTCTTCTCCAGGGAAGAGCCACCCCTCTCTCAGG 66
Db 85 gccatcagatgttagcagcagctacttagccctgggtaccagagagaacccctggccaggct 144
QY 67 GCGACTCAGAGTGTTAGCAGCAATTAATTAAGCTGGTACCAGCAGAGACCTGGCCAGGCT 126
Db 145 cccagctccctcatctataggtgctaccagcagggccacctggcatccagacagagttcagt 204
QY 127 CCCAGGCTCCCTCATCTATGGTGCAATCCAGCAGAGGCGCCACTGGTCATCCAGACAGGTCAGT 186
Db 205 ggcagtcgctctggagacagcttcactctccatccatcagcagagctggagcctgaagatttt 264
QY 187 GCGAGTGGGCTGGACAGAGATTACCTCTCCATCAATCAGTACAGTGGAGCCGTAAGATTIT 246
Db 265 gcaatgtattactatcagcagctatggtaattccacagtggaagctgggccaagggaacaaag 324
QY 247 GCAAGTATTAATGACATGACATTTAATGGTAACACAGATGGAGAGGTTGGAGAGAGACCAAG 306
Db 325 atggaatacaaa 336
QY 307 GTGGAGATCAAA 318

Search completed: Tue Feb 24 07:09:30 1998
Job time : 544 secs.

WQRELE

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:29:34 1998 Master time 4.94 Seconds
454,909 Million cell updates/sec
Tabular output not generated

Title: >US-08-844-215-14
Description: (1-105) from US08844215.pep
Perfect Score: 749
Sequence: 1 AELTQSPSTLSLSPGEPATL YCCOYGTPTFGQTKVEIK 106

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs 21010399 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 40.434 Variance 69.990 scale 0.578

Pred. No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description Pred. No.
1	695	92 8	129 5 KV3L_HUMAN IG KAPPA CHAIN PRECUR 1 26e-133
2	679	90 7	129 5 KV3M_HUMAN IG KAPPA CHAIN PRECUR 7 77e-130
3	677	90 4	109 5 KV3E_HUMAN IG KAPPA CHAIN V-III 2 31e-129
4	676	90 3	109 5 KV3D_HUMAN IG KAPPA CHAIN V-III 3 98e-129
5	655	88 8	104 5 KV3A_HUMAN IG KAPPA CHAIN V-III 1 59e-126
6	654	88 0	104 5 KV3G_HUMAN IG KAPPA CHAIN V-III 4 16e-125
7	658	87 9	109 5 KV3C_HUMAN IG KAPPA CHAIN V-III 7 15e-125
8	602	80 4	100 5 KV3K_HUMAN IG KAPPA CHAIN PRECUR 1 11e-111
9	602	80 4	129 5 KV3L_HUMAN IG KAPPA CHAIN PRECUR 1 11e-111
10	600	80 1	104 5 KV3H_HUMAN IG KAPPA CHAIN V-III 3 29e-111
11	599	80 0	129 5 KV3H_HUMAN IG KAPPA CHAIN PRECUR 5 60e-111
12	560	74 8	115 5 KV3I_HUMAN IG KAPPA CHAIN PRECUR 7 62e-102
13	543	72 5	116 5 KV3J_HUMAN IG KAPPA CHAIN PRECUR 7 06e-98
14	540	72 1	108 5 KV1H_HUMAN IG KAPPA CHAIN V-I RE 3 53e-97
15	531	70 9	108 5 KV1M_HUMAN IG KAPPA CHAIN V-I RE 4 40e-95
16	530	70 8	108 5 KV1N_HUMAN IG KAPPA CHAIN V-I RE 7 53e-95
17	524	70 0	108 5 KV1K_HUMAN IG KAPPA CHAIN V-I RE 1 87e-93
18	523	69 8	107 5 KV1D_HUMAN IG KAPPA CHAIN V-I RE 3 19e-93
19	521	69 6	104 5 KV1F_HUMAN IG KAPPA CHAIN V-I RE 9 29e-93
20	519	69 3	114 5 KV4C_HUMAN IG KAPPA CHAIN PRECUR 2 71e-92
21	513	68 5	133 5 KV4B_HUMAN IG KAPPA CHAIN PRECUR 6 69e-91
22	512	68 4	108 5 KV1B_HUMAN IG KAPPA CHAIN V-I RE 1 14e-90

RESULT 1
ID KV3L_HUMAN STANDARD: PRI: 129 AA.
AC P18135;
DI 01-NOV-1990 (REL. 16, CREATED)
DI 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DI 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAH).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
OC EUTHERIA, PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.:
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10022; K3H0HA.
DR HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14073 MW: 2044885E CRC32:
Query Match 92 98; Score 695; DB 5; Length 129;
Best Local Similarity 94 10; Pred. No. 125e-133;
Matches 99; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 24 140spstlsdgeratiscragssy1aw7qgkqaprllyqasaraaipdrf 83
QY 3 140spstlsdgspefatulscpaslskylaw7qgkqaprllyqasaraaipdrf 62
Db 84 sqsgsqdftltistlepdefvyyvgygysprtfgggtkveik 128
QY 63 SQSGSGIDILISLRLLEDFAVYVCUUYGI-PRTFGGGSIKVEIK 105

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RESULT 2
ID KV3D_HUMAN STANDARD: PRT: 129 AA.
AC P01620:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (HIC)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 8611307.
RA KIPPS T.J., TOMHAVE F., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P00021; K3HUHI.
DR HSSP; P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 22 45 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; D030C369 CRC32;

Query Match 90.7%; Score 679; DB 5; Length 129;
Best Local Similarity 91.4%; Pred. No. 7,77e-130;
Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Db 24 ltqspgtlslspgeratlscrasqssvssylawyqkpgqaprllygassratgipdrf 83
QY 3 LTQSPGTLSPGERATLSRASQSLSSKYLAWYQKPGQAPRLFIYDASSRATGIPDRF 62

Db 84 sgsqsgtdftlslrlepddfavyyccqygssptfaggkveik 128
QY 63 SSGSGGDTFTLSRLEPEDFAVYYCQYGT-PRTFGGGKVEIK 106

RESULT 3
ID KV3B_HUMAN STANDARD: PRT: 109 AA.
AC P01620:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR; A01892; K3HUST.
DR HSSP; P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 00B5DD5D CRC32;

Query Match 90.4%; Score 677; DB 5; Length 109;

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Best Local Similarity 89.5%; Pred. No. 2.31e-129;
Matches 94; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

Db 4 ltqspgtlslspgeratlscrasqssvssylawyqkpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSRASQSLSSKYLAWYQKPGQAPRLFIYDASSRATGIPDRF 62

Db 64 sgsqsgtdftlslrlepddfavyyccqygssptfaggkveik 108
QY 53 SSGSGGDTFTLSRLEPEDFAVYYCQYGT-PRTFGGGKVEIK 106

RESULT 4
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01623:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR; A01896; K3HULW.
DR HSSP; P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 7D8F5D75 CRC32;

Query Match 90.3%; Score 676; DB 5; Length 109;
Best Local Similarity 91.4%; Pred. No. 3.08e-129;
Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltqspgtlslspgeratlscrasqssvssylawyqkpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSRASQSLSSKYLAWYQKPGQAPRLFIYDASSRATGIPDRF 62

Db 64 sgsqsgtdftlslrlepddfavyyccqygslgrtfaggkveik 108
QY 63 SSGSGGDTFTLSRLEPEDFAVYYCQYGT-PRTFGGGKVEIK 106

RESULT 5
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01622:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TI)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 72188439.
RA SUITEP L., BARNIKOL H., WATANABE S., HILSCHMANN N.;
PL HOPPE-SPELTER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01895; K3HUTI.
DR HSSP; P01607; 2IMW.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; D03795B1 CRC32;

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Query Match 4 98.8% Score 645; DB 5; Length 109;
 Best Local Similarity 78.5% Pred No. 159-159;
 Matches 94; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 63
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 QY 3 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 62
 |||||

Db 64 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 108
 |||||
 QY 63 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 106
 |||||

RESULT 6
 ID KV3C_HUMAN STANDARD: PRT: 108 AA.
 AC P01619;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN PFCUPSOR V-III REGION (NG9) (FRAGMENT).
 DE IG KAPPA CHAIN V-III REGION (B6).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE; 84093600.
 RA BENTLEY D.L.;
 RL NATURE 307:77-80(1984).
 CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9 1 HYBRIDOMA.
 DE PIR: A01894; K3HUNG.
 DR HSP: P01607; IMGP.
 KW IMMUNOGLOBULIN V REGION; RENCE-JONES PROTEIN.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON-TER 108 108
 SQ SEQUENCE 108 AA; 11635 MW; 4805868E CRC32;

Query Match 88.0% Score 659; DB 5; Length 108;
 Best Local Similarity 83.8% Pred. No. 4.15e-125;
 Matches 88; Conservative 13; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 63
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 QY 3 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 62
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Db 64 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 108
 |||||
 QY 63 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 106
 |||||

RESULT 7
 ID KV3C_HUMAN STANDARD: PRT: 109 AA.
 AC P04205;
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-III REGION (NG9) (PHEMATELID FAVOR)
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE; 86230578.
 RA NEWKIRK M., CHEN P., CAPSON D.A., DOSNETT D., CAPPA J.D.;
 RL MOL. IMMUNOL. 23:239-244(1986).
 DR PIR: A01893; K3HUNG.
 DR HSP: P01607; IDPB.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON-TER 109 109
 SQ SEQUENCE 109 AA; 11830 MW; 893DC04A CRC32;

Query Match 87.9% Score 658; DB 5; Length 109;
 Best Local Similarity 88.7% Pred No. 7.16e-125;
 Matches 94; Conservative 7; Mismatches 2; Indels 3; Gaps 2;

Db 4 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 62
 |||||
 QY 3 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 61
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Db 63 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 108
 |||||
 QY 62 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 106
 |||||

RESULT 8
 ID KV3C_HUMAN STANDARD: PRT: 100 AA.
 AC P01621;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN PFCUPSOR V-III REGION (NG9) (FRAGMENT).
 DE IG KAPPA CHAIN PFCUPSOR V-III REGION (NG9) (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE; 84093600.
 RA BENTLEY D.L.;
 RL NATURE 307:77-80(1984).
 CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9 1 HYBRIDOMA.
 DE PIR: A01894; K3HUNG.
 DR HSP: P01607; IMGP.
 KW IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA.
 FT NON-TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).
 FT DISULFID 27 93 BY SIMILARITY.
 FT NON-TER 100 100
 SQ SEQUENCE 100 AA; 10729 MW; 99A7E223 CRC32;

Query Match 80.4% Score 602; DB 5; Length 100;
 Best Local Similarity 89.2% Pred. No. 1.11e-111;
 Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 8 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 67
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 QY 3 ltsqptslsppgratlsctasqslsnylawyqkqgqaprllyvassratgipdrf 62
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Db 68 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 100
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 QY 63 sdsqsgtdftltisrlepedfavyvccqygsspsatfgqgkveik 95
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RESULT 9
 ID KV3C_HUMAN STANDARD: PRT: 128 AA.
 AC P06311;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN PFCUPSOR V-III REGION (IARC/RL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE; 86041852.
 RA KLORECH H.G., WEINFLA., GUMPERT G., ELLMANN A., RAHBE H.3.;
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL; 200021; G33179; .
 DR PIR: A01899; K3HUNG.
 DR HSP: P01607; 3HEM.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON-TER 1 20
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/RL41).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 60 FRAMEWORK 2.

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DR EMRI; M12740; G553486; -
DR DR PIR: A01898; K3H0CL
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (CLL).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 2F344868 CRC32;

Query Match 80.08; Score 599; DB 5; Length 129;
Best Local Similarity 79.28; Pred No. 5 60e-111;
Matches 84; Conservative 15; Mismatches 4; Indels 3; Gaps

Db 24 mtqspatlsppgratlsracsqssvnn-lavyqkqkqpprlllyqasrtaqparf 82
QY 3 LTQSPGDTLSLSPGPATLSLSPASQSSSKYLAWYQQKPKAPRLFIYASSPATGIPPPF 42
DB 83 sgsqsgtdftltisrlgsdfavyqqqynnpwplfgqgtveik 128
QY 63 SSGSGTDTLTLISLPLEPDPFAVYQQYGT--PPTFGGTTKVEIK 106

RESULT 12
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (PEL C5, CREATED)
DD 13-AUG-1987 (PEL C5, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (PEL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VC) (FRAGMENT).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA, PRIMATES.
RN [1]
RS SEQUENCE FROM N.A.
RP RP MEDLINE: 85087932
RA PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES 12:9239-9236(1984)
RE EMBL; X01668; -- NOT_ANNOTATED_CDS.
RF PIR: A01908; K3H0VG
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 ~115 IG KAPPA CHAIN V-III REGION (VC).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E182FC CRC32;

Query Match 74.88; Score 560; DB 5; Length 115;
Best Local Similarity 90.94; Pred. No. 7.52e-102;
Matches 80; Conservative 5; Mismatches 2; Indels 1; Gaps

Db 24 itqspatlsppgratlsracsqssv-lavyqkqkqpprlllyqasrtaqparf 82
QY 3 LTQSPGDTLSLSPGPATLSLSPASQSSSKYLAWYQQKPKAPRLFIYASSPATGIPPPF 42
DB 83 sgsqsgtdftltisrlgsdfavyqqq 110
QY 63 SSGSGTDTLTLISLPLEPDPFAVYQQ 90

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RESULT 13
ID KVAL_HUMAN STANDARD: PRT: 116 AA.
AC P0434:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932
RA PECH M., ZACHAU H.G.:
PE NUCLEIC ACID RES. 12:9220-9236(1984).
DR EMBL: X02725: -; NOT_ANNOTATED_CDS.
DR PIR: A01901: K3HUVH.
DR HSP: P01607: LMCP.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 22 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 23 56 70 FRAMEWORK 2.
FT DOMAIN 24 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 25 78 109 FRAMEWORK 3.
FT DOMAIN 26 110 116 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA: 12757 MW: 27FAIRCE CPC32:
Query Match 72.5% Score 543. DB 5. Length 116.
Best Local Similarity 84.1% Pred No. 7 Use-aa:
Matches 74: Conservative 8: Mismatches 6: Indels 0: Gaps 0:

Db 24 mtqspstlsppgervtlscrasgssvssytlwqqkqgqprlllygastratsiparf 83
QY 3 LTQSPGTLSPGPATLSCPASQSSSKYLAWYTKPKQAPPLFIYDASSPAIGIKV 62

Db 84 sgsqsttdftlslapdfavyyccq 111
QY 63 SSGSGGTDFTLSISPLEPEFAVYYCCQ 90

RESULT 14
ID KVAL_HUMAN STANDARD: PRT: 108 AA.
AC P01600:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 05, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (HAU).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 71032830.
RA WATANABE S., HILSCHMANN M.:
RL HOPPE-SEILER S. Z. PHYSIOL. CHEM. 351:1291-1295(1970).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (I) SAKREF.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01968: KIHUHG.
DR HSP: P01607: IFVC.
KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 25 35 49 FRAMEWORK 2.
FT DOMAIN 26 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 27 57 88 FRAMEWORK 3.
FT DOMAIN 28 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 29 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11934 MW: 2228RQC CPC32:
Query Match 70.9% Score 531. DB 5. Length 108.
Best Local Similarity 65.1% Pred No. 4 Use-aa:
Matches 69: Conservative 27: Mismatches 12: Indels 2: Gaps 2:

Db 3 gntdspslsasvdrvtlscrasgssvssytlwqqkqgqprlllygastratsiparf 61
QY 2 ELTSPGTLSPGPATLSCPASQSSSKYLAWYTKPKQAPPLFIYDASSPAIGIKV 61

Db 62 fsgsgsttdftlslapdfavyyccq 107
QY 62 PSGSGGTDFTLSISPLEPEFAVYYCCQYCT-PPFEGGQIKVEIK 106

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Search completed: Tue Feb 24 07:29:48 1998
Job time : 14 secs.

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FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11671 MW: C9A2EE86 CPC32:
Query Match 72.1% Score 540. DB 5. Length 108.
Best Local Similarity 69.8% Pred No. 3 Use-aa:
Matches 74: Conservative 19: Mismatches 11: Indels 2: Gaps 2:

Db 3 gntdspslsasvdrvtlscrasgssvssytlwqqkqgqprlllygastratsiparf 61
QY 2 ELTSPGTLSPGPATLSCPASQSSSKYLAWYTKPKQAPPLFIYDASSPAIGIKV 61

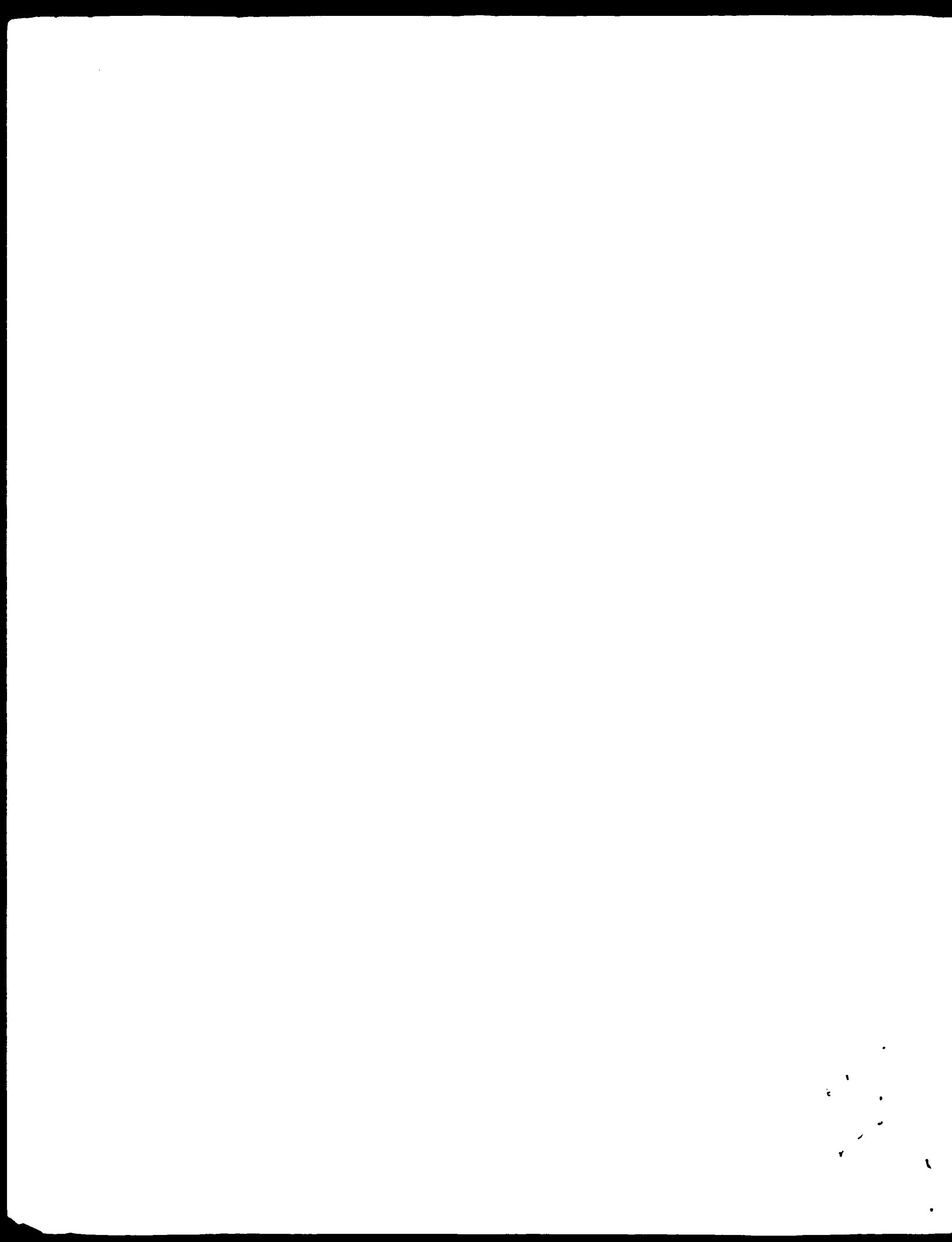
Db 62 fsgsgsttdftlslapdfavyyccq 107
QY 62 PSGSGGTDFTLSISPLEPEFAVYYCCQYCT-PPFEGGQIKVEIK 106

RESULT 15
ID KVAL_HUMAN STANDARD: PRT: 108 AA.
AC P01605:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAY).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 77038198.
RA CAPPA J.D., KLAPPEP D.G.:
PE SCAND. J. IMMUNOL. 5:677-684(1976).
CC -1- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN FCμ V-III KAPPA CHAIN. WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
DR PIR: A01871: KIHULY.
DR HSP: P01607: 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 25 35 49 FRAMEWORK 2.
FT DOMAIN 26 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 27 57 88 FRAMEWORK 3.
FT DOMAIN 28 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 29 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11934 MW: 2228RQC CPC32:
Query Match 70.9% Score 531. DB 5. Length 108.
Best Local Similarity 65.1% Pred No. 4 Use-aa:
Matches 69: Conservative 27: Mismatches 12: Indels 2: Gaps 2:

Db 3 gntdspslsasvdrvtlscrasgssvssytlwqqkqgqprlllygastratsiparf 61
QY 2 ELTSPGTLSPGPATLSCPASQSSSKYLAWYTKPKQAPPLFIYDASSPAIGIKV 61

Db 62 fsgsgsttdftlslapdfavyyccq 107
QY 62 PSGSGGTDFTLSISPLEPEFAVYYCCQYCT-PPFEGGQIKVEIK 106

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W P E R E H

(TM)

Release 2.10 John F. Collins, Biocomputing Research Unit
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MPSrch_pp1 protein - protein database search using Smith-Waterman algorithm

Run on: Tue Feb 24 07:57:15 1998: MasPar time 4.09 Seconds
Tabular output not generated: 131 950 Million cell updates/sec

Title: >US-08-844-215-14
Description: (1-106) from US08844215.pep
Perfect Score: 749
Sequence: 1 AELTQSPGTLSPGERATL.....YCCQYGTPTFGGKTKVEIK 106

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1.back1 2.51 3.52 4.53 5.54 6.55 7.56 8.PCT90 9.PCT91
10.PCT92 11.PCT93 12.PCT94 13.PCT95 14.PCT96

Statistics: Mean 27.184: Variance 144.390: scale 0.188

Pred. No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Pred No
1	676	90.3	108	7	US-08-474-	Sequence 86, Applicati	5.02e-44
2	676	90.3	108	7	US-08-487-	Sequence 86, Applicati	5.02e-44
3	676	90.3	108	6	US-08-477-	Sequence 86, Applicati	5.02e-44
4	675	90.3	108	6	US-07-634-	Sequence 86, Applicati	5.02e-44
5	675	90.1	109	13	PCT-US95-0	Sequence 147, Applicat	6.02e-44
6	675	90.1	109	7	US-08-276-	Sequence 99, Applicati	6.02e-44
7	670	89.5	104	7	US-08-276-	Sequence 99, Applicati	1.50e-43
8	670	89.5	104	13	PCT-US95-0	Sequence 99, Applicati	1.50e-43
9	666	88.9	104	7	US-08-276-	Sequence 86, Applicati	3.10e-43
10	666	88.9	104	13	PCT-US95-0	Sequence 86, Applicati	3.10e-43
11	666	88.9	111	13	US-08-276-	Sequence 149, Applicat	3.10e-43
12	665	88.9	111	13	PCT-US95-0	Sequence 149, Applicat	3.10e-43
13	663	88.5	107	13	PCT-US95-0	Sequence 90, Applicati	5.36e-43
14	663	88.5	107	7	US-08-276-	Sequence 90, Applicati	5.36e-43
15	656	87.6	104	11	PCT-US93-0	Sequence 23, Applicati	1.92e-42
16	650	86.8	104	13	PCT-US95-0	Sequence 100, Applicat	5.71e-42
17	650	86.8	104	7	US-08-276-	Sequence 100, Applicat	5.71e-42
18	641	85.6	108	7	US-08-276-	Sequence 110, Applicat	2.94e-41
19	641	85.6	108	13	PCT-US95-0	Sequence 110, Applicat	2.94e-41
20	628	83.8	107	7	US-08-276-	Sequence 87, Applicati	3.12e-40
21	628	83.8	107	13	PCT-US95-0	Sequence 87, Applicati	3.12e-40
22	626	83.4	104	13	PCT-US95-0	Sequence 95, Applicati	4.49e-40

23	626	83.6	108	7	US-08-276-	Sequence 96, Applicati	4.49e-40
24	619	82.6	104	11	PCT-US93-0	Sequence 24, Applicati	1.50e-39
25	618	82.5	112	7	US-08-276-	Sequence 151, Applicat	1.92e-39
26	618	82.5	112	13	PCT-US95-0	Sequence 151, Applicat	1.92e-39
27	616	82.2	104	13	PCT-US95-0	Sequence 94, Applicati	2.76e-39
28	616	82.2	104	7	US-08-276-	Sequence 94, Applicati	2.76e-39
29	612	81.7	105	7	US-08-276-	Sequence 93, Applicati	5.71e-39
30	612	81.7	105	13	PCT-US95-0	Sequence 93, Applicati	5.71e-39
31	611	81.6	116	7	US-08-053-	Sequence 183, Applicat	5.85e-39
32	610	81.4	108	13	PCT-US95-0	Sequence 88, Applicati	8.21e-39
33	610	81.4	108	7	US-08-276-	Sequence 88, Applicati	8.21e-39
34	594	79.3	107	13	PCT-US95-0	Sequence 118, Applicat	1.50e-37
35	594	79.3	107	7	US-08-276-	Sequence 118, Applicat	1.50e-37
36	594	79.3	107	7	US-08-276-	Sequence 116, Applicat	1.50e-37
37	594	79.3	107	13	PCT-US95-0	Sequence 116, Applicat	1.50e-37
38	591	78.9	107	7	US-08-276-	Sequence 117, Applicat	2.58e-37
39	591	78.9	107	13	PCT-US95-0	Sequence 117, Applicat	2.58e-37
40	590	78.8	104	13	PCT-US95-0	Sequence 92, Applicati	3.10e-37
41	590	78.8	104	7	US-08-276-	Sequence 92, Applicati	3.10e-37
42	586	78.2	107	7	US-08-487-	Sequence 63, Applicati	6.39e-37
43	586	78.2	107	6	US-08-477-	Sequence 63, Applicati	6.39e-37
44	586	78.2	107	6	US-08-477-	Sequence 87, Applicati	6.39e-37
45	586	78.2	107	7	US-08-474-	Sequence 63, Applicati	6.39e-37

ALIGNMENTS

RESULT 1
ID US-08-474-040-86 STANDARD: PRI: 108 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE Sequence 86, Application US/08474040.
XX
CC Sequence 86, Application US/08474040
CC Patent No. 5693761
CC GENERAL INFORMATION:
CC APPLICANT: OUEEN, Cary L.
CC APPLICANT: CO, Man Sung L.
CC APPLICANT: SCHNEIDER, William P
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/410,252
CC FILING DATE: 19-FEB-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975

CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;
CC
CC Query Match 90.3%; Score 676; DB 7; Length 108;
CC Best Local Similarity 91.4%; Pred. No. 5.02e-44;
CC Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
CC
D6 4 LTQSPGTLSPGERATLSPASQSVSSGVLGWYQKPGQAPPLIYGASSRATGIPDRF 63
QY 3 LTQSPGTLSPGERATLSPASQSVSSGVLGWYQKPGQAPPLIYGASSRATGIPDRF 62
D6 64 SGSGSGDTFTLTISPLEPEDFAVYVCOQYGLGPTFGQGTKEIK 108
QY 63 SGSGSGDTFTLTISPLEPEDFAVYVCOQYGLGPTFGQGTKEIK 106
CC
CC RESULT 2
CC ID US-08-487-200-86 STANDARD: PRT: 108 AA
CC XX xxxxxx
CC XX 01-JAN-1900
CC DE Sequence 86, Application US/08487200.
CC XX
CC Sequence 86, Application US/08487200
CC Patent No. 5693762
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: CORLEIGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: 379 Lytton Avenue
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/487,200
CC FILING DATE: 7-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/310,352
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002610
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;
CC
CC Query Match 90.3%; Score 676; DB 7; Length 108;
CC Best Local Similarity 91.4%; Pred. No. 5.02e-44;
CC Matches 96; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
CC
D6 4 LTQSPGTLSPGERATLSPASQSVSSGVLGWYQKPGQAPPLIYGASSRATGIPDRF 63
QY 3 LTQSPGTLSPGERATLSPASQSVSSGVLGWYQKPGQAPPLIYGASSRATGIPDRF 62
D6 64 SGSGSGDTFTLTISPLEPEDFAVYVCOQYGLGPTFGQGTKEIK 108
QY 63 SGSGSGDTFTLTISPLEPEDFAVYVCOQYGLGPTFGQGTKEIK 106
CC
CC RESULT 3
CC ID US-08-477-728-86 STANDARD: PRT: 108 AA
CC XX xxxxxx
CC XX 01-JAN-1900
CC DE Sequence 86, Application US/08477728
CC XX
CC Sequence 86, Application US/08477728
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/210,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 54079 CN:

Query Match 90.3% Score 676: DB 6: Length 108;
Best Local Similarity 91.4% Pred No 5 02e-44;
Matches 96: Conservative 5: Mismatches 3: Indels 1: Gaps 1:

DB 4 LTQSPGTLSPGEPATLSPASQSVSSGYLWYQKPGQAPRLIYGCASSPATGIPDRF 63
QY 3 LTQSPGTLSPGEPATLSPASQSVSSGYLWYQKPGQAPRLIYGCASSPATGIPDRF 62

DB 64 SSGSGTDFTLTISPLEPEFAVYCCQYQSLGRTFGQKVEIK 108
QY 63 SSGSGTDFTLTISPLEPEFAVYCCQYGT-PRTFQGIKVEIK 105

RESULT 4
ID US-07-634-278-86 STANDARD: PPT: 108 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 86, Application US/07634278.
CC Sequence 86, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO. Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELING, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 170 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274

CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/210,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 54079 CN:

Query Match 90.3% Score 676: DB 6: Length 108;
Best Local Similarity 91.4% Pred No 5 02e-44;
Matches 96: Conservative 5: Mismatches 3: Indels 1: Gaps 1:

DB 4 LTQSPGTLSPGEPATLSPASQSVSSGYLWYQKPGQAPRLIYGCASSPATGIPDRF 63
QY 3 LTQSPGTLSPGEPATLSPASQSVSSGYLWYQKPGQAPRLIYGCASSPATGIPDRF 62

DB 64 SSGSGTDFTLTISPLEPEFAVYCCQYQSLGRTFGQKVEIK 108
QY 63 SSGSGTDFTLTISPLEPEFAVYCCQYGT-PRTFQGIKVEIK 105

RESULT 5
ID PCT-US95-08743-147 STANDARD: PPT: 109 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 147, Application PC/TUS9508743.
CC Sequence 147, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNOEFFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (LPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: Pct/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 147:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA: 11779 MW: 55550 CN:

Query Match 90.1% Score 675: DB 13: Length 109;
Best Local Similarity 88.7% Pred. No 5 02e-44;
Matches 94: Conservative 8: Mismatches 4: Indels 0: Gaps 0:

Db 2 AELTSPGTLSPGERVIVSCRASQSSVSNLYAWYQKQKQAPRLIYGASNRATGIPD 61
 QY 1 AELTSPGTLSPGERATLSCRASQSSLSKYLAUWQKQKQAPPLFIYDASSRATGIPD 60
 Db 62 RFSGSGGTDTLTISRLEPEDFAVYVCOQYSGSGTGQGTKEIK 107
 QY 61 RFSGSGGTDTLTISRLEPEDFAVYVCOQYGTPTFTGQGTKEIK 106

RESULT 6
 ID US-08-276-852-147 STANDARD: PRT: 109 AA.
 AC xxxxxx
 XX 01-JAN-1900
 DE Sequence 147, Application US/08276852.
 CC Sequence 147, Application US/08276852.
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis P
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10466 No 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC FILING DATE: 30-SEP-1992
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCPI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 147:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 109 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 109 AA: 11779 MW: 65550 CN;

Query Match 90.1%; Score 675; DB 7; Length 109;
 Best Local Similarity 88.7%; Pred. No. 6.02e-44;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0.

Db 2 AELTSPGTLSPGERVIVSCRASQSSVSNLYAWYQKQKQAPRLIYGASNRATGIPD 61
 QY 1 AELTSPGTLSPGERATLSCRASQSSLSKYLAUWQKQKQAPPLFIYDASSRATGIPD 60
 Db 62 RFSGSGGTDTLTISRLEPEDFAVYVCOQYSGSGTGQGTKEIK 107
 QY 61 RFSGSGGTDTLTISRLEPEDFAVYVCOQYGTPTFTGQGTKEIK 106

QY 1 AELTSPGTLSPGERATLSCRASQSSLSKYLAUWQKQKQAPRLFIYDASSRATGIPD 60
 Db 62 RFSGSGGTDTLTISRLEPEDFAVYVCOQYSGSGTGQGTKEIK 107
 QY 61 RFSGSGGTDTLTISRLEPEDFAVYVCOQYGTPTFTGQGTKEIK 106

RESULT 7
 ID US-08-276-852-99 STANDARD: PRT: 108 AA.
 AC xxxxxx
 XX 01-JAN-1900
 DE Sequence 99, Application US/08276852.
 CC Sequence 99, Application US/08276852.
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis P
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10466 No 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCPI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 99:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA: 11738 MW: 63142 CN;

Query Match 89.5%; Score 670; DB 7; Length 108;
 Best Local Similarity 89.6%; Pred. No. 1.50e-43;
 Matches 95; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

Db 1 ELTOSPGTLSPGERATLSCRASQSSVSNLYAWYQKQKQAPPLIYGASNRATGIPD 60
 QY 2 ELTOSPGTLSPGERATLSCRASQSSLSKYLAUWQKQKQAPPLFIYDASSRATGIPD 61
 Db 61 RFSGSGGTDTLTISRLEPEDFAVYVCOQYGTPTFTGQGTKEIK 106

QY 62 FSGSGGDTFTLSISRLPEPEFAVYQQYGT-PPFQGGTKVEIK 106

RESULT 8
ID PCT-US95-08743-86 STANDARD: PRI: 106 AA.

XX XXXXXX

DT 01-JAN-1900

DE Sequence 86, Application PCT/US9508743

XX Sequence 86, Application PCT/US9508743

CC GENERAL INFORMATION:

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1 0, Version #1 25 (EPO)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/08743

CC FILING DATE: 11-JUL-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/276,852

CC FILING DATE: 18-JUL-1994

CC INFORMATION FOR SEQ ID NO: 99:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 108 AA: 11738 MW: 63142 CN:

Query Match 89.5%; Score 670; DB 13; Length 108;

Best Local Similarity 89.6%; Pred No. 1,50e-43;

Matches 95; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

Db 1 ELTQSGTSLSPGERATLSRPAQSISNNYLAWYQKPGQAPRLIYGSNRAIGIFDR 60

QY 2 ELTQSGTSLSPGERATLSRPAQSISNNYLAWYQKPGQAPRLIYGSNRAIGIFDR 61

Db 61 FSGSGGDTFTLSISRLPEPEFAVYQQYGTSPYIFGGTGLDIK 106

QY 62 FSGSGGDTFTLSISRLPEPEFAVYQQYGT-PPFQGGTKVEIK 106

RESULT 9

ID US-08-276-852-86 STANDARD: PRI: 108 AA.

XX XXXXXX

DT 01-JAN-1900

CC STREET: Mail Drop IPCB

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1 0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US 08/276,852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCR1452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 86:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 108 AA: 11769 MW: 65957 CN:

Query Match 88.9%; Score 566; DB 7; Length 106;

Best Local Similarity 89.6%; Pred. No. 3.10e-43;

Matches 95; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Db 1 ELTQSGTSLSPGERATLSRPAQSISNNYLAWYQKPGQAPRLIYGSNRAIGIFDR 60

QY 2 ELTQSGTSLSPGERATLSRPAQSISNNYLAWYQKPGQAPRLIYGSNRAIGIFDR 61

Db 61 FSGSGGDTFTLSISRLPEPEFAVYQQYGTSPYIFGGTGLDIK 106

QY 62 FSGSGGDTFTLSISRLPEPEFAVYQQYGT-PPFQGGTKVEIK 106

RESULT 10

ID PCT-US95-08743-86 STANDARD: PRI: 108 AA.

XX XXXXXX

DT 01-JAN-1900

DE Sequence 86, Application PCT/US9508743.

XX Sequence 86, Application PCT/US9508743

CC GENERAL INFORMATION:

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1 0, Version #1.25 (EPO)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/08743

CC FILING DATE: 11-JUL-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/276,852

CC FILING DATE: 18-JUL-1994

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCR1452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 86:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 108 AA: 11769 MW: 65957 CN:

Query Match 88.9%; Score 566; DB 7; Length 106;

Best Local Similarity 89.6%; Pred. No. 3.10e-43;

Matches 95; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Db 1 ELTQSGTSLSPGERATLSRPAQSISNNYLAWYQKPGQAPRLIYGSNRAIGIFDR 60

QY 2 ELTQSGTSLSPGERATLSRPAQSISNNYLAWYQKPGQAPRLIYGSNRAIGIFDR 61

Db 61 FSGSGGDTFTLSISRLPEPEFAVYQQYGTSPYIFGGTGLDIK 106

QY 62 FSGSGGDTFTLSISRLPEPEFAVYQQYGT-PPFQGGTKVEIK 106

CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65967 CN;
Query Match 88.9%; Score 666; DB 13; Length 108;
Best Local Similarity 86.8%; Pred No 3 10e-43;
Matches 95; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
Db 1 ELTQSPGTLISLSPGERATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 60
QY 2 ELTQSPGTLISLSPGERATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 61
Db 61 FSGSGSGDTFTLSISPLEPDEFVAVYCCQYGTSPWTFGGTKVEIK 106
QY 62 FSGSGSGDTFTLSISPLEPDEFVAVYCCQYGTSPWTFGGTKVEIK 106
RESULT 11
ID US-08-276-852-149 STANDARD: PRT: 111 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE Sequence 149, Application US/08276852.
XX
XX Sequence 149, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10566 No. 56521st Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-534-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA; 11956 MW; 63169 CN;
Query Match 88.9%; Score 666; DB 7; Length 111;
Best Local Similarity 86.8%; Pred No 3 10e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db 2 AELTQSPGTLISLSPGERATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 61
QY 1 AELTQSPGTLISLSPGERATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 60
Db 62 FSGSGSGADFTLAIISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 107
QY 61 FSGSGSGADFTLAIISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 106
RESULT 12
ID PCT-US95-08743-149 STANDARD: PRT: 111 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE Sequence 149, Application PC/TUS9508743.
XX
XX Sequence 149, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA; 11956 MW; 63169 CN;
Query Match 88.9%; Score 666; DB 13; Length 111;
Best Local Similarity 86.8%; Pred No 3 10e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db 2 AELTQSPGTLISLSPGERATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 61
QY 1 AELTQSPGTLISLSPGERATLSPPASQSVSNLYAWYQKPGAPRLIYGVSNRATGIPDP 60
Db 62 FSGSGSGADFTLAIISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 107
QY 61 FSGSGSGADFTLAIISPLEPDEFVAVYCCQYAGSHTFGGTKVEIK 106
RESULT 13
ID PCT-US95-08743-90 STANDARD: PRT: 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE

DE • Sequence 90, Application PC/TUS9508743.
 XX
 CC Sequence 90, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PC/TUS95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 90:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 107 AA: 11705 MW: 62938 CN:
 SQ
 Query Match 88.5%: Score 663; DB 13; Length 107;
 Best Local Similarity 85.8%: Pred. No. 5,36e-43;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
 Db 1 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGQAPRLIYSSSTRTGIGIPDP 60
 QY 2 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGQAPRLIYSSSTRTGIGIPDP 61
 Db 61 FSGGSGGTDTLTISRLPEDEFAVYQCHYGNVYTFQGTKEIK 106
 QY 62 FSGGSGGTDTLTISRLPEDEFAVYQCHYGNVYTFQGTKEIK 106
 RESULT 14
 ID US-08-276-852-90 STANDARD: PRT: 107 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 90, Application US/08276852
 XX
 CC Sequence 90, Application US/08276852
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R.
 CC APPLICANT: Barbas, Carlos F.
 CC APPLICANT: Leiner, Richard A.
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/176,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCP1452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 90:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 107 AA: 11705 MW: 62938 CN:
 SQ
 Query Match 88.5%: Score 563; DB 7; Length 107;
 Best Local Similarity 85.8%: Pred. No. 5,36e-43;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
 Db 1 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGQAPRLIYSSSTRTGIGIPDP 60
 QY 2 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGQAPRLIYSSSTRTGIGIPDP 61
 Db 61 FSGGSGGTDTLTISRLPEDEFAVYQCHYGNVYTFQGTKEIK 106
 QY 62 FSGGSGGTDTLTISRLPEDEFAVYQCHYGNVYTFQGTKEIK 106
 RESULT 15
 ID PCT-US93-08786-23 STANDARD: PRT: 109 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 23, Application PC/TUS9308786.
 XX
 CC Sequence 23, Application PC/TUS9308786
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R.
 CC APPLICANT: Barbas, III, Carlos F.
 CC APPLICANT: Chanock, Robert M.
 CC APPLICANT: Murphy, Brian P.
 CC APPLICANT: Crowe, Jr., James E.
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1860 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08786
 CC FILING DATE: 16-SEP-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:

```

CC NAME: Wetherell, Jr., Ph.D., John R.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: FD-2791
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 6L; 11L; 21L; anad 22L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
SQ SEQUENCE 109 AA; 12099 MW; 62556 CN;

Query Match      87.6%; Score 656; DB 11; Length 109;
Best Local Similarity 86.0%; Pred.No. 1.92e-42;
Matches 92; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

Db      2 AELTQSPGTLSPGERATLSGCRATOSISSNYLAWYQORPGQAPRLLIYGASNRATDIPD 61
Qy      1 AELTQSPGTLSPGERATLSGCRATOSISSNYLAWYQORPGQAPRLLIYGASNRATDIPD 60

Db      62 RFSGSGSGTDFTLTISRLEPEDFAVYQCQYDISPYTFGQGTKEIK 108
Qy      61 RFSGSGSGTDFTLTISRLEPEDFAVYQCQYG-TPRTFGQGTKEIK 106

```

Search completed: Tue Feb 24 07:57:22 1998
 Job time : 6 secs.

M05RELH

(TM)

Release 2 ID John F Collins, Biocomputing Research Unit
Copyright (c) 1993, 1994, 1995 University of Edinburgh, UK
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:25:04 1998. MasPar time 4.88 Seconds
Tabular output not generated. 464,957 Million cell updates/sec

Title: >US-08-844-215-12
Description: (1-107) from US08844215.pep
Perfect Score: 769
Sequence: 1 AELTQSPGILSLVGERAIL. QQQYQSPPVTFGGTKVEIK 107

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 40.305; Variance 68.586; scale 0.588
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	676	87.9	129	5	KV3M_HUMAN IG KAPPA CHAIN PRECUR	1.78e-131	
2	673	87.5	129	5	KV3L_HUMAN IG KAPPA CHAIN PRECUR	9.36e-131	
3	672	87.4	109	5	KV3E_HUMAN IG KAPPA CHAIN V-III	1.63e-130	
4	669	87.0	109	5	KV3R_HUMAN IG KAPPA CHAIN V-III	8.58e-130	
5	658	85.6	108	5	KV3A_HUMAN IG KAPPA CHAIN V-III	3.79e-127	
6	655	85.2	109	5	KV3D_HUMAN IG KAPPA CHAIN V-III	1.99e-126	
7	642	83.5	109	5	KV3G_HUMAN IG KAPPA CHAIN V-III	2.63e-123	
8	625	81.3	129	5	KV3H_HUMAN IG KAPPA CHAIN PRECUR	3.12e-119	
9	604	78.5	128	5	KV3K_HUMAN IG KAPPA CHAIN PRECUR	3.30e-114	
10	598	77.8	109	5	KV3F_HUMAN IG KAPPA CHAIN V-III	8.95e-113	
11	587	76.3	100	5	KV3C_HUMAN IG KAPPA CHAIN PRECUR	3.77e-110	
12	552	71.8	108	5	KV1M_HUMAN IG KAPPA CHAIN V-I RE	8.65e-102	
13	544	70.7	108	5	KV1V_HUMAN IG KAPPA CHAIN V-I RE	6.37e-100	
14	544	70.7	114	5	KV4A_HUMAN IG KAPPA CHAIN V-IV R	6.37e-100	
15	542	70.5	115	5	KV3I_HUMAN IG KAPPA CHAIN PRECUR	1.90e-99	
16	538	70.0	108	5	KV1N_HUMAN IG KAPPA CHAIN V-I RE	1.68e-98	
17	536	69.7	134	5	KV4C_HUMAN IG KAPPA CHAIN PRECUR	5.02e-98	
18	534	69.4	108	5	KV1B_HUMAN IG KAPPA CHAIN V-I RE	1.49e-97	
19	532	69.2	108	5	KV1S_HUMAN IG KAPPA CHAIN V-I RE	4.46e-97	
20	529	68.9	107	5	KV1D_HUMAN IG KAPPA CHAIN V-I RE	2.58e-96	
21	529	68.9	108	5	KV1Y_HUMAN IG KAPPA CHAIN V-I RE	2.58e-96	
22	523	68.8	115	5	KV3J_HUMAN IG KAPPA CHAIN PRECUR	2.58e-96	

23	524	68.1	108	5	KV1K_HUMAN IG KAPPA CHAIN V-I RE	3.47e-95
24	524	68.1	108	5	KV1O_HUMAN IG KAPPA CHAIN V-I RE	3.47e-95
25	523	68.0	108	5	KV1L_HUMAN IG KAPPA CHAIN PRECUR	5.98e-95
26	522	67.9	132	5	KV4B_HUMAN IG KAPPA CHAIN PRECUR	1.03e-94
27	520	67.6	108	5	KV1F_HUMAN IG KAPPA CHAIN V-I RE	3.26e-94
28	518	67.4	108	5	KV1P_HUMAN IG KAPPA CHAIN V-I RE	9.10e-94
29	517	67.2	108	5	KV1Q_HUMAN IG KAPPA CHAIN V-I RE	1.57e-93
30	515	67.0	111	5	KV3M_MOUSE IG KAPPA CHAIN V-III	4.65e-94
31	509	66.2	108	5	KV1E_HUMAN IG KAPPA CHAIN V-I RE	1.21e-91
32	508	66.1	108	5	KV1P_HUMAN IG KAPPA CHAIN V-I RE	2.09e-91
33	508	66.1	111	5	KV3L_MOUSE IG KAPPA CHAIN V-III	2.09e-91
34	506	65.8	111	5	KV3O_MOUSE IG KAPPA CHAIN V-III	6.18e-91
35	506	65.8	129	5	KV1W_HUMAN IG KAPPA CHAIN PRECUR	6.18e-91
36	504	65.5	120	5	KV1X_HUMAN IG KAPPA CHAIN PRECUR	1.82e-90
37	504	65.4	112	5	KV3B_MOUSE IG KAPPA CHAIN V-III	3.15e-90
38	503	65.4	135	5	KV5B_MOUSE IG KAPPA CHAIN PRECUR	3.15e-90
39	501	65.1	108	5	KV1C_HUMAN IG KAPPA CHAIN V-I RE	9.43e-90
40	501	65.1	111	5	KV3N_MOUSE IG KAPPA CHAIN V-III	9.43e-90
41	499	64.9	111	5	KV3D_MOUSE IG KAPPA CHAIN V-III	2.76e-89
42	499	64.9	111	5	KV3H_MOUSE IG KAPPA CHAIN V-III	2.76e-89
43	496	64.5	110	5	KV3P_MOUSE IG KAPPA CHAIN V-III	1.40e-88
44	496	64.5	111	5	KV3Q_MOUSE IG KAPPA CHAIN V-III	1.40e-88
45	495	64.4	109	5	KV1T_HUMAN IG KAPPA CHAIN V-I RE	2.42e-88

ALIGNMENTS

RESULT 1
ID KV3M_HUMAN STANDARD: PRT: 129 AA.
AC P18136:
DT 01-NOV-1990 (PEL 16, CREATED)
DT 01-NOV-1990 (REL 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (PEL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
PA KIPPS T J, TOMHAVE E, CHEN P P, CAPSON D A.;
PL J EXP MED 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC ANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10021: K3HUH1.
DR HSSP: P01607: 1DPB.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: DD09C359 CRC32:

Query Match 87.9%; Score 576; DB 5; Length 129;
Best Local Similarity 88.6%; Pred. No. 1.78e-131;
Matches 93; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltsqgtlslspgeratiscrasgsvssylawqgkpgqgprlllygssratgipdrf 83
|||||
QY 3 LTQSGTILSLVGERATISCRASGNIYSGYLOWTQKQKQPPRLLYGASNNATGIPDRF 62
|||
DE 94 ssssgtgrfllststfexkfayvvyggygsspflyggtkvsk 128
|||||
QY 49 SSSGSGTFTLLISLESEETFAVYVYQYGGSPFTTGGTAVELY 107
|||||

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RESULT 2
ID KV3L_HUMAN STANDARD: PRT: 129 AA.
AC P18135.
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAH).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOCANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10022; K3HUHA.
DR HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; 2C44B85E CRC32;

Query Match 87.5%; Score 673; DB 5; Length 129;
Best Local Similarity 86.6%; Pred. No. 9,36e-131;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltqspgtlslspgeratlscrasqsvssylawyqkqpgqprlllygassratgipdrf 83
QY 3 LTQSPGTLSSLVGERATLSQASQNIYSGYLQWYQKPGQPPRLIYGASNPATGIPDPF 62
|||||
Db 84 sqsgsgtdftltisrlepedfavyycqyqgtsprtfgggtkveik 128
QY 63 SGSGSGTDFTLISRLSEDFAVYICQYQSGPPYTFGGGTKEIK 107
|||||

RESULT 3
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01623.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01896; K3HUL.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 7D8F5D75 CRC32;

Query Match 87.4%; Score 672; DB 5; Length 109;
Best Local Similarity 86.6%; Pred. No. 9,36e-131;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

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Best Local Similarity 90.5%; Pred. No. 1.63e-130;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 4 ltqspgtlslspgeratlscrasqsvssylawyqkqpgqprlllygassratgipdrf 63
QY 3 LTQSPGTLSSLVGERATLSQASQNIYSGYLQWYQKPGQPPRLIYGASNPATGIPDPF 62
|||||
Db 64 sqsgsgtdftltisrlepedfavyycqyqgtsprtfgggtkveik 108
QY 63 SGSGSGTDFTLISRLSEDFAVYICQYQSGPPYTFGGGTKEIK 107
|||||

RESULT 4
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01620.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUSI.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 00B5DD5D CRC32;

Query Match 87.0%; Score 669; DB 5; Length 109;
Best Local Similarity 86.7%; Pred. No. 8.58e-130;
Matches 91; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspgtlslspgeratlscrasqsvssylawyqkqpgqprlllygassratgipdrf 63
QY 3 LTQSPGTLSSLVGERATLSQASQNIYSGYLQWYQKPGQPPRLIYGASNPATGIPDPF 62
|||||
Db 64 sqsgsgtdftltisrlepedfavyycqyqgtsprtfgggtkveik 108
QY 63 SGSGSGTDFTLISRLSEDFAVYICQYQSGPPYTFGGGTKEIK 107
|||||

RESULT 5
ID KV3A_HUMAN STANDARD: PRT: 108 AA.
AC P01619.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (B6).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 2,301-334(1969).
RA FEBS LETT. 2,301-334(1969).
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3HUR6.
DR HSSP: P01607; 1MCP.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 46D4668E CRC32;

Query Match 85.6%; Score 658; DB 5; Length 108;
Best Local Similarity 80.0%; Pred. No. 3.75e-127;

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Query Match      83.58; Score 542; DB 5; Length 109-
Best Local Similarity 85.79; Pct Id 50.123
Matches          90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

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RESULT	9	STANDARD	PRT:	128 AA.
AD	KV3K_HUMAN			
IC	P06311			
DI	01-JAN-1988	(REL 06, CREATED)		
DI	01-JAN-1988	(REL 06, LAST SEQUENCE UPDATE)		
DI	01-JAN-1990	(REL 16, LAST ANNOTATION UPDATE)		
DI	01-NOV-1990	(REL 16, LAST ANNOTATION UPDATE)		
DI	IG KAPPA CHAIN PREPUSCOP V-III REGION (IAPC/YBL41).			
OS	DE HOMO SAPIENS (HUMAN).			
OS	EU KARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUKARYOTA; METAFOA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE: 86041852.			
EX	KLOBECK H G, METINDI A, COMBETALOG, SOULIMAN A, ZACHAR H G.			
PL	NUCLEIC ACIDS RES 13:6499-6513(1985).			
EF	EMBL 200321, G31179.			
DR	PIR: A01899; K3HU41.			

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DR HSP: P01607; 3HPM.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20 IG KAPPA CHAIN V-III REGION (IAPC/RI41)
FT CHAIN 21 128
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 77 104 FRAMEWORK 3
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 318E08AF CPC32;

Query Match 78.5%; Score 694; DB 5; Length 128;
Best Local Similarity 81.0%; Pred. No. 3.30e-114;
Matches 85; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

Db 24 ltqspdtlslsgpgeratlscrasqsv-ssnlwlyqkrgqsprrllldasrarqgiedrf 82
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3 LTQSPDTLSVSGERATLSGPASQNIYSGLWYQCKQKQPRLIIYGASNPATGIPDPF 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 83 sgsasgtftllisrlepedfavyycqygsptfsggtrveik 127
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 SSGSGTDTLTISRLESEDFAVYCYQYGSPPYTFGGTKVEIK 107
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (POM)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RA KLAPPER D.G., CAPPA J.D.;
PL ANN INST PASTEUR IMMUNOL. 127:261-271(1976)
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01897; K3HUPM
DR HSP: P01607; IDPR
KW IMMUNOGLOBULIN V REGION
FT DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA; 11922 MW; A0C42C88 CPC32;

Query Match 77.8%; Score 598; DB 5; Length 109;
Best Local Similarity 79.2%; Pred. No. 8.95e-113;
Matches 84; Conservative 12; Mismatches 8; Indels 2; Gaps 2;

Db 4 mtqspvtlsvsgpgeratlscrasqslsnylawyqkqsgsprrlliygastratgiparf 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3 LTQSPDTLSVGERATLSGPASQNIYSGLWYQCKQKQPRLIIYGASNPATGIPDPF 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 64 sgsasgtftllisrlepedfavyycqygsptfsggtrveik 108
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 SSGSGTDTLTISRLESEDFAVYCYQYGS-PPYTFGGTKVEIK 107
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
ID KV3C_HUMAN STANDARD; PRT; 100 AA
AC P01621;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (NG9) (PEPAMENT)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
FX MERLINE; 84093600
RA BENTLEY D.L.;
RL NATURE 307:77-80(1984).
CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9 1 HYBRIDOMA.
DR PIR: A01894; K3HUNG.
DR HSP: P01607; LAAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 92A75223 CPC32;

Query Match 76.3%; Score 587; DB 5; Length 100;
Best Local Similarity 85.9%; Pred. No. 3.77e-110;
Matches 79; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Db 8 ltqspdtlslsgpgeratlscrasqsvssylwlyqkqgqgafrrlliygatsratgipdrf 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3 LTQSPDTLSVSGERATLSGPASQNIYSGLWYQCKQKQPRLIIYGASNPATGIPDPF 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 68 sgsasgtftllisrlepedfavyycqygs 99
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 SSGSGTDTLTISRLESEDFAVYCYQYGS 94
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAY).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RA CAPPA J.D., KLAPPER D.G.;
PL SCAND. J. IMMUNOL. 5:677-684(1976)
CC -!- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01871; K1HULY.
DR HSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11934 MW; 22228B0C CPC32;

Query Match 71.8%; Score 552; DB 5; Length 108;
Best Local Similarity 68.2%; Pred. No. 4.05e-102;
Matches 73; Conservative 22; Mismatches 9; Indels 3; Gaps 3;

Db 3 gntqspstlsvsgpgeratlscrasqsv-naylnwlyqkqgqgafrrlliygastratgipdrf 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2 ELTQSPDTLSVSGERATLSGPASQNIYSGLWYQCKQKQPRLIIYGASNPATGIPDPF 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 62 fsgsgsgtftllisrlepedfavyycqygsptfsggtrveik 107
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

QY 62 FSGSGSGDTLTISRLESEDFAVYCOQYGS-PPTFGQGTKEIK 107

RESULT 13
ID KVIIV_HUMAN STANDARD: PRI: 108 AA.
AC P04430:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (BAN)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 86174817.
RA DWILET F E, O'CONNOR T P, BENSON M D.;
PL MOL IMMUNOL. 23:73-79(1986).
DR PIR: A01878; K1HUBN.
DR HSP: P01607; 1FVC.
KW IMMUNOGLOBULIN V REGION; AMYLOID.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32.

Query Match 70.7%; Score 544; DB 5; Length 108.
Best Local Similarity 66.0%; Pred. No. 6.37e-100;
Matches 70; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Db 3 qltqpsissasvgrvltitcrasgsv-yvawfqqkpkapksliydastlqsgvpsn 61
QY 2 ELTQSPGTLISLVSGEPATLSCPASQNTYSGYLGWYCKPGCPPELLIYGASNRATGIPDR 61

Db 62 ftqsgsdtdltlsslqaedvavvyccqyyspysfqqgtkvik 107
QY 62 FSGSGSGDTLTISRLESEDFAVYCOQYGS-PPTFGQGTKEIK 107

RESULT 14
ID KVAIA_HUMAN STANDARD: PRI: 114 AA.
AC P01625:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-IV REGION (LEN)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 76004342.
RA SCHNEIDER M., HILSCHMANN N.;
PL HOPPE-SEYLER'S Z PHYSIOL CHEM. 356:507-557(1975).
DR [2]
RP REVISION TO 9.
RA SALOMON A.;
RL SUBMITTED (AUG-1996) TO THE SWISS-PROT DATA BANK.
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MAPREP.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01903; K4HULN.
DR HSP: P01607; 1MCP.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 41 55 FRAMEWORK 2.

FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 63 94 FRAMEWORK 3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 113 FRAMEWORK 4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; EEICE0BE CRC32;

Query Match 70.7%; Score 544; DB 5; Length 114;
Best Local Similarity 70.0%; Pred. No. 6.37e-100;
Matches 77; Conservative 20; Mismatches 8; Indels 5; Gaps 2;

Db 4 ltqspdlslslqeratlnckssqsv-ysnsknvjlawyqckpqgkplliydastlqsg 61
QY 3 LTQSPGTLISLVSGEPATLSCPASQNT-YSG-----YLGWYCKPSPPELLIYGASNRATG 57

Db 64 vpdrlfsgsgsdtdltlsslqaedvavvyccqyyspysfqqgtkvik 113
QY 58 LPDRLFSGSGSGDTLTISRLESEDFAVYCOQYGSPPYTFGQGTKEIK 107

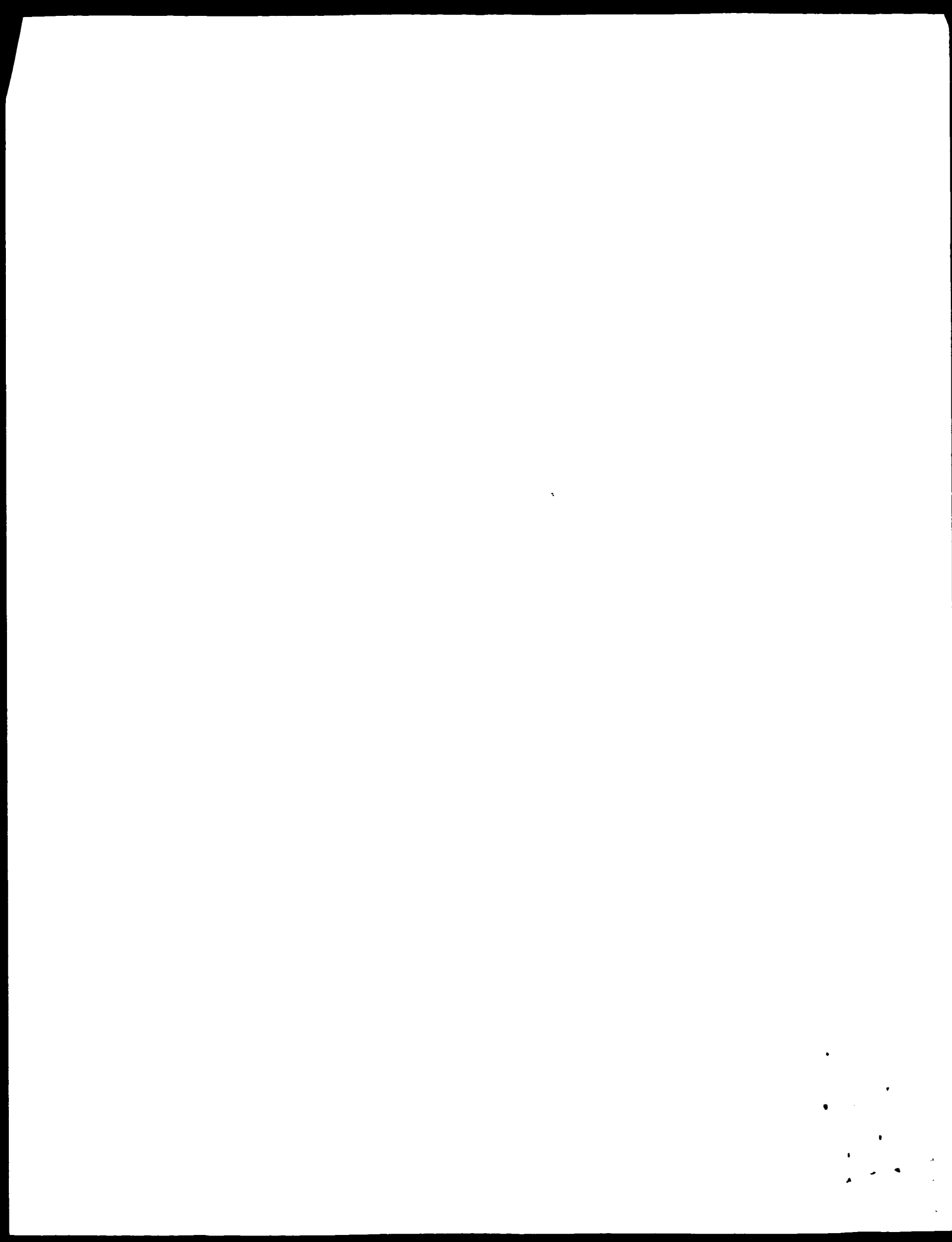
RESULT 15
ID KVIIV_HUMAN STANDARD: PRI: 115 AA.
AC P04433:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 13-AUG-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PPECURSOR V-III REGION (V5) (FRAGMENT).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932.
RA PECH M., ZACHAU H.G.;
PL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL: X01668; -; NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT CHAIN 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (V5).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E182FC CRC32;

Query Match 70.5%; Score 542; DB 5; Length 115;
Best Local Similarity 86.4%; Pred. No. 1.50e-99;
Matches 76; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

Db 24 ltqspdlslslqeratlnckssqsv-ssylawyqckpqgkplliydastlqsg 62
QY 3 LTQSPGTLISLVSGEPATLSCPASQNTYSGYLGWYCKPGCPPELLIYGASNRATGIPDR 62

Db 83 sgsqsgtdltlsslqaedvavvyccqyyspysfqqgtkvik 110
QY 63 SSGSGSGDTLTISRLESEDFAVYCOQ 90

Search completed: Tue Feb 24 07:25:27 1998
Job time : 18 secs.



WQERLH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrchLff protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:53:13 1998. Master time 3.04 Seconds
Tabular output not generated. 179.068 Million cell updates/sec

Title: >US-08-844-215-12
Description: (1-107) from US08844215.pep
Perfect Score: 769
Sequence: 1 AELTQSPGTLTSLVSGEPATL CQOYQSPPTPGGKVEIK 107
Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10:PC192 11:PC193 12:PC194 13:PC195 14:PC196
Statistics: Mean 27.220 Variance 114.082 scale 0.203

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	583	98.8	108	13	PCT-US95-0 Sequence 99, Applicat	3.18e-48
2	583	88.8	108	7	US-08-276- Sequence 99, Applicat	3.18e-48
3	672	87.4	108	6	US-08-477- Sequence 86, Applicat	2.76e-47
4	672	87.4	108	6	US-07-534- Sequence 86, Applicat	2.76e-47
5	672	87.4	108	7	US-08-474- Sequence 86, Applicat	2.76e-47
6	672	87.4	108	7	US-08-487- Sequence 86, Applicat	2.76e-47
7	672	87.4	108	11	PCT-US93-0 Sequence 23, Applicat	4.09e-47
8	670	87.1	108	13	PCT-US95-0 Sequence 86, Applicat	4.09e-47
9	670	87.1	108	7	US-08-276- Sequence 90, Applicat	2.39e-46
10	661	86.0	107	13	PCT-US95-0 Sequence 90, Applicat	2.39e-46
11	658	85.6	108	13	PCT-US95-0 Sequence 147, Applicat	4.31e-46
12	658	85.6	108	13	US-08-276- Sequence 147, Applicat	4.31e-46
13	649	84.4	108	13	PCT-US95-0 Sequence 110, Applicat	2.52e-45
14	649	84.4	108	7	US-08-276- Sequence 110, Applicat	2.52e-45
15	640	84.4	108	7	US-08-276- Sequence 100, Applicat	3.06e-45
16	648	84.3	104	7	PCT-US95-0 Sequence 100, Applicat	3.06e-45
17	648	84.3	104	7	US-08-276- Sequence 100, Applicat	3.06e-45
18	647	84.1	111	7	US-08-276- Sequence 149, Applicat	3.73e-45
19	647	84.1	111	13	PCT-US95-0 Sequence 149, Applicat	3.73e-45
20	645	83.9	109	11	PCT-US93-0 Sequence 24, Applicat	5.52e-45
21	644	83.7	107	7	US-08-276- Sequence 27, Applicat	6.71e-45
22	644	83.7	107	13	PCT-US95-0 Sequence 87, Applicat	6.71e-45

RESULT 2
ID US-08-276-852-99 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 99, Application US/08276852.
XX CC Sequence 99, Application US/08276852.
XX CC Patent No. 5652138
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis R
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Lerner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10666 N. 5652138th Torrey Pines Road, Suite 220,
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent Release #1 0, Version #1.25
XX CC CURRENT APPLICATION NUMBER: US/08/276.852
XX CC FILING DATE: 18-JUL-1994
XX CC CLASSIFICATION: 514
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/178,302
XX CC FILING DATE: 30-SEP-1993
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/954,148
XX CC FILING DATE: 30-SEP-1992
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Fitting, Thomas
XX CC REGISTRATION NUMBER: 34,163
XX CC REFERENCE/DOCKET NUMBER: SCPI452P
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 619-554-2937
XX CC TELEFAX: 619-554-6312
XX CC INFORMATION FOR SEQ ID NO. 99:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 108 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 108 AA; 11738 MW; 63142 CN;
Query Match 88.8%; Score 683; DB 7; Length 108;
Best Local Similarity 86.8%; Pred No. 3 18e-48;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGEPATLSCRAGQSSNYLAWYQOKPGQAPRLIYVGNPNATGIPDP 60
QY 2 ELTQSPGTLSPGEPATLSCRAGQSSNYLAWYQOKPGQAPRLIYVGNPNATGIPDP 61
Db 61 FSGSGSGDTFTLISRLPEDEFAVYVCOQYGTSPYTFGQGTOLDIK 106
QY 62 FSGSGSGDTFTLISRLPEDEFAVYVCOQYGTSPYTFGQGTOLDIK 107
RESULT 3
ID US-08-477-728-86 STANDARD: PRT: 108 AA.

XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/08477728.
XX CC Sequence 86, Application US/08477728
XX CC Patent No. 5585089
XX CC GENERAL INFORMATION:
XX CC APPLICANT: QUEEN, Gary L.
XX CC APPLICANT: SCHNEIDER, William P.
XX CC APPLICANT: SELICK, Harold E.
XX CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
XX CC NUMBER OF SEQUENCES: 113
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: Townsend and Townsend and Crew LLP
XX CC STREET: Two Embarcadero Center, 8th Floor
XX CC CITY: Palo Alto
XX CC STATE: California
XX CC COUNTRY: US
XX CC ZIP: 94111
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent Release #1 0, Version #1.25
XX CC CURRENT APPLICATION NUMBER: US/08/477,728
XX CC FILING DATE: 07-JUN-1995
XX CC CLASSIFICATION: 424
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/634,278
XX CC FILING DATE: 19-DEC-1990
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/590,274
XX CC FILING DATE: 28-SEP-1990
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/310,252
XX CC FILING DATE: 13-FEB-1989
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/240,975
XX CC FILING DATE: 28-DEC-1988
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Smith, William M.
XX CC REGISTRATION NUMBER: 30,223
XX CC REFERENCE/DOCKET NUMBER: 11843-002500
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: (415) 326-2400
XX CC TELEFAX: (415) 326-2422
XX CC INFORMATION FOR SEQ ID NO. 86:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 108 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: single
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: peptide
XX CC SEQUENCE 108 AA; 11590 MW; 64079 CN;
Query Match 87.4%; Score 672; DB 6; Length 108;
Best Local Similarity 90.5%; Pred No. 2 75e-47;
Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Db 4 LTQSPGTLSPGEPATLSCRAGQSSNYLAWYQOKPGQAPRLIYVGNPNATGIPDP 53
QY 3 LTQSPGTLSPGEPATLSCRAGQSSNYLAWYQOKPGQAPRLIYVGNPNATGIPDP 52
Db 64 FSGSGSGDTFTLISRLPEDEFAVYVCOQYGTSPYTFGQGTOLDIK 108
QY 63 FSGSGSGDTFTLISRLPEDEFAVYVCOQYGTSPYTFGQGTOLDIK 107
RESULT 4

QY 63 SGGSGTDLTISPLESEDFAVYCOQYGSPPYTFGQGTKEIK 107

RESULT 6

ID US-08-487-200-86 STANDARD: PRT: 108 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 86, Application US/08487200.

XX Sequence 86, Application US/08487200

CC Patent No. 5693762

CC GENERAL INFORMATION:

CC APPLICANT: QUEEN, Cary L.

CC APPLICANT: CO, Man Sung

CC APPLICANT: SCHNEIDER, William P.

CC APPLICANT: LANDOLEI, Nicholas F.

CC APPLICANT: COELINGH, Kathleen L.

CC APPLICANT: SELICK, Harold E.

CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

CC NUMBER OF SEQUENCES: 113

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend and Crew

CC STREET: 379 Lytton Avenue

CC CITY: Palo Alto

CC STATE: California

CC COUNTRY: US

CC ZIP: 94301

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/487,200

CC FILING DATE: 7-JUN-1995

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION NUMBER: US 07/634,278

CC FILING DATE: 19-DEC-1990

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/590,274

CC FILING DATE: 28-SEP-1990

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/310,252

CC FILING DATE: 13-FEB-1989

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/290,975

CC FILING DATE: 28-DEC-1988

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Smith, William M.

CC REGISTRATION NUMBER: 30,223

CC REFERENCE/DOCKET NUMBER: 11823-002610

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 326-2400

CC TELEFAX: (415) 326-2422

CC INFORMATION FOR SEQ ID NO: 86:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 108 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 87.4%; Score 672; DB 7; Length 108;

Best-Local Similarity 90.5%; Pred No 2 76e-47;

Matches 95; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 4 LTQSGTSLISLSPGERATLSGPGATISGASVSSYGLGWYQKPGQAPPLIYGASNPATIPDPF 63

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QY 3 LTQSGTSLISLSPGERATLSGPGATISGASVSSYGLGWYQKPGQAPPLIYGASNPATIPDPF 62

DB 64 SGGSGTDLTISPLESEDFAVYCOQYGSPPYTFGQGTKEIK 108

QY 63 SGGSGTDLTISPLESEDFAVYCOQYGSPPYTFGQGTKEIK 107

RESULT 7

ID PCT-US93-08786-23 STANDARD: PRT: 109 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 23, Application PC/TUS9308786.

XX Sequence 23, Application PC/TUS9308786

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R.

CC APPLICANT: Barbas, III, Carlos F.

CC APPLICANT: Chanoock, Robert M.

CC APPLICANT: Murphy, Brian R.

CC APPLICANT: Crowe, Jr., James E.

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC NUMBER OF SEQUENCES: 29

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Spensley Horn Jubas & Lubitz

CC STREET: 1880 Century Park East, Suite 500

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90067

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/08786

CC FILING DATE: 16-SEP-1993

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Wetherell, Jr., Ph.D., John P.

CC REGISTRATION NUMBER: 31,678

CC REFERENCE/DOCKET NUMBER: FD-2791

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110

CC INFORMATION FOR SEQ ID NO: 23:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 109 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC IMMEDIATE SOURCE:

CC CLONE: rsv 6L; 11L; 21L; anad 22L

CC FEATURE:

CC NAME/KEY: Peptide

CC LOCATION: 1..109

CC SEQUENCE 109 AA: 12099 MW: 62556 CN:

Query Match 87.4%; Score 672; DB 11; Length 109;

Best-Local Similarity 86.0%; Pred No 2 76e-47;

Matches 92; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

DB 2 AELTQSGTSLISLSPGERATLSGPGATISGASVSSYGLGWYQKPGQAPPLIYGASNPATIPDP 61

QY 1 AELTQSGTSLISLSPGERATLSGPGATISGASVSSYGLGWYQKPGQAPPLIYGASNPATIPDP 60

DB 62 RFSGSGSTDTLTISPLESEDFAVYCOQYGSPPYTFGQGTKEIK 108

|||||

QY * 61 FSGSGGDTFTLTISPLESEDFAVYCCQYSGSPPTFGGKVEIK 107

RESULT 8
ID PCT-US95-08743-86 STANDARD: PPT: 108 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 86, Application PC/TUS9508743
XX
CC Sequence 86, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 25 (EPQ)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65957 CN;

Query Match 87.1%; Score 670; DB 13; Length 108;
Best Local Similarity 87.7%; Pred. No. 4.09e-47;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGERATLSRASOSVTSNYLAWYQKPGQAPRLIYGVSNRATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSRASOSVTSNYLAWYQKPGQAPRLIYGVSNRATGIPDR 61
Db 61 FSGSGGDTFTLTISPLESEDFAVYCCQYSGSPPTFGGKVEIK 106
QY 62 FSGSGGDTFTLTISPLESEDFAVYCCQYSGSPPTFGGKVEIK 107

RESULT 9
ID US-08-276-852-86 STANDARD: PPT: 108 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 86, Application US/08276852.
XX
CC Sequence 86, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 N. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA

CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SC1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11769 MW; 65957 CN;
Query Match 87.1%; Score 670; DB 7; Length 108;
Best Local Similarity 87.7%; Pred. No. 4.09e-47;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGERATLSRASOSVTSNYLAWYQKPGQAPRLIYGVSNRATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSRASOSVTSNYLAWYQKPGQAPRLIYGVSNRATGIPDR 61
Db 61 FSGSGGDTFTLTISPLESEDFAVYCCQYSGSPPTFGGKVEIK 106
QY 62 FSGSGGDTFTLTISPLESEDFAVYCCQYSGSPPTFGGKVEIK 107
RESULT 10
ID US-08-276-852-90 STANDARD: PPT: 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 90, Application US/08276852.
XX
CC Sequence 90, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 N. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA


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XX Sequence 147, Application US/98/276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10556 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 147:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA: 11779 MW: 55550 CN:

Query Match 85.6%; Score 658; DB 7; Length 109;
Best Local Similarity 86.9%; Pred. No. 4,31e-46;
Matches 93; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Db 2 AELTQSPGTLSPGEPATLSGPRASQVSNVYLVYQKPGQCAPPLLYGASNPATGIPO 61
QY 1 AELTQSPGTLSPGEPATLSGPRASQVSNVYLVYQKPGQCAPPLLYGASNPATGIPO 60
Db 62 PFSGSGSGDTLTISPLPEPFVAVYCOQYQVSSG-TFGQTKVEIK 107
QY 61 RFSGSGSGDTLTISPLPESEDFAVYCOQYQVSPPTTFGQTKVEIK 107

RESULT 14
ID PCT-US95-08743-110 STANDARD: PRT: 108 AA
XX
XX AC xxxxxx
XX DT 01-JAN-1990
XX Sequence 110, Application PC/TUS9508743
XX Sequence 110, Application PC/TUS9508743
XX Sequence 110, Application PC/TUS9508743
XX GENERAL INFORMATION:

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CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPC)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 110:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11981 MW: 63187 CN:

Query Match 84.4%; Score 649; DB 13; Length 108;
Best Local Similarity 92.1%; Pred. No. 2,52e-45;
Matches 87; Conservative 11; Mismatches 8; Indels 3; Gaps 0;

Db 1 ELTQSPGTLSPGEPATLSGPRASQVSNVYLVYQKPGQCAPPLLYGASNPATGIPO 67
QY 2 ELTQSPGTLSPGEPATLSGPRASQVSNVYLVYQKPGQCAPPLLYGASNPATGIPO 61
Db 61 FSGSGSGDTLTISPLPEPFVAVYCOQYQVSSG-TFGQTKVEIK 105
QY 62 PFSGSGSGDTLTISPLPESEDFAVYCOQYQVSPPTTFGQTKVEIK 107

RESULT 15
ID US-08-276-852-110 STANDARD: PRT: 108 AA
XX
XX AC xxxxxx
XX DT 01-JAN-1990
XX Sequence 110, Application US/08276852
XX Sequence 110, Application US/08276852
XX Patent No. 5652138
XX GENERAL INFORMATION:
XX APPLICANT: Burton, Dennis R
XX APPLICANT: Barbas, Carlos F
XX APPLICANT: Lerner, Richard A
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX NUMBER OF SEQUENCES: 170
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: The Scripps Research Institute, Office of
XX ADDRESSEE: Patent Counsel
XX STREET: 10556 No. 5652138th Torrey Pines Road, Suite 220,
XX CITY: La Jolla
XX STATE: CA
XX COUNTRY: USA
XX ZIP: 92037
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX OPERATING SYSTEM: IBM PC compatible
XX SOFTWARE: Patentin Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994
XX CLASSIFICATION: 514
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US/08/276,852
XX FILING DATE: 18-JUL-1994
XX INFORMATION FOR SEQ ID NO: 110:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 108 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
XX SEQUENCE 108 AA: 11981 MW: 63187 CN:

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WATERMAN

(TW)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:25:26 1998; MasPar time 6.55 Seconds
Tabular output not generated. 226,930 Million cell updates/sec
Title: >US-08-844-215-12
Description: (1-107) from US08844215.pep
Perfect Score: 769
Sequence: 1 AELTQSPGTLSLVGERATL ... CQYGSPPYTFGGQIKVEIK 107

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 29.627; Variance 158.010; scale 0.187
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	588	89.5	129	7	R38672	7.87e-44	
2	583	88.8	108	9	R54316	1.94e-43	
3	583	88.8	108	9	W01278	1.94e-43	
4	572	97.4	109	9	P50217	1.42e-42	
5	570	97.1	108	10	P54307	2.04e-42	
6	570	97.1	108	19	W01265	2.04e-42	
7	561	86.0	107	10	P54311	1.04e-41	
8	561	86.0	107	19	W01269	1.04e-41	
9	560	85.8	107	19	R38593	1.24e-41	
10	558	85.6	109	19	W01320	1.78e-41	
11	558	85.6	109	19	P54275	1.78e-41	
12	549	84.4	108	19	W01289	9.06e-41	
13	548	84.3	104	19	W01279	1.09e-40	
14	548	84.3	104	9	R54317	1.09e-40	
15	547	94.1	111	19	W01322	1.09e-40	
16	547	94.1	111	10	P54277	1.30e-40	
17	545	83.9	109	9	P50218	1.87e-40	
18	545	83.9	129	7	R38673	1.87e-40	
19	544	83.7	107	19	W01266	2.24e-40	
20	544	83.7	107	10	P54308	2.24e-40	

21	644	83.7	124	22	W04539	Immunoglobulin r101.2	2.24e-40
22	644	83.7	129	7	R41286	F105 rearranged variab	2.24e-40
23	643	83.6	215	19	W05216	Ulcerative colitis-as	2.58e-40
24	642	83.5	109	10	P54263	Anti-HIV gp120 immuno	2.21e-40
25	640	83.2	134	20	W11155	Anti-lung tumour anti	4.60e-40
26	637	82.8	112	10	W01324	VL of Fab, SS 41 B, b	7.91e-40
27	637	82.8	112	10	P54279	Anti-HIV gp41 immuno	7.91e-40
28	630	81.9	109	10	P56286	light chain of Abt a1	2.79e-39
29	630	81.9	214	19	W05215	Ulcerative colitis-as	2.79e-39
30	628	81.7	108	19	W01267	VL region of HIV neut	4.01e-39
31	625	81.3	108	10	P54255	Anti-HIV gp120 immuno	6.89e-39
32	625	81.3	108	19	W01275	VL region of HIV neut	6.89e-39
33	620	80.6	107	19	W01295	VL region of HIV neut	1.69e-38
34	620	80.6	107	19	W01294	VL region of HIV neut	1.69e-38
35	620	80.6	137	9	R54325	Anti-HIV gp120 immuno	1.69e-38
36	616	80.1	107	19	W01297	VL region of HIV neut	3.48e-38
37	616	80.1	107	10	R54265	Anti-HIV gp120 immuno	3.48e-38
38	615	80.0	108	10	P54309	Anti-HIV gp120 immuno	4.17e-38
39	613	79.7	107	9	R54326	Anti-HIV gp120 immuno	5.98e-38
40	613	79.7	107	19	W01296	VL region of HIV neut	5.98e-38
41	610	79.3	105	9	R54314	Anti-HIV gp120 immuno	1.03e-37
42	510	79.3	105	19	W01272	VL region of HIV neut	1.03e-37
43	606	78.8	116	7	R38650	Human V-kappa fragmen	2.11e-37
44	606	78.8	116	11	P52930	Human V-kappa vk65.8	2.11e-37
45	606	78.8	116	20	W03048	DNA fragment vk65.8,	2.11e-37

ALIGNMENTS

RESULT 1
ID R38672 standard; Protein: 129 AA.
AC R38672;
DT 01-NOV-1993 (first entry)
DE vk325-Jk2.
KW Monoclonal antibody, MAB, envelope, glycoprotein, gp120, HIV; AIDS;
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Protein 21..129
FT /label= mat_protein
FT Region 1..115
FT /label= vk325
FT Region 117..129
FT /label= Jk2
FT Region 44..55
FT /label= CDR1
FT Region 71..77
FT /label= CDR2
FT Region 110..117
FT /label= CDR3
FT Misc.difference 1
FT /note= Met encoded by ATC (sic)
FT Misc.difference 35
FT /note= "Frc encoded by GCA (sic)"
FT Misc.difference 99
FT /note= "Ileu encoded by GTG (sic)"
FT Misc.difference 113
FT /note= "Gly encoded by GAT (sic)"
FT Misc.difference 114
FT /note= "Ser encoded by AAC (sic)"
FT Misc.difference 116
FT /note= "Pro encoded by GTT (sic)"
PN W09312232-A.
PD 24-JUN-1993.
PF 10-DEC-1992; U10298.
PP 10-DEC-1991; US-904652.
PA (DAND) DANA FABER CANCER INST INC.
PA (NEWB-) NEW ENGLAND DEACONESS HOSPITAL CORP.
PI Resolving WA, KARASC WA, POSENY MR, SODICKSI JG;
DE WFI: 93-214174/26.

DR N-PSDB; Q42706.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV for treating AIDS, and for diagnosing and
PT monitoring HIV infection.
PS Disclosure; Page 74-75; 109pp; English.
CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
CC other F105 VK sequences given elsewhere in the specification) was
CC compared with germline gene HumVK325 (Q42706), showing 97.7%
CC similarity. By nucleotide sequence analysis, F105 appears to
CC be derived from a member of the VK III subgroup gene family.
SQ Sequence 129 AA;

Query Match 89.5%; Score 688; DB 7; Length 129;
Best Local Similarity 89.5%; Pred. No. 7.87e-44;
Matches 94; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Db 24 ltqspgtlslspgeratlsragsvssylawyyqkpgqaprllygssratgipdrf 83
QY 3 LTQSPGTLSLVGRPATLSRAGSNIVSGYLGWYQKPGQPPPLLYGASNPATGIPDRF 62

Db 84 sgsgsgtdftltisrlepafavyqygsspytfgqgkcleik 128
QY 63 SGSGSGTDFTLTISRLESEDFAVYQYQYGGSPYTFGQGTKEIK 107

RESULT 2 Location/Qualifiers
ID F54316 standard; protein: 108 AA
AC R54316
DE 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region b6.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
PN W09602273-A1
PD 01-FEB-1996.
PF 11-JUL-1995; U08743
PR 18-JUL-1994; US-276852.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example; Fig 11: 366pp; English.
CC The sequences given in W01361-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the Jk2
CC gene clone, b6. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 88.8%; Score 683; DB 9; Length 108;
Best Local Similarity 86.8%; Pred. No. 1.94e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlsragsvssylawyyqkpgqaprllygssratgipdr 60
QY 2 ELTQSPGTLSLVGRPATLSRAGSNIVSGYLGWYQKPGQPPPLLYGASNPATGIPDR 61

Db 61 fsgsgsgtdftltisrlepafavyqygsspytfgqgkcleik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYQYQYGGSPYTFGQGTKEIK 107

RESULT 4
ID F50217 standard; protein: 109 AA.

Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlsragsvssylawyyqkpgqaprllygssratgipdr 60
QY 2 ELTQSPGTLSLVGRPATLSRAGSNIVSGYLGWYQKPGQPPPLLYGASNPATGIPDR 61

Db 61 fsgsgsgtdftltisrlepafavyqygsspytfgqgkcleik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYQYQYGGSPYTFGQGTKEIK 107

RESULT 3
ID W01278 standard; protein: 108 AA.
AC W01278;
DE 29-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone b6.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
PN W09602273-A1
PD 01-FEB-1996.
PF 11-JUL-1995; U08743
PR 18-JUL-1994; US-276852.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example; Fig 11: 366pp; English.
CC The sequences given in W01361-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the Jk2
CC gene clone, b6. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 88.8%; Score 683; DB 19; Length 108;
Best Local Similarity 86.8%; Pred. No. 1.94e-43;
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlsragsvssylawyyqkpgqaprllygssratgipdr 60
QY 2 ELTQSPGTLSLVGRPATLSRAGSNIVSGYLGWYQKPGQPPPLLYGASNPATGIPDR 61

Db 61 fsgsgsgtdftltisrlepafavyqygsspytfgqgkcleik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYQYQYGGSPYTFGQGTKEIK 107

RESULT 4
ID F50217 standard; protein: 109 AA.

AC R50217:
 DT 31-OCT-1994 (first entry)
 DE HSV glycoprotein F binding, MAB clone rsv6/11/21/22L VH/VL domain
 KW Complementarity determination region; CDR3; human; bronchiolitis;
 KW monoclonal antibody; epitope; glycoprotein F; influenza virus;
 KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;
 KW lung; pneumonia.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..99
 FT /label= FR3
 FT Region 90..98
 FT /label= CDR3
 FT Region 99..109
 FT /label= FR4
 FT /label= FR4
 PN WO9406448-A.
 PF 31-MAR-1994.
 PF 16-SEP-1993: U08786.
 PR 16-SEP-1992: US-945515.
 PA (SCR1) SCRIPPS RES INST.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Barbas CF, Burton DR, Chanock RM, Crowe JE, Murphy BR.
 DR WPI: 94-118147/14.
 PT Human neutralising monoclonal antibodies to respiratory syncytial
 PT virus - for treatment prophylaxis and diagnosis of psv and other
 PT diseases of the respiratory tract
 PS Disclosure: Fig 4: 104pp: English.
 CC The sequences given in R5015-19 represent the heavy and light chain
 CC variable domains of various clones of a human monoclonal antibody
 CC which binds to an epitope on glycoprotein F of respiratory syncytial
 CC virus (RSV). These antibodies may be used as a reagent for the
 CC diagnosis of RSV disease and other viral mucosal diseases, eg.
 CC influenza virus, rhinovirus and coronavirus. They are particularly
 CC useful in ameliorating RSV when delivered directly to the lungs, and
 CC may also be used for treating pneumonia and bronchiolitis.
 SQ Sequence 109 AA;

Query Match 87.4%; Score 672; DB 9; Length 109;
 Best Local Similarity 86.0%; Pred No. 1,42e-42;
 Matches 92: Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 2 aeltsgptglspgertatlsratqstssnylawyqgqpqapqprllygsnratdipd 61
 QY 1 AELTSGPTGLSPGERTATLSRATQSTSSNYLAWYQGPQAPQAPRLLYGSNRAIPD 60

Db 62 rfsgsqatdftltisrlepafayvcsqyqdispytfgqtkleik 108
 QY 61 PFGSGSGTFTLTISPLESEDFAVYCVQYGSPPYIFEQGIRKVEIK 107

RESULT 5
 ID R54307 standard; protein: 108 AA.
 AC R54307:
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region b24.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48

FT /label= FR2 49..55
 FT Region /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN WO9407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993: U09328.
 PR 30-SEP-1992: US-954148.
 PA (SCR1) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example: Page 177-178; 248pp: English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence K4307 is from a gp120-
 CC specific clone.
 SQ Sequence 108 AA;

Query Match 87.1%; Score 670; DB 10; Length 108;
 Best Local Similarity 87.7%; Pred No. 2,04e-42;
 Matches 93: Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltgspgtglspgertatlsratqstssnylawyqgqpqapqprllygsnratdipdr 60
 QY 2 ELTSGPTGLSPGERTATLSRATQSTSSNYLAWYQGPQAPQAPRLLYGSNRAIPDR 61

Db 61 fsgsqatdftltisrlepafayvcsqyqdispytfgqtkleik 106
 QY 62 PFGSGSGTFTLTISPLESEDFAVYCVQYGSPPYIFEQGIRKVEIK 107

RESULT 6
 ID W01265 standard; Protein: 108 AA.
 AC W01265:
 DT 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b24.
 KW Heavy chain, light chain, variable region, VH; monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor; gp120; immunodeficiency; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN WO9602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995: U08743.
 PR 18-JUL-1994: US-276952.

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PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno:therapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK1
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match 87.1%; Score 670; DB 19; Length 108;
Best Local Similarity 87.7%; Pred. No. 2.04e-42;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltspgtltispggeratlscrasqslsnnylawyqgkpgqaprllygvsnratgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSRASQNIYSGYLGWYQKPGPPRLIYGASNPATGIPDP 61
Db 61 fsgsgsgtdftltisrlepefavyycqygtspwtfgggtkveik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYCYQYGGSPPTFGQGTKEIK 107

RESULT 7
ID R54311 standard; protein; 107 AA.
AC R54311;
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
FT W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 180: 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC distrophic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive

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CC clones. The light chain VK region sequence R54311 is from a gp120-
CC specific clone.
SQ Sequence 107 AA;

Query Match 86.0%; Score 661; DB 10; Length 107;
Best Local Similarity 83.0%; Pred. No. 1.04e-41;
Matches 88; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltspgtltispggeratlscrasqslsnnylawyqgkpgqaprllygvsnratgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSRASQNIYSGYLGWYQKPGPPRLIYGASNPATGIPDP 61
Db 61 fsgsgsgtdftltisrlepefavyycqygtspwtfgggtkveik 106
QY 62 FSGSGSGTDFTLTISRLESEDFAVYCYQYGGSPPTFGQGTKEIK 107

RESULT 8
ID W01269 standard; Protein; 107 AA.
AC W01269;
DT 28-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone B20.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 98..107
FT /label= FR4
FT W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno:therapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match 86.0%; Score 661; DB 19; Length 107;
Best Local Similarity 83.0%; Pred. No. 1.04e-41;
Matches 88; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltspgtltispggeratlscrasqslsnnylawyqgkpgqaprllygvsnratgipdr 60
QY 2 ELTQSPGTLSLSVGERATLSRASQNIYSGYLGWYQKPGPPRLIYGASNPATGIPDP 61
Db 61 fsgsgsgtdftltisrlepefavyycqygtspwtfgggtkveik 106

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QY 62 FSSGSGIDFTLIISRLSEDEFAVYCYGSGPPYIFGQIKVEIK 107
|||||

RESULT 9

ID R38593 standard; peptide; 107 AA.
AC R38593;
DT 28-OCT-1993 (first entry)
DE Human lambda light chain subgroup 3 (HL3).
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 96
FT /note- residue conserved in less than 50% of the
FT known sequences of HL3*
PN WO9411794-A.
PD 24-JUN-1993.
PF 14-DEC-1992; U10906
PF 13-DEC-1991; US-900464
PA (XOMA) XOMA CORP.
PI Fishwild DM, Kohn PP, Little PG, Studnicka GM.
DI WPI: 93-213827/26.
PT Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc
PS Claim 2: Page 93-94; 130pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (hk1 - R38590, hk3 - NGK, hk2 - GST, hL1 - R38591, hL2 -
CC R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
CC hH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA:

Query Match 85.8%; Score 650; DB 7; Length 107;

Best Local Similarity 87.6%; Pred. No. 1.24e-41;
Matches 92; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Db 4 ltqspstlslpggeratlsrassvssylawygqkpgqgprlllygssratgipdrf 62
|||||

QY 3 LTQSPSTLSLVGERATLSRASSVSSYLGWYCYGSGPPYIFGQIKVEIK 62
|||||

Db 63 sgsqsgtdftltisrlpqrdfavycggygsspxtfqgtdveik 107
|||||

QY 63 SSGSGSIDFTLIISRLSEDEFAVYCYGSGPPYIFGQIKVEIK 107
|||||

RESULT 10

ID WO1320 standard; Protein; 109 AA.
AC WO1320;
DT 29-JAN-1997 (first entry)
DE VL of Fab, DL 4119, binds to HIV gp41.
KW Heavy chain, light chain, variable region, VH monoclonal antibody;
KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..23
FT /label- FR1
FT Region 24..35
FT /label- CDR1
FT Region 36..50
FT /label- FR2

FT Region 51..57
FT /label- CDR2
FT Region 58..89
FT /label- FR3
FT Region 90..97
FT /label- CDR3
FT Region 98..109
FT /label- FR4
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PF 18-JUL-1994; US-276852.
PA (SCPI) SCRIPPS PES INST.
PI Barbas CF, Burton DR, Lerner RA;
DI WPI: 96-179601/1R
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
FS Example 3, Fig 19, 36pp; English.
CC The sequences given in WO1320-24 represent the light chain variable
CC regions (VH) of a series of antibody fragments (FAB's) which are
CC immunoreactive with HIV glycoprotein gp41. This sequence represents
CC the sequence of the clone, DL 4119. These sequences represent light
CC chains which bind to the heavy light chain clones given in WO1315-19. A
CC monoclonal antibody containing one of these Fab sequences may have the
CC capacity to reduce HIV infectivity titre in an *in vivo* virus infectivity
CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
CC The MAb may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 109 AA:

Query Match 85.6%; Score 658; DB 19; Length 109;

Best Local Similarity 86.9%; Pred. No. 1.78e-41;
Matches 93; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Db 2 aeltqspstlslpggeratlsrassvssylawygqkpgqgprlllygssratgipdrf 61
|||||

QY 1 AELTQSPSTLSLVGERATLSRASSVSSYLGWYCYGSGPPYIFGQIKVEIK 60
|||||

Db 62 rfsqsgsgtdftltisrlpqrdfavycggygsspxtfqgtdveik 107
|||||

QY 61 RFSQSGSIDFTLIISRLSEDEFAVYCYGSGPPYIFGQIKVEIK 107
|||||

RESULT 11

ID R54275 standard; protein; 109 AA.

AC R54275;

DI 10-NOV-1994 (first entry)

DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 4119.
KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW neutralisation; monoclonal antibody; light chain; variable region;
KW framework region; complementarity determining region.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..23

FT /label- FR1

FT Region 24..35

FT /label- CDR1

FT Region 36..50

FT /label- FR2

FT Region 51..57

FT /label- CDR2

FT Region 58..89

FT /label- FR3

FT Region 90..97

FT /label- CDR3

FT Region 98..109

FT /label- FR4

PN WO9407923-A.

PD 14-APR-1994.

PF 30-SEP-1993; U09328.

PP 30-SEP-1992; US-954148.

PA (SCPI) SCRIPPS PES INST.

PI Barbas CF, Burton DR, Lerner RA;

WPI; 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 11, Page 215-216, 248pp, English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive HIV
 CC clones. The light chain VL region sequence R542/5 neutralises HIV1
 CC gp41.
 SQ Sequence 109 AA:

Query Match 85.6%; Score 658; DB 10; Length 109;
 Best Local Similarity 86.9%; Pred. No. 1,78e-41;
 Matches 93; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 Db 2 aeltspgtlslspqervivscrasqsvssnylawyqgkpgqprlliygasmratgipd 61
 QY 1 AELTSPGTLSSLVGERATLSPASQNIYSGYLGMWQKPGQPPPELLIYGASNRATGIPD 60
 Db 62 rfsgsgsgtdftltisrlepedfavyycqygssg-tfgggtkveik 107
 QY 61 RFSGSGSGTDFTLTISRLESEDFAVYQCQYGSPPYTFGGGTKEIK 107

RESULT 12
 ID W01289 standard; Protein; 108 AA.
 AC W01289;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b11.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB, HIV, human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence, human.
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

Key Location/Qualifiers

FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIpps RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI; 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, b11. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV

antibody and in the detection of HIV infection.
 SQ Sequence 109 AA:
 Query Match 85.6%; Score 658; DB 10; Length 109;
 Best Local Similarity 86.9%; Pred. No. 1,78e-41;
 Matches 93; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 Db 2 aeltspgtlslspqervivscrasqsvssnylawyqgkpgqprlliygasmratgipd 61
 QY 1 AELTSPGTLSSLVGERATLSPASQNIYSGYLGMWQKPGQPPPELLIYGASNRATGIPD 60
 Db 62 rfsgsgsgtdftltisrlepedfavyycqygssg-tfgggtkveik 107
 QY 61 RFSGSGSGTDFTLTISRLESEDFAVYQCQYGSPPYTFGGGTKEIK 107

CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 84.4%; Score 649; DB 19; Length 108;
 Best Local Similarity 82.1%; Pred. No. 9.06e-41;
 Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1 eltsptlslspqervivscrasqsvssnylawyqgkpgqprlliygasmratgipdr 60
 QY 2 ELTSPGTLSSLVGERATLSPASQNIYSGYLGMWQKPGQPPPELLIYGASNRATGIPDR 61
 Db 61 fsgsgsgtdftltisrlepedfavyycqygsgdaqytfgggtkveik 106
 QY 62 FSGSGSGTDFTLTISRLESEDFAVYQCQYGSPPYTFGGGTKEIK 107

RESULT 13
 ID W01279 standard; Protein; 104 AA.
 AC W01279;
 DT 29-JAN-1997 (first entry)

DE VL region of HIV neutralising MAB, clone s6.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB, HIV, human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

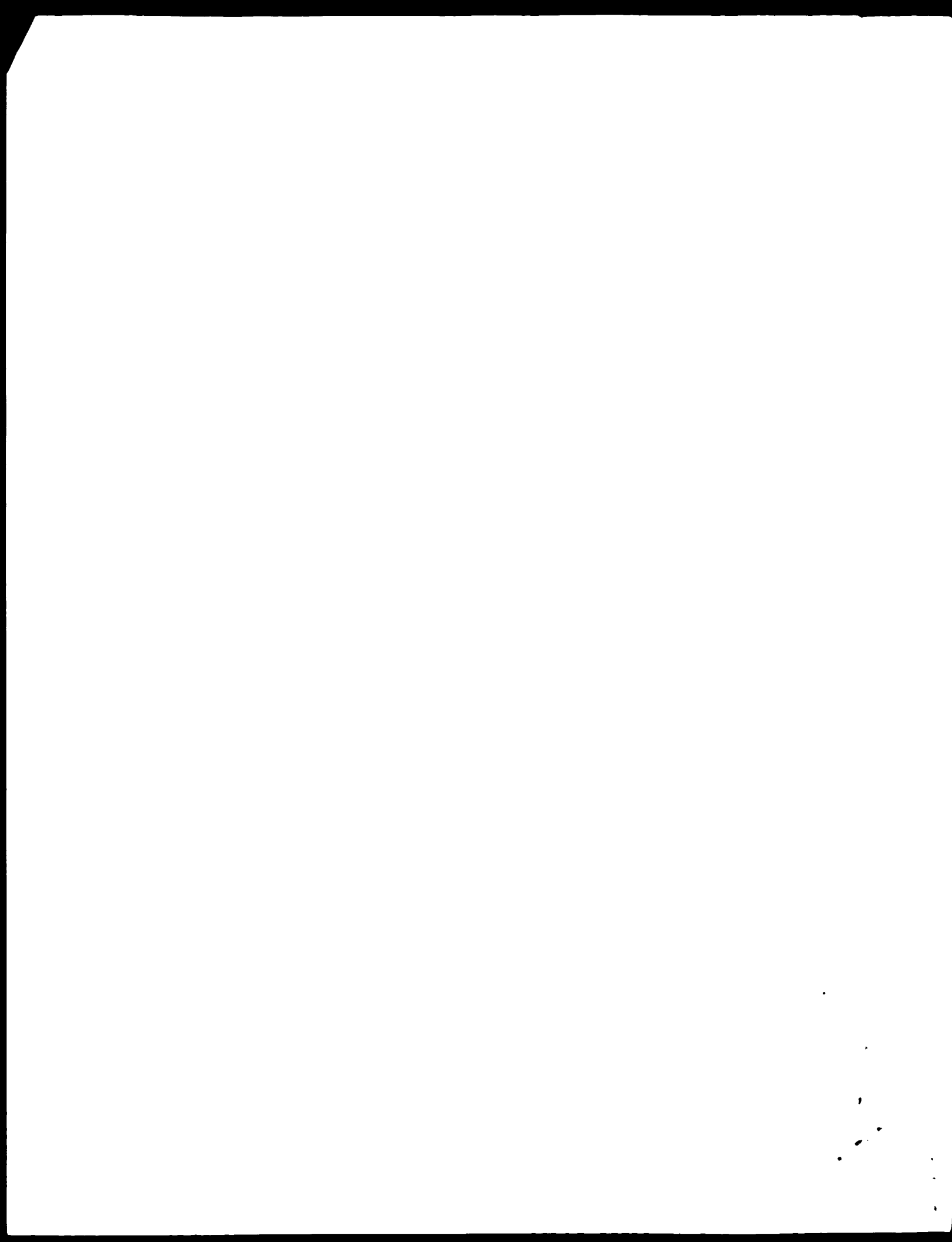
Key Location/Qualifiers

FT Region 1..18
 FT /label= FR1
 FT Region 19..30
 FT /label= CDR1
 FT Region 31..45
 FT /label= FR2
 FT Region 46..52
 FT /label= CDR2
 FT Region 53..84
 FT /label= FR3
 FT Region 85..93
 FT /label= CDR3
 FT Region 94..104
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIpps RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI; 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, s6. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 104 AA;

Query Match 84.3%; Score 648; DB 19; Length 104;
 Best Local Similarity 84.5%; Pred. No. 1.04e-40;
 Matches 87; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Db 1 qspptlslspqervivscrasqsvssnylawyqgkpgqprlliygasmratgipdrfsq 60
 QY 5 QSPPTLSSLVGERATLSPASQNIYSGYLGMWQKPGQPPPELLIYGASNRATGIPDRFSQ 64
 Db 61 gsgsgtdftltisrlepedfavyycqygsgsvytfgggtkveik 103
 QY 62 FSGSGSGTDFTLTISRLESEDFAVYQCQYGSPPYTFGGGTKEIK 107

Abstract



 W O R L D

 (TM)

Release - ID John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, UK
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 MParch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 07:23:21 1998; MaxPar time 7.30 Seconds
 442,233 Million cell updates/sec
 Tabular output not generated.
 Title: >US-08-844-215-11
 Description: (1-106) from US08844215.pep
 Perfect Score: 746
 Sequence: 1 AELQSPATLSVSPGEPASL ..COHYSTWPLTFGGTKVPEK 106
 Scoring Table: PAM 150
 Gap 11
 Searched: 95051 seqs, 30459580 residues
 Post-processing: Minimum Match 48
 Listing first 45 summaries

Database: pif53
 1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:unann2 7:unann3
 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
 13:unann9 14:unann10 15:unann11 16:unann12 17:unann
 18:unrev
 Statistics: Mean 39.648; Variance 128.596; scale 0.308
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

Result No	Score	Query Match	Length	DB ID	Description	Pred No
1	672	90.1	117	7	Ig kappa chain - hum	1.52e-67
2	647	86.7	127	7	Ig kappa chain V reg	2.21e-64
3	627	84.0	124	7	Ig kappa light chain	7.42e-62
4	624	83.6	144	7	Ig kappa chain precu	1.77e-61
5	622	83.4	108	7	Ig kappa chain V reg	3.17e-61
6	614	82.3	108	7	Ig kappa chain V reg	3.23e-60
7	613	82.2	109	7	Ig kappa chain V-reg	4.32e-60
8	612	82.0	109	7	Ig kappa chain V-reg	5.78e-60
9	611	81.9	108	7	Ig kappa chain V-reg	7.72e-60
10	610	81.8	109	7	Ig kappa chain V-reg	1.03e-59
11	610	81.8	114	7	Ig kappa chain V reg	1.03e-59
12	610	81.8	131	7	Ig kappa chain - hum	1.03e-59
13	609	81.6	109	7	Ig kappa chain V-reg	1.38e-59
14	609	81.6	109	7	Ig kappa chain V-reg	1.38e-59
15	606	81.2	115	7	Ig kappa chain V-reg	3.28e-59
16	605	81.1	109	7	Ig kappa chain V reg	4.40e-59
17	604	81.0	111	7	Ig kappa chain V reg	5.88e-59
18	603	80.8	129	2	Ig kappa chain precu	7.85e-58
19	602	80.7	129	2	Ig kappa chain V-reg	1.05e-58
20	601	80.6	128	7	Ig kappa chain V reg	1.40e-58

SUMMARIES

21 600 80.4 109 7 D30601 Ig kappa chain V-reg 1.47e-58
 22 599 80.3 125 7 S43344 Ig kappa light chain 2.50e-58
 23 599 80.2 109 7 PH0963 Ig kappa chain V reg 3.34e-58
 24 596 79.9 109 7 F30607 Ig kappa chain V-reg 5.97e-58
 25 596 79.9 109 7 H30601 Ig kappa chain V-reg 5.97e-58
 26 595 79.8 130 7 S40360 Ig kappa chain - hum 7.57e-58
 27 594 79.6 108 7 C30608 Ig kappa chain V-reg 1.04e-57
 28 594 79.6 109 2 K3HUT1 Ig kappa chain V-reg 1.06e-57
 29 594 79.6 129 2 K3HUT1 Ig kappa chain precu 1.06e-57
 30 594 79.6 129 7 S40325 Ig kappa chain - hum 1.06e-57
 31 593 79.5 107 7 PH0965 Ig kappa chain V reg 1.42e-57
 32 592 79.4 129 7 S43369 Ig light chain varia 1.90e-57
 33 592 79.4 134 7 S38643 Ig kappa chain V reg 1.90e-57
 34 591 79.2 91 7 S37525 Ig kappa chain V reg 2.54e-57
 35 591 79.2 104 7 G30601 Ig kappa chain V-reg 2.54e-57
 36 591 79.2 128 7 S40379 Ig kappa light chain 2.54e-57
 37 590 79.1 108 2 K3HUB6 Ig kappa chain V-reg 3.39e-57
 38 590 79.1 115 2 K3HUC1 Ig kappa chain precu 3.39e-57
 39 590 79.1 128 7 S20636 Ig kappa chain V reg 3.39e-57
 40 589 79.0 129 7 S29627 Ig kappa chain V reg 4.53e-57
 41 587 78.7 110 7 S20635 Ig kappa chain V reg 8.07e-57
 42 587 78.7 115 7 A30553 Ig kappa chain precu 8.07e-57
 43 586 78.6 128 7 S40345 Ig kappa light chain 1.08e-56
 44 586 78.6 129 7 S45432 anti-Sm antibody V 1.04e-56
 45 585 78.4 108 7 E30609 Ig kappa chain V-reg 1.44e-56

ALIGNMENTS

RESULT 1
 ENTRY S40362 #type complete
 TITLE Ig kappa chain - human
 ORGANISM Homo sapiens #common_name man
 DATE 06-Mar-1994 #sequence_revision 26-May-1996 #text_change 16-Aug-1996
 S40362
 S40312
 Klein, R.; Juenichen, R.; Zachau, H.G.
 Eur. J. Immunol. (1993) 23:3249-3271
 Expressed human immunoglobulin chi genes and their
 hypermutation.
 #accession S40362
 #status preliminary; translation not shown
 #molecule_type mRNA
 #residues 1-117 #label KLE
 #cross-references EMBL:X72472
 CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 117 #molecular-weight 12513 #checksum 8309

Query Match 90.1% Score 672; DB 7; Length 117;
 Best Local Similarity 87.5%; Pred. No 1.52e-67;
 Matches 91; Conservative 10; Mismatches 3; Indels 0; Gaps 0

Db 14 mtspstlsvspgertlscragssslawyyqyqpgqprlllygstratgiparis 73
 QY 3 ITSPATLSVSPGEPASLSCPSQSGVNNLAWYQKPSAPPELLYNGTIPATIS-PDRFS 42

Db 74 qsgsgteftlsslsgsfavyyqggnwpltfqgqtkveik 117
 QY 63 GSGSGTEFTLSSLSGSEFAFYVQHYSTWPLTFGGTKVPEK 106

RESULT 2
 ENTRY S34005 #type complete
 TITLE Ig kappa chain V region - human
 ORGANISM Homo sapiens #common_name man
 DATE 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 S34005; S30524
 S34001
 Mariette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. (1993) 23:846-851

```

#title      Nucleotide sequence analysis of the variable domains of four
#accession  S34005
#status     preliminary
#molecule_type mRNA
#residues   1-107 #label MAR
#cross-references EMBL:Z18330
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 107 #molecular-weight 11659 #checksum 7893

Query Match      86.7% Score 647 DB 7 Length 107
Best Local Similarity 85.6% Pred No 2 21e-64
Matches 89; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 4 mtgspatlsppgeratlsrsgsvsnlwyqkpgqaprllygastratgiparfs 63
QY 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQKPGQAPRLLYGGNTRATGTPDRFS 62

Db 64 gsgsgtftltisslqsdafvyyccqyrnwrptfsggtkveik 107
QY 63 GSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 3
ENTRY   S40343 #type complete
TITLE   Ig kappa light chain (VJ) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     19-May-1994 #sequence_revision 26-May-1995 #text_change
16-Aug-1996
ACCESSIONS S40343
REFERENCE  S40312
#authors   Klein, P.; Jaenichen, P.; Zachau, H G
#journal   Eur. J. Immunol. (1993) 23:3248-3271
#title     Expressed human immunoglobulin chi genes and their
           hypermutation.
#accession S40343
#status    preliminary; translation not shown
#molecule_type mRNA
#residues  1-128 #label KLE
#cross-references EMBL:X72453
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 128 #molecular-weight 13950 #checksum 6935

Query Match      84.0% Score 627 DB 7 Length 128
Best Local Similarity 82.7% Pred. No. 7.42e-62
Matches 86; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 24 mtgspatlsppgeratlsrsgsvsnlwyqkpgqaprllygastratgiparfs 83
QY 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQKPGQAPRLLYGGNTRATGTPDRFS 62

Db 84 gsgsgtftltisslqsdafvyyccqyrnwrptfsggtkveik 127
QY 63 GSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 4
ENTRY   PL0106 #type fragment
TITLE   Ig kappa chain precursor V-J-C region (LS1) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
16-Aug-1996
ACCESSIONS PL0106
REFERENCE  PL0106
#authors   Silberstein, L.E.; Litwin, S.; Carmack, C E
#journal   J. Exp. Med. (1989) 169:1631-1643
#title     Relationship of variable region genes expressed by a human B
           cell lymphoma secreting pathologic anti-pr-2 erythrocyte
           autoantibodies.

```

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#cross-references MUID:89235383
#accession  PL0106
#molecule_type mRNA
#residues   1-144 #label SIL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURES      1-20
1-20      #domain signal sequence #status predicted #label SIG
21-115    #domain V region #label VRE
44-54     #region complementarity-determining 1\
70-76     #region complementarity-determining 2\
109-115   #region complementarity-determining 3\
116-127   #domain J region #label JRG
128-144   #domain C region (fragment) #label CPE
SUMMARY     #length 144 #checksum 3623

Query Match      83.6% Score 624 DB 7 Length 144
Best Local Similarity 80.8% Pred. No. 1.77e-61
Matches 84; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Db 24 ltgspatlsppgeratlsrsgsvsnlwyqkpgqaprllydasrnatgiparfs 83
QY 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQKPGQAPRLLYGGNTRATGTPDRFS 62

Db 84 gsgsgtftltisslqsdafvyyccqyrnwrptfsggtkveik 127
QY 63 GSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 5
ENTRY   G44151 #type fragment
TITLE   Ig kappa chain V region (JM-10) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS G44151
REFERENCE  A44151
#authors   Zehedee, S L.; Barbas III, C F.; Hom, Y L.; Caothien, R.H.;
           Graff, R.; DeGraw, J.; Pyati, J.; LaPolla, R.; Burton,
           D.R.; Lerner, P.A.; Thornton, G.B.
           Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
           Human combinatorial antibody libraries to hepatitis B surface
           antigen.
#accession  G44151
#status     Preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues   1-108 #label ZEB
#note       nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 108 #checksum 770

Query Match      83.4% Score 622 DB 7 Length 108
Best Local Similarity 80.2% Pred. No. 3.17e-61
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Db 1 aeltgspatlsppgeratlsrsgsvsnlwyqkpgqaprllydasrnatgipar 60
QY 1 AELTQSPATLSVSPGERASLSCRASQSVGNLAWYQKPGQAPRLLYGGNTRATGTPDRFS 60

Db 61 fsgsgtftltisslqsdafvyyccqyrnwrptfsggtkveik 106
QY 61 FSGSGTEFTLTISLQSDFAVYFCQHYSTWPLTFGGGKVEFK 106

RESULT 6
ENTRY   H44151 #type fragment
TITLE   Ig kappa chain V region (JM-15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS H44151
REFERENCE  A44151

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#authors      Zehedee, S.L.; Barbas III, C.F.; Hom, Y.I.; Coathien, R.H.;
              Graff, R.; DeGraw, J.; Pyati, J.; Capella, R.; Burton,
              D.R.; Lerner, P.A.; Thornton, G.B.
#journal      Proc Natl Acad Sci U S A (1992) 89:3175-3179
#title        Human combinatorial antibody libraries to hepatitis B surface
              antigen.
#accession    H44151
#status       preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues     1-108 ##label ZEB
#note         nucleotide translation not given
#classification #superfamily immunoglobulin V region: immunoglobulin homology
              heterotetramer: immunoglobulin
#keywords      #length 108 #checksum 1576
#summary

Query Match      82.3%  Score 613; DB 7; Length 108;
Best Local Similarity 79.0%  Pred No 3.23e-60;
Matches 85; Conservative 17; Mismatches 3; Indels 2; Gaps 2.

Db 1 aeltqspqtislsperatiscrasqssvssylawyqgkpgqaprllygassratgipd 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 AELTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPGQAPRLLYSGNTPATGTPDF 59
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 fsgsgstetfltlsslsqsdafavyqcgqyassp-tfgggtkveik 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 RFGSGSGTEFTLTSSLSQSDFAVFYFCQHYSTWPLTFGGGTKEVEK 106

RESULT 7
ENTRY   B30601
TITLE   Ig kappa chain V-III region (Glo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
#accessions B30601
#status       preliminary
#molecule_type protein
#residues     1-109 ##label GON
#classification #superfamily immunoglobulin V region: immunoglobulin homology
              heterotetramer: immunoglobulin
#keywords      #length 109 #checksum 5911
#summary

Query Match      82.2%  Score 613; DB 7; Length 109;
Best Local Similarity 79.0%  Pred No 4.32e-60;
Matches 83; Conservative 17; Mismatches 4; Indels 1; Gaps 1.

Db 4 ltspqtislsperatiscrasqssvssylawyqgkpgqaprllygassratgipdrf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 LTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPGQAPRLLYSGNTPATGTPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 64 ssgsgstetfltlsslsqsdafavyqcgqyassp-ltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGTEFTLTSSLSQSDFAVFYFCQHYSTWPLTFGGGTKEVEK 106

RESULT 8
ENTRY   K3HUPM
TITLE   Ig kappa chain V-III region (Pom) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     06-Sep-1995
#accessions A01897
#status       preliminary
#molecule_type protein
#residues     1-109 ##label GON
#classification #superfamily immunoglobulin V region: immunoglobulin homology
              heterotetramer: immunoglobulin
#keywords      #length 109 #checksum 1177
#summary

Query Match      81.9%  Score 611; DB 7; Length 108;
Best Local Similarity 76.2%  Pred No 7.72e-60;
Matches 80; Conservative 21; Mismatches 3; Indels 1; Gaps 1.

Db 4 ltspqtislsperatiscrasqssvssylawyqgkpgqaprllygassratgipdrf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 LTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPGQAPRLLYSGNTPATGTPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 64 ssgsgstetfltlsslsqsdafavyqcgqyassp-ltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGTEFTLTSSLSQSDFAVFYFCQHYSTWPLTFGGGTKEVEK 106

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#title        The amino acid sequence of the variable regions of the light
              chains from two idiotypically cross reactive IgM anti-gamma
              globulins.
#accession    A01897
#molecule_type protein
#residues     1-109 ##label KLA
#comment       This chain was isolated from an IgM with anti-gamma globulin
              activity.
#status       preliminary
#molecule_type protein
#residues     1-109 ##label KLA
#comment       This chain was isolated from an IgM with anti-gamma globulin
              activity.
#status       preliminary
#molecule_type protein
#residues     1-109 ##label GON
#classification #superfamily immunoglobulin V region: immunoglobulin homology
              heterotetramer: immunoglobulin
#keywords      #length 108 #checksum 1177
#summary

Query Match      82.0%  Score 612; DB 2; Length 109;
Best Local Similarity 79.0%  Pred No 5.78e-60;
Matches 83; Conservative 14; Mismatches 7; Indels 1; Gaps 1.

Db 4 mtspvtlspsgeratiscrasqssvssylawyqgkpgqaprllygassratgiparf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 LTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPGQAPRLLYSGNTPATGTPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 64 ssgsgstetfltlsslsqsdafavyqcgqygnwpptfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGTEFTLTSSLSQSDFAVFYFCQHYSTWPLTFGGGTKEVEK 106

RESULT 9
ENTRY   B30608
TITLE   Ig kappa chain V-III region (Sca) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
#accessions B30608
#status       preliminary
#molecule_type protein
#residues     1-108 ##label GON
#classification #superfamily immunoglobulin V region: immunoglobulin homology
              heterotetramer: immunoglobulin
#keywords      #length 108 #checksum 1177
#summary

Query Match      81.9%  Score 611; DB 7; Length 108;
Best Local Similarity 76.2%  Pred No 7.72e-60;
Matches 80; Conservative 21; Mismatches 3; Indels 1; Gaps 1.

Db 4 ltspqtislsperatiscrasqssvssylawyqgkpgqaprllygassratgipdrf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 LTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPGQAPRLLYSGNTPATGTPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 64 ssgsgstetfltlsslsqsdafavyqcgqyassp-ltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 SGSGSGTEFTLTSSLSQSDFAVFYFCQHYSTWPLTFGGGTKEVEK 106

RESULT 10

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ENTRY          C30601      #type fragment
TITLE          Ig kappa chain V-III region (Pay) - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
ACCESSIONS     C30601
REFERENCE       A30601
#authors       Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
                Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
                Frangione, B.
#journal       J. Immunol. (1989) 142:3158-3163
#title        Structural and idiotypic characterization of the L chains of
                human IgM autoantibodies with different specificities.
#cross-references EMBL:X82934
#accession    C30601
#status       preliminary
#molecule_type protein
#residues     1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 6191

Query Match      81.8%; Score 610; DB 7; Length 109.
Best Local Similarity 78.1%; Pred. No. 1.03e-59;
Matches          82; Conservative 18; Mismatches 4; Indels 1; Gaps 1;

Db 4 ltspgtlspgertatlsrscasqsvssylawygqpgqaprllygassratgipdrf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPATLSVSPGERASLSCASQSVGNLAWYQKPKQAPPLIYGGNTPATGTDPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 64 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
ENTRY          S54905      #type fragment
TITLE          Ig kappa chain V region - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS     S54905
REFERENCE       S54905
#authors       Esposito, G.; Traboni, C.
#submission    submitted to the EMBL Data Library, November 1994
#description    Cloning and sequencing of cDNA coding for the variable
                domains of a human antibody against Hepatitis C virus
                helicase.
#accession    S54905
#status       preliminary
#molecule_type mRNA
#residues     1-114 #label ESP
#cross-references EMBL:X82934
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 114 #checksum 5831

Query Match      81.8%; Score 610; DB 7; Length 114.
Best Local Similarity 80.0%; Pred. No. 1.03e-59;
Matches          84; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 4 mtgspatlspgertatlsrscasqsvssylawygqpgqaprllydsrratgiparfs 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPATLSVSPGERASLSCASQSVGNLAWYQKPKQAPPLIYGGNTPATGTDPDF 62
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 64 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY -63 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPL-LTFGGGKVEFK 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
ENTRY          S40328      #type complete
TITLE          Ig kappa chain - human

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ORGANISM       #formal_name Homo sapiens #common_name man
DATE           06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS     S40328
REFERENCE       S40312
#authors       Klein, R.; Jaenichen, P.; Zachau, H.G.
#journal       Eur. J. Immunol. (1993) 23:3248-3271
#title        Expressed human immunoglobulin chi genes and their
                hypermutation.
#accession    S40328
#status       preliminary; translation not shown
#molecule_type mRNA
#residues     1-131 #label KLE
#cross-references EMBL:X72438
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 131 #molecular-weight 14270 #checksum 0795

Query Match      81.8%; Score 610; DB 7; Length 131.
Best Local Similarity 81.4%; Pred. No. 1.03e-59;
Matches          86; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 23 mtgspatlspgertatlsrscasqsvitnlawygqgqgqprllyggytratygtarfs 82
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPATLSVSPGERASLSCASQSVGNLAWYQKPKQAPPLIYGGNTPATGTDPDF 62
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 83 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 127
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPL-LTFGGGKVEFK 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
ENTRY          G30607      #type fragment
TITLE          Ig kappa chain V-III region (Kas) - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
ACCESSIONS     G30607
REFERENCE       A30601
#authors       Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
                Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
                Frangione, B.
#journal       J. Immunol. (1989) 142:3158-3163
#title        Structural and idiotypic characterization of the L chains of
                human IgM autoantibodies with different specificities.
#cross-references EMBL:X8215279
#accession    G30607
#status       preliminary
#molecule_type protein
#residues     1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 4998

Query Match      81.6%; Score 609; DB 7; Length 109.
Best Local Similarity 78.1%; Pred. No. 1.03e-59;
Matches          82; Conservative 18; Mismatches 4; Indels 1; Gaps 1;

Db 4 ltspgtlspgertatlsrscasqsvssylawygqpgqaprllygassratgipdrf 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 3 LTQSPATLSVSPGERASLSCASQSVGNLAWYQKPKQAPPLIYGGNTPATGTDPDF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 64 sgsgsgtdftltisrlepedfavyycqgysppltfgggtkveik 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 SGSGSGTEFTLTSSLOSEDFAVYFCQHYSTWPL-LTFGGGKVEFK 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
ENTRY          A30608      #type fragment
TITLE          Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change

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QY 301 COTCCAGATATGCGAGTGGTGGTAGAGGCTAC 333
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RESULT 12 HS20364 525 bp RNA PRI 03-AUG-1995
LOCUS H sapiens mRNA for immunoglobulin variable region (clone 203-G4)
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 203-G4)
ACCESSION 247271
NID g619492
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Euteria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 525)
REFERENCE Lebecque, S.
AUTHORS Direct Submission
TITLE Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
JOURNAL Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, France, 69572, FRANCE
2 (bases 1 to 525)
REFERENCE Galibert, L., van Dooren, J., Durand, I., Pousset, F., Jefferis, P.,
AUTHORS Bancheureau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur J Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/clone="203-G4"
/tissue_type="blood"
/cell_type="B-lymphocyte"
BASE COUNT 99 a 144 c 173 g 109 t
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Best Local Similarity 80.8%; Pred. No. 7.02e-120;
Matches 311; Conservative 0; Mismatches 60; Indels 14; Gaps 6;
Db 67 ctatgacagctctgggctgaagctaaagcctggctcctggctcctctcctcgaag 126
QY 1 CTCGAGCAGCTCTGGGCTGAGGTCAGAGAGGCTGGGCTGGTGAAGGCTCTGCGAAG 60
Db 127 gctctgagagcaccctcagcagctatctatcagctgggtggcgagcagccctcgaaca 186
QY 61 GCTTCGAGGAGCAGCTTCAGGGGCTATGTTATCAGCTGGGCTGGGAGGAGGAGGAG 120
Db 187 ggccttgagtgagtgaggagatcctcctctcttgggt-----ac-a-gc---aaac 234
QY 121 GGACTTCAGTGGTGGAGAGAGGATGCTATCTTGGTTCGGGAAAGTACGCTCAAAAC 180
Db 235 tacacacagaagttccaggcagagatcacgattaccgcgacacaaatccacacacagcc 294
QY 181 TACGCTTCAGAAATTCGGGAGCAGAGTCTGATTAACGGGACGAAATCCAGAGAGCTGG 240
Db 295 tacatggagctgagcagcctgagatctgagagacacggcgcctgattactgtgcgagagg 354
QY 241 TTCATTGAGCTGAGTAACCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 300
Db 355 gggagcta-aggtcgaattttggagtggtttcagtgagtggtttcagtgagtggtttcag 413
QY 301 COTCCAGATATGCGAGTGGTGGTAGAGGCTAC 333
|||||
Db 414 gggaaacctggctcagctcctcca 438
QY 360 GGGACCCCTGCTCAGCGTCTCTCTCA 384
|||||
RESULT 14 HUMIGHVAN 421 bp mRNA PRI 06-NOV-1994
LOCUS Human (fetal) Ig rearranged H-chain VDJ-region mRNA, clone 51P1.
DEFINITION Human (fetal) Ig rearranged H-chain VDJ-region mRNA, clone 51P1.
ACCESSION M18516
NID g185545
KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
immunoglobulin mu-chain; processed gene; variable region subgroup
VH-1.
SOURCE Homo sapiens foetus liver cDNA to mRNA.
ORGANISM Homo sapiens

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Search completed: Tue Feb 24 09:37:00 1998
Job time : 511 secs.

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OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; .

JOURNAL
Unpublished (1997)


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FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/cclone="810346"
/clonelib="Soares ovary tumor NbHOT"
/sex="Female"
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Best Local Similarity 90.0%; Pred. No. 2.53e-239;
Matches 190; Conservative 0; Mismatches 16; Indels 5; Gaps 3;
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QY 10 ACGCAGTCTCCAGCGCACCCCTGTCTGTCTCCAGGGGAAGAGCCCTCTCTCGAGG 69
Db 140 gccagtcagagtgtagcagcaaa---cttagcctgtaccagcagattcctggccagct 196
QY 70 GCCAGTCACAGCTTTAGTACCAATACCTTAGCTGTGTACCAAGAACTCTGCTTGTATAG 129
Db 197 cccaggtctctcatctatgtgtatccacagggccacttggtatccacagcagattcaga 256
QY 130 CCCAGGCTCTTCATTTATCATGCATCCAGCAGGCGCACTGGCATCCACAGAGCTTTCAG- 188
Db 257 tggcagtgaggtctaggacagagttcactct 287
QY 189 TGGCAGTGGGTCT-TGGGACAGACTTCACCTCT 218
RESULT 11
LOCUS AA494059 217 bp mpNA EST 10-JUL-1997
DEFINITION ng61b01.s1 NCI-CCAP-Lip2 Homo sapiens cDNA clone 939241 similar to
gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION AA494059
NID 92223900
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo;
REFERENCE 1 (bases 1 to 217)
AUTHORS NCI-CCAP.
TITILE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Location/Qualifiers
FEATURES

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/organism="Homo sapiens"
/note="Vector: pAMP10. mRNA made from liposarcoma. cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
/clone="939241"
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BASE COUNT
ORIGIN

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Matches 154: Conservative 0: Mismatches 17: Indels 0: Gaps 0:

Db 47 acgcaactcgcagcaccctcttcttcacagggaaacagcaccctctctgcagg 106
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Db 107 gccagtcagagtgtagcaccagtaacttagccttgtagcagcagcagcagcagc 166
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QY 70 GCCAGTCAGAGTCITAGAGCAAAATACIIASINIGGACCAAGAAAGAAAGCAAGCT 129
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Db 167 cccagctctcattatgtatgttcacagggagggagggagggagggagggagggag 217
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 130 CCCAGCTCTTTCATTATGATGATCCAGGAGGGGACATGGCATCCAGAC 180
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RESULT 12
ID HS1284569 standard: RNA: EST: 217 BP.
AC AA444039:
NI 92223900
DT 28-JUN-1997 (Rel. 52, Created)
DE n61b01.s1 NCI-CGAP Lip2 Homo sapiens cDNA clone 939241 similar to
DE qb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
OC Homo.
RN [1]
RP 1-217
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,
CC M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:
CC David B. Krizman, Ph.D. cDNA Library Arrayed by Greg Lennon, Ph.D.
CC DNA Sequencing by: Washington University Genome Sequencing Center
CC Clone distribution: NCI-CGAP clone distribution information can be
CC found through the I.M.A.G.E. Consortium/LLNL at:
CC www.bio.llnl.gov/bbrp/image/image.html Insert Length: 922 Std
CC Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham.
CC Location/Qualifiers
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FH source
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/organism="Homo sapiens"
/note="Vector: pAMP10. mRNA made from liposarcoma. cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
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<1..217
44 a 75 c 55 g 43 t
BASE COUNT
ORIGIN

Query Match 43.5% Score 138: DB 38: Length 217:
Best Local Similarity 90.1%: Prod. No. 8.85e-225:
Matches 154: Conservative 0: Mismatches 17: Indels 0: Gaps 0:

Db 47 acgcaactcgcagcaccctcttcttcacagggaaacagcaccctctctgcagg 106
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QY 10 ACCGAGTCTCCAGGACACCTCTCTCTCTCCAGGAAAGGACACCTCTCTCTCAGG 69
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Db 107 gccagtcagagtgtagcaccagtaacttagccttgtagcagcagcagcagcagc 166
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QY 70 GCCAGTCAGAGTCITAGAGCAAAATACIIASINIGGACCAAGAAAGAAAGCAAGCT 129
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Db 167 cccagctctcattatgtatgttcacagggagggagggagggagggagggagggag 217
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QY 130 CCCAGCTCTTTCATTATGATGATCCAGGAGGGGACATGGCATCCAGAC 180
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RESULT 13
ID HS1145281 standard: PNA: EST: 260 BP.
AC AA225858:
NI 91847166
DT 23-FEB-1997 (Rel. 51, Created)
DE 26-JUL-1997 (Rel. 52, Last updated, Version 5)
DE n627d05.s1 NCI-CGAP Pri Homo sapiens cDNA clone 1009353 similar to
DE qb:Z11894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
OC Homo.
RN [1]
RP 1-260
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: W. Marston Linehan,
CC M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA
CC Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed
CC by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone distribution:
CC NCI-CGAP clone distribution information can be found through the
CC I.M.A.G.E. Consortium/LLNL at:
CC www.bio.llnl.gov/bbrp/image/image.html Insert Length: 1066 Std
CC Error: 0.00 Seq primer: -41ml3 fwd. ET from Amersham High quality
CC sequence stop: 250.
CC Location/Qualifiers
FH
FH source
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/organism="Homo sapiens"
/note="Vector: pAMP10. Site: 3. Not. Site: 2. EcoRI: 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal prostatic
epithelial cells. Double-stranded cDNA was ligated to EcoR
adaptors, 5 cycles of PCR applied to the cDNA with an
adaptor-specific primer, and the resulting PCR product
subcloned into pAMP10 by the topo-cloning method (Life
Technologies). Average insert size is 600 bp. Note: Not
directionally cloned. This library was constructed by David
Krizman."
/clone="1009353"
/clone_lib="NCI-CGAP_Pri1"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"

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FT mRNA <1..>260
SQ Sequence 260 RF: 57 A, 84 C, 66 G, 49 T, 4 others:

Query Match 42.9%; Score 136; DB 49; Length 260;
Best Local Similarity 91.6%; Pred No. 1,24e-220;
Matches 153; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Db 90 cgcagctccaggccacctgttcttctccaggaggagccaccctctctcgcagg 149
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QY 11 CGCAGCTCCAGGCACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCTGCA 70

Db 150 ccagtcagagtgatcagcagcagatacttagccctgggtaccacaaacccctgcccaggct 209
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QY 71 CCAGTCCAGAGTCTTAGCAGCAATACCTTAGCN-TGCTACCAACAGAACTGGCCAGGCT 129

Db 210 cccaggtcctcatatgctgctgctccagggagggccactggtatccc 256
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QY 130 CCCAGGCTCTTCATTATGATGCATCCAGCAGGCGCCACTGGCATCCC 176

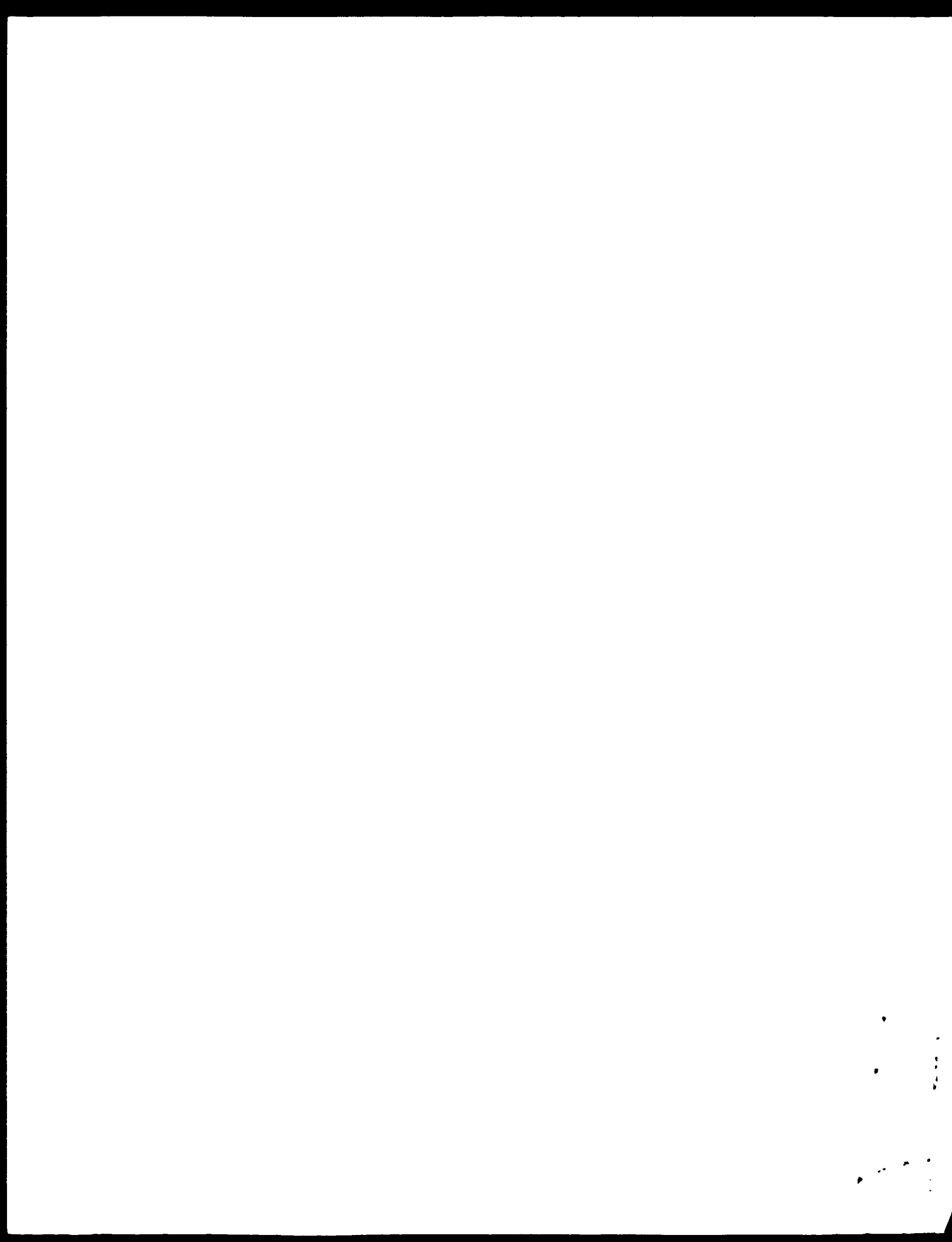
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gb:211894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION AA225858
NID 91847166
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes, Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria, Primates, Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS NCI-CGAP.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph D
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,
M D, Michael Emmert-Buck, M D, Ph D
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1066 Std Error: 0.00
Seq primer: -4lm13 fwd. ET from Amersham
High quality sequence stop: 250
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/notes="vector: pAMP10; Site_1: NotI, Site_2: EcoRI, 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
/clone="3490"
/clone_lib="NCI_CGAP_Prl"
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mRNA

BASE COUNT 57 a 84 c 66 g 49 t 4 others
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Best Local Similarity 89.5%; Pred No. 2,72e-210;
Matches 153; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Db 93 acgagctccaggccacctgttcttctccaggaggagccaccctctctcgcagg 152

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SUMMARIES

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	240	75.7	400	11	AA356778	rw27f11_r1 Soares ova	5 000-00
2	233	73.5	349	59	AA379044	EST11990 Skin tumor r1	0 000-00
3	227	71.6	341	21	AA350582	EST13447 Testis tumor	0 000-00
4	220	69.4	345	33	AA345486	EST11505 Gall bladder	0 000-00
5	217	68.5	405	52	AA360232	EST19341 Lymph node r1	0 000-00
6	201	63.4	328	24	AA295311	EST100471 Pancreas tu	0 000-00
7	190	59.9	370	24	AA295093	EST100400 Pancreas tu	0 000-00
8	177	55.8	277	24	AA295377	EST100548 Pancreas tu	0 000-00
9	173	54.6	289	37	AA337318	EST10586 Colon r1 Hom	1 150-000
10	168	53.0	284	24	AA256154	EST100323 Pancreas tu	4 710-220
11	161	50.8	294	55	AA366461	EST17408 Pancreas tum	3 160-275
12	156	49.2	253	25	AA295941	EST10156 Thymus r1 r1	1 160-264
13	156	49.2	269	87	AA343001	rw25f01_r1 Soares ova	2 160-264
14	156	49.2	263	55	AA367405	EST178511 Pancreas tu	1 160-264
15	143	45.1	283	53	AA361578	EST100041 T-cell lymph	2 630-237
16	142	44.8	209	100	AA392250	rw20a12_r1 Soares ova	3 340-235
17	140	44.2	209	100	AA392250	rw20a12_r1 Soares ova	5 190-231
18	139	43.8	238	62	AA333934	EST17307 Thymus r1 Ho	6 450-229
19	136	42.9	260	71	AA325588	nc27305_s1 NC1 CGAP F	1 220-222
20	129	40.7	230	87	AA434180	rw27b10_s1 Soares ova	4 880-208
21	129	40.7	243	99	AA284594	rw20a11_r1 Soares ova	4 880-208
22	126	40.7	243	93	AA422162	rw31a03_r1 Soares ova	4 880-208
23	127	40.1	256	90	AA234462	rw24a03_r1 Soares ova	4 960-204
24	125	39.4	253	100	AA291691	rw39e12_r1 Soares ova	1 010-199
25	119	37.5	244	85	AA420555	rw23h09_r1 Soares ova	2 730-187
26	117	36.9	249	79	AA432153	rw5e05_r1 Soares ova	3 700-183
27	117	36.9	345	39	AA350866	EST130457 Esophagus tu	3 700-183
28	116	36.6	255	100	AA392247	rw20a12_r1 Soares ova	4 280-181
29	113	35.6	352	27	AA331261	EST14181 Testis tumor	6 490-175
30	106	33.4	240	86	AA419046	rw34c09_r1 Soares ova	1 490-160
31	106	33.4	248	86	AA430449	rw20f11_r1 Soares ova	1 490-160
32	106	33.4	357	53	AA331497	EST171040 T-cell lymph	1 490-160
33	106	33.4	413	27	AA301347	EST14279 Testis tumor	1 490-160
34	105	33.1	362	25	AA295786	EST100987 Pancreas tu	1 650-158
35	102	32.2	233	25	AA300732	EST113847 Testis tumor	2 370-152
36	99	31.2	239	72	AA230271	nc13b04_r1 NC1 CGAP F	2 750-146
37	99	31.2	235	33	AA318177	EST10620 Spleen r1 Hom	2 750-146
38	94	29.7	263	26	AA303631	EST117654 Testis tumor	3 450-136
39	93	29.3	334	37	AA373254	EST140547 Colon r1 Hom	3 810-134
40	92	29.0	303	26	AA300890	EST130431 Testis tumor	3 940-132
41	92	29.0	298	84	AA422447	rw00a03_r1 Soares ova	3 940-132
42	91	29.0	297	22	AA350788	EST13648 Testis tumor	4 060-130
43	89	28.1	442	80	AA405445	rw56302_r1 Soares ova	4 220-126
44	84	26.5	292	24	AA295508	EST100751 Pancreas tu	4 350-116
45	82	25.9	292	26	AA295508	EST12403 Testis tumor	3 940-110

Comments

[illegible]

REFERENCE 1 (bases 1 to 264)

AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Buit, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C., Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, E., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Sauder, D.M., Shirley, P., Small, K.V., Spriggs, J.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Fertle, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Other ESTs: THCL69106
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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/organism="Homo sapiens"
/note="Organ: pancreas. Vector: pBluescript SK-, Site_1."
ECORI: Site_2: XhoI
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
BASE COUNT 53 a 79 c 69 g 56 t 7 others
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Best Local Similarity 91.88; Pred. No. 4,71e-290;
Matches 178; Conservative 0; Mismatches 16; Indels 0; Gaps 0.

Db 71 acgagctnccagcaccctgttttcttccaggggaagagccaccctctcttcgagg 130
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QY 10 ACGTAGTCTAGGTAACCTGCTTTTCTGCTCAGGGGAAAGAGACACCTCTCTTCCAGG 69
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Db 131 gccagttagagtttagcagcagctacttagctgtaccagcagaacacctggcagct 190
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QY 70 GCCAGTCAGAGCTTTAGCAGCAAAATAGTGNIGTATGACCAACAGAAACCTGGCAGGCT 129
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Db 191 ccagagctctnattctatgttgcattccagagagggccactggcattccagcagagttcagt 250
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QY 130 CCCAGGCTTTTCAITATGATGATATGACAGAGGGGAGGATGAGTATCCACAGAGGTTCAST 189
|||||
Db 251 gccagtgaggtctgag 264
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QY 190 GGCAGTGGGTCTGG 203
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RESULT 11
LOCUS AA366461 294 bp mRNA EST 21-APR-1997
DEFINITION EST77408 Pancreas tumor III Homo sapiens cDNA, end similar to similar to immunoglobulin kappa light chain, V region.
ACCESSION AA366461
NID Q2018779

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 294)

AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Buit, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C., Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, E., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Sauder, D.M., Shirley, P., Small, K.V., Spriggs, J.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Fertle, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Other ESTs: THCL68243
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.

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/note="Organ: pancreas. Vector: pBluescript SK-, Site_1."
ECORI: Site_2: XhoI
/clone_lib="Pancreas tumor III"
/dev_stage="adult"
BASE COUNT 64 a 87 c 77 g 64 t 2 others
ORIGIN
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Best Local Similarity 88.88; Pred. No. 3,15e-275;
Matches 182; Conservative 0; Mismatches 23; Indels 0; Gaps 0.

Db 85 acgaattctccagcaccctctgttcttccaggggaagagccaccctctcttcgagg 144
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QY 10 ACGCAGTCTCCAGGACCTGCTGTTTGTCTCAGGGGAAAGAGACACCTCTCTTCCAGG 69
|||||
Db 145 gccagttagagtttagcagcagctacttagctgtaccagcagaacacctggcagct 204
|||||
QY 70 GCCAGTCAGAGCTTTAGCAGCAAAATAGTGNIGTATGACCAACAGAAACCTGGCAGGCT 129
|||||
Db 205 ccagagctctctatctatgttgcattccagagagggccagttgttccagcagaattcagt 264
|||||
QY 130 CCCAGGCTTTTCAITATGATGATATGACAGAGGGGAGGATGAGTATCCACAGAGGTTCAST 189
|||||

Db 265 gccagtgaggtctggcagagattca 289
|||||

QY 190 GGCAGTGGGTCTGGGACAGACTTCA 214
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RESULT 12

LOCUS AA295941 253 bp mRNA EST 18-Apr-1997
 DEFINITION EST101165 Thymus III Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:Y00640).
 ACCESSION AA295941
 NID Q1948286
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
 Homo.
 REFERENCE 1 (bases 1 to 253)
 AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S. Jr., Kelley,J.M., Kelley,J.C., Liu,L.T., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,P.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Pyder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarek,D.P., Gao,L., Cepeda,M.A., Coleman,T.A., Collins,F.J., Dimke,D., Feng,D.-F., Perlie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,P.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Rubin,S.M., Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
 MEDLINE 96026280
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
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 /note="Organ: thymus; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
 /clone_lib="Thymus III"
 /dev_stage="adult"
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 Best Local Similarity 86.8%; Pred. No. 116c-264;
 Matches 197; Conservative 0; Mismatches 27; Indels 3; Gaps 3.
 Db 6 acttagctgtaccagcagcaaaacctggccagntcccccaggtcctctatctatgtgcat 65
 Qy 95 ACTTAGCTGTGTAACACAGAAACCTGGCCAGGCTCCCGAGGCTCTTCATTATGATGAT 154
 Db 66 ccacagggccactgattccacagcaggttcagtgccagtggtctgggacagattca 125
 Qy 155 CCACAGGGCCACTGATTCTTATAGAGTTTASTGGTCTGGACAGACTTCA 214
 Db 126 ctctccaccatcagcagcagctcagctgaagattttncagctttattactgtcagcagata 185
 Qy 215 CTCTCCACATCAGCAGTAAGTGAAGCTGAAGATTTTCAGCTGATTAATGTCAGCAGTATG 274
 Db 186 aaaactggccagagacgtcttcggccagggacccaagtggaatacaaa 232

Qy 275 GAA-CACCTC-GC-ACCTTCGCCAGGGGACCAAGGTGGAAATCAAA 318
 RESULT 13
 LOCUS AA434001 269 bp mRNA EST 20-MAY-1997
 DEFINITION ZW25f01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 770329 5' similar to gb:Z11894 IG KAPPA CHAIN PREPUSOP V-III REGION (HUMAN).
 ACCESSION AA434001
 NID Q2138915
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
 Homo.
 REFERENCE 1 (bases 1 to 269)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marfa,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisinger,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through INM: contact the IMAGE Consortium (info@image.liml.grv) for further information.
 Seq primer: -28ml3 rev2 ET from Amersham.
 FEATURES
 source
 1..269
 /organism="Homo sapiens"
 /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGGGGGGTTTITTTTITTTTITTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
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 BASE COUNT 59 a 90 c 67 g 53 t
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 Best Local Similarity 95.3%; Pred. No. 116c-264;
 Matches 163; Conservative 0; Mismatches 8; Indels 0; Gaps 0.
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 Db 159 gccagtcagagtggttagcagcagctacttaccctgggtaccacagaacacagcagct 218
 Qy 70 GCCAGTCAGAGTCTTAGCAGCAATACCTTAGCCTTAGCCTTAGCCTTAGCCTTAGCCT 129
 Db 219 ccagggtcctcatctatgttgctccagcagggccagcagcagcagcagcagcagcagc 269
 Qy 130 CCAGGCTCTTCAATTTATTSATGATCCAGCAAGGAGGCAATGCAATGCAATGCAATG 180

RESULT 14 AA367405 363 bp mRNA EST 21-APR-1997
LOCUS ES17851: Pancreas tumor 11: Homo sapiens cDNA 5' end similar to
DEFINITION similar to immunoglobulin kappa light chain.
ACCESSION AA367405
NID Q2019753
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C.,
 Clayton, P.A., Cline, J.K., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Pyder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.Y.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
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 Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M. and Venter, J.C.
TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (5547 Suppl), 3-174 (1995)
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COMMENT Contact: Kerlavage, AR
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 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavage@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M3 Reverse.
FEATURES source
 location/Qualifiers
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 /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
 /clone_lib="Pancreas tumor III"
 /dev_stage="adult"
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 Db 118 tctctatcatcagtgatgtgtccagggccacgtggtactccgcgcaccttcaagtcagtggt 177
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Db 178 ggctcgacacagaattcaactctccatccatccagggcgcgcgtgcactctgaggaattttacatat 247
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 Db 238 actattgtacacatatataactggacctctcaactctctctctctctctctctctctctctct 247
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 QY 257 ATTACTGTACGACGATATGG-AACA--CTTCGCACTCTTCCGCGAGGAGGACACACGAGAA 313
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 Db 298 tcaa 301
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 QY 314 TCAA 317
RESULT 15 AA361678 283 bp mRNA EST 21-APR-1997
LOCUS ES170893: T-cell lymphoma Homo sapiens cDNA 5' end similar to
DEFINITION similar to immunoglobulin kappa variable region (JH:100640).
ACCESSION AA361678
NID Q2013998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C.,
 Clayton, P.A., Cline, J.K., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
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 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Pyder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.Y.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M. and Venter, J.C.
TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (5547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESTs: THC168243
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavage@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M3 Reverse.
FEATURES source
 location/Qualifiers
 1..283
 /organism="Homo sapiens"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"
 /clone_lib="T-cell lymphoma"
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 Best Local Similarity 98.5%; Pred. No. 2166-237;

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Db 147	agagtgttagcag--aa-acttagcctgggtccagcagaaacctggccagcctcccaggc	203			
Qy 77	AGAGTCTTAGCAGCAAAATACCTTAGCTGTACCAACAGAAACCTGGCCAGGCTCCACAGGC	136			
Db 204	tectnttctatgggtccctccaccaggccactgggtatcccagccaggttcaagtggcaagt	263			
Qy 137	TCTTCATTATGATGTCATCCAGCAGGGCCACTGSCATCCACAGAGGTTTAGTGGCAGTG	196			
Db 264	ggtctggccacagagtttcaact	283			
Qy 197	GGTCTGGGACAGACTTCACT	216			

Search completed: Tue Feb 24 09:25:31 1998
 Job time : 130 secs.

WATERMAN

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MPsrch_nnn n a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 09:19:27 1998 Maspar time 204 25 Seconds
768,844 Million cell updates/sec
Tabular output not generated

Title: >US-08-844-215-21
Description: (1-118) from US08844215.seq
Perfect Score: 317
N.A. Sequence: 1 GCGCAGGTCACGCAATGTCG
Comp: CGCTTCAGTGTCTCAAGCG

Scoring table:
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 565703 seqs, 246912890 bases x 2
Post-processing: Minimum Match 84
Listing first 45 summaries

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1-EST1 2-EST2 3-EST3 4-EST4 5-EST5 6-EST6 7-EST7 8-EST8	9-EST9 10-EST10 11-EST11 12-EST12 13-EST13 14-EST14
15-EST15 16-EST16 17-EST17 18-EST18 19-EST19 20-EST20	21-EST21 22-EST22 23-EST23 24-EST24 25-EST25 26-EST26
27-EST27 28-EST28 29-EST29 30-EST30 31-EST31 32-EST32	33-EST33 34-EST34 35-EST35 36-EST36 37-EST37 38-EST38
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63-EST63 64-EST64 65-EST65 66-EST66 67-EST67 68-EST68	69-EST69 70-EST70 71-EST71 72-EST72 73-EST73 74-EST74
75-EST75 76-EST76 77-EST77 78-EST78 79-EST79 80-EST80	81-EST81 82-EST82 83-EST83 84-EST84 85-EST85 86-EST86
87-EST87 88-EST88 89-EST89 90-EST90 91-EST91 92-EST92	93-EST93 94-EST94 95-EST95 96-EST96 97-EST97 98-EST98
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184-EST184 185-EST185 186-EST186 187-EST187 188-EST188
189-EST189 190-EST190 191-EST191 192-EST192 193-EST193
194-EST194 195-EST195 196-EST196

Statistics: Mean 3.928; Variance 1.999; scale 5.292

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	228	71.9	381.58	T29114	EST69430 Homo sapiens	0.00e+00
2	217	68.5	383.59	T29145	EST99471 Homo sapiens	0.00e+00
3	211	66.6	383.58	T27870	EST19007 Homo sapiens	0.00e+00
4	192	60.6	575.34	P75233	Y38138 H1 Homo sapiens	0.00e+00
5	184	58.0	463.34	H45532	Y38286 H1 Homo sapiens	0.00e+00
6	183	57.7	389.69	H44798	YF4410 H1 Homo sapiens	0.00e+00
7	182	57.4	401.40	P10529	YF4186 H1 Homo sapiens	0.00e+00
8	181	57.1	332.58	T29342	EST77121 Homo sapiens	0.00e+00
9	180	56.8	359.64	H27642	Y15107 H1 Homo sapiens	0.00e+00
10	159	50.2	451.10	T90236	Y15d10 H1 Homo sapiens	1.38e-271
11	146	45.1	171.64	H25498	Y14786 H1 Homo sapiens	4.31e-274
12	143	45.1	385.64	H45475	Y15195 H1 Homo sapiens	9.02e-238
13	136	42.9	421.27	P48043	Y35581 H1 Homo sapiens	4.64e-223
14	127	40.1	360.37	P39907	Y35501 H1 Homo sapiens	3.12e-204
15	125	39.4	261.28	P51942	Y37167 H1 Homo sapiens	4.1e-200
16	124	39.1	438.23	R45693	Y122109 H1 Homo sapiens	5.58e-198
17	122	38.5	235.65	H28891	Y30311 H1 Homo sapiens	8.08e-194
18	115	36.3	232.63	H21646	Y33361 H1 Homo sapiens	2.65e-179
19	114	36.0	219.64	H27031	Y15591 H1 Homo sapiens	2.09e-177
20	109	34.4	201.64	H25206	Y13532 H1 Homo sapiens	5.22e-167
21	108	34.1	493.58	T27593	EST10965 Homo sapiens	7.21e-165
22	100	31.5	130.59	H44328	Y304110 H1 Homo sapiens	1.74e-148
23	97	30.6	176.81	H54909	Y35510 H1 Homo sapiens	2.22e-142
24	96	30.3	151.81	H22088	Y134205 H1 Homo sapiens	2.40e-140
25	96	30.3	364.58	T27594	EST10964 Homo sapiens	2.40e-140
26	93	29.2	470.81	H22117	Y34301 H1 Homo sapiens	2.89e-134
27	91	28.7	447.84	H26746	Y35512 H1 Homo sapiens	3.18e-130
28	87	27.4	516.23	P75559	Y14241 H1 Homo sapiens	3.55e-122
29	86	27.1	279.58	T26456	EST29311 Homo sapiens	3.61e-120
30	85	26.8	503.22	P28231	Y35508 H1 Homo sapiens	3.61e-120
31	85	26.8	295.58	T29112	EST69384 Homo sapiens	3.61e-118
32	85	26.8	433.11	T29119	Y34287 H1 Homo sapiens	3.61e-118
33	82	26.5	330.41	H25942	Y32214 H1 Homo sapiens	3.62e-116
34	82	25.9	488.64	H25535	Y14839 H1 Homo sapiens	3.74e-112
35	79	24.9	457.64	H27034	Y15535 H1 Homo sapiens	2.22e-106
36	75	23.7	297.29	P49711	Y35503 H1 Homo sapiens	2.54e-98
37	74	23.3	261.27	P45879	Y34503 H1 Homo sapiens	2.94e-96
38	73	23.0	210.34	P28493	Y23633 H1 Homo sapiens	1.74e-94
39	71	22.4	288.58	T27721	EST13641 Homo sapiens	1.74e-90
40	71	22.4	359.58	T27597	EST10975 Homo sapiens	1.74e-90
41	70	22.1	203.68	H39742	Y36307 H1 Homo sapiens	1.54e-88
42	69	21.8	189.51	P29213	Y14d10 H1 Homo sapiens	1.35e-86
43	69	21.8	438.24	P29535	Y14212 H1 Homo sapiens	1.35e-86
44	67	21.1	288.58	T27591	EST190107 Homo sapiens	1.01e-82
45	67	21.1	366.64	H27048	Y35516 H1 Homo sapiens	1.01e-82

ALIGNMENTS

RESULT 1
LOCUS T29114 381 bp mRNA EST 06-SEP-1995
DEFINITION EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V(LII),J(V) regions (GB:227176) (H1:3121).
ACCESSION T29114
NID g611212
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human Lymphoid tissue.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 381)

AUTHORS
Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
Buit,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Chiu,M.-W.,
Clayton,P.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudak,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,F.J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Fannon,M.P., Rosen,C.A.,
Yu,G.-L., Puhon,S.M., Dillon,P.J., Fannon,M.P., Rosen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.

TITLE
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence

JOURNAL
Unpublished (1995)

COMMENT
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org)

FEATURES
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/organism
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QY 17 ctccaggcaccctgtcttntccagggtatagaccacccctctctgcaggccagtc 76
Db 147 agagtgttagcagcaactacctagctgtgtaccagcagaaacctggccaggtcccagc 206
QY 77 AGAGCTTTAGCAGCAAACTACTAGTGTGTACCAACAGAACTGTGCTAGGCTCCAGGC 136
Db 207 tctctatctatgatcatccacagagggcgcgtggcgtatccagacagagttcaactggcagtg 266
QY 137 TCTTCATTTATCATCCAGCAGGGGCCACTGGCATCCCAAGACAGGTTTCAGTGGCAGTG 196
Db 267 ggtctgggacagacttcaactcaccatcagcagacttgagcctgaagattttgagtg 326
QY 197 GGTCTGGGACAGACTTCTCTCATCATCATAGATAGATAGATAGATAGATAGATAG 255
Db 327 tattnctgtcagcagatg 346
QY 256 TATTACTGTACAGATATGG 275

RESULT 2
LOCUS T29916 383 bp mRNA EST 06-SEP-1995
DEFINITION EST99871 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
light chain, V region (GB:M27025) (HT:3778).

ACCESSION T29916

9612014
EST.
human primer=M13 Reverse library-Human Pancreas.
Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 383)

AUTHORS
Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
Buit,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
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FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudak,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,F.J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Fannon,M.P., Rosen,C.A.,
Yu,G.-L., Puhon,S.M., Dillon,P.J., Fannon,M.P., Rosen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.

TITLE
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence

JOURNAL
Unpublished (1995)

COMMENT
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org)

FEATURES
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/organism
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Best Local Similarity 88.5%; Pred. No. 0.00e-00;
Matches 278; Conservative 0; Mismatches 30; Indels 6; Gaps 4;
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QY 10 ACCGAGCTCTCCAGGCACTGTCTTTTCTCTCAGAGGAAAGAGCACTCTCTCTCAGG 69
Db 111 gccagtcagagtggttagcaacaactcttagcctgtatccacagcaaacacctggccagnt 170
QY 70 GCCAGTCAGAGTCCTTAGCAGTAATACTTAGCTGTGATCAACAGAACTCTGCCAGGT 129
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QY 130 CCTAGGCTCTCTCATTTATGATGCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 189
Db 231 ggcagtggtggtctgggacagacttctactcttgaacctcagcagcagcagcagcagc 290
QY 190 GGCAGTGGGTCTGGACAGAGACTT-CAGTCTC-AGCAGTACAGAGTGGAGTGGAGT 247
Db 291 ttgcagctgattactgctcagcagtgatgtgtgactcaccgggagcgttctggagagagc 350
QY 248 TT-TCAGTGTATTACTGTCACTA31ATGGAAA---CAGCTCTCTCAGTCTCTCTCAGG 303
Db 351 aagctggaagtc 364
QY 304 AAGGTGGAAATCAA 317

Db 266 ggtctgggacagagttctttctcaccatcagcagcctgcagcctgaagattttgcagttt 325

Dh 250 qtgacagtggtctgggacagacttcactctaccattcaccagactgcggagcctgaag 309

[illegible]

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 RS1922
 NID g813824
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 SOURCE human clone-154165 library-Soares breast 2NBHst vector-pT73D
 (Pharmacia) with a modified polylinker host-DH10B (ampicillin
 resistant) primer-M13Rpi Rsite1-Not I Rsite2-Eco RI Adult female.
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATGAGGAGCGGCCCTTTTITTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned into the Not I and Eco RI sites of a
 modified pT73 vector (Pharmacia). Library went through one round
 of normalization to a Cot - 230. Library constructed by Bento
 Soares and M.Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 361)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewarton.wustl.edu
 High quality sequence stops: 308
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 Matches 224; Conservative 0; Mismatches 30; Indels 12; Gaps 11;
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 QY 136 CTCTTCATTTATGATG-CATCTATCTAGGCT-CTATCTGGAAT-CCACAGAGGTTTCACTGG- 191
 Db 268 cagtgaggtctggagacagagttccatttccaccatcagcagcctgcagttctgaagattt 327
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 QY 249 TCCAGTGTATTACTGT-CAGCAGTAT 273

Search completed: Tue Feb 24 09:23:01 1998
 Job time : 214 secs.



Release 2 to John F. Collins, BioComputing Research Unit
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MPSrch_n n a - n a database search using Smith-Waterman algorithm

Run on: Tue Feb 24 14:53:12 1998: Maspar time 19 75 Seconds
Tabular output not generated. 740 666 Million cell updates/sec

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N.A. Sequence: 317
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Scoring table: TABLE default
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Searched: 87531 seqs, 2299521 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Statistics: Mean 7.643: Variance 4 250: scale 1 798

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description	Prod No
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2	258	91.4	646 12	PCT-US94-0	Sequence 2, Application	1 728-172
3	259	91.4	646 7	US-08-290	Sequence 2, Application	1 728-172
4	247	77.9	900 7	US-08-053	Sequence 182, Application	3 856-164
5	238	75.1	325 11	PCT-US93-1	Sequence 1, Application	2 578-157
6	215	67.8	812 7	US-08-053	Sequence 178, Application	6 488-140
7	209	65.9	900 7	US-08-053	Sequence 190, Application	2 190-135
8	197	62.1	729 13	US-08-276	Sequence 152, Application	2 440-126
9	197	62.1	729 13	PCT-US95-0	Sequence 152, Application	2 440-126
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11	197	62.1	729 7	US-08-276	Sequence 156, Application	2 440-126
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13	197	62.1	13254 13	PCT-US95-0	Sequence 170, Application	2 440-126
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15	197	62.1	350 5	US-08-026	Sequence 3, Application	3 836-71
16	123	39.8	387 5	US-08-217	Sequence 1, Application	2 096-70
17	112	37.5	280 7	US-08-200	Sequence 52, Application	3 358-68
18	119	37.5	280 13	PCT-US95-1	Sequence 52, Application	3 358-68
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20 117 36.9 381 7 US-08-474- Sequence 82, Applicati 9 866-67
21 117 36.9 381 6 US-07-634- Sequence 82, Applicati 9 866-67
22 117 36.9 381 5 US-08-477- Sequence 82, Applicati 9 866-67
23 117 36.9 381 7 US-08-487- Sequence 82, Applicati 9 866-67
24 117 36.9 847 7 US-08-053- Patent 184, Applicat 9 866-67
25 117 36.9 6238 1 5453363-1 Patent No. 5453363 9 866-67
26 114 36.0 599 6 US-08-339- Sequence 3, Applicatio 1 560-64
27 114 36.0 729 1 5455030-1b Patent No. 5455030 1 560-64
28 113 36.6 360 7 US-08-447- Sequence 13, Applicati 8 448-64
29 113 35.6 1848 7 US-08-447- Sequence 15, Applicati 8 448-64
30 112 35.3 333 11 PCT-US93-0 Sequence 8, Applicatio 4 558-63
31 112 35.3 648 7 US-08-353- Patent No. 5455030 4 558-63
32 109 34.4 940 7 US-08-353- Sequence 24, Applicati 7 110-61
33 108 34.1 327 12 PCT-US94-0 Sequence 3, Applicatio 3 628-60
34 107 33.9 329 11 PCT-US93-0 Sequence 5, Applicatio 2 058-59
35 107 33.8 339 11 PCT-US93-0 Sequence 7, Applicatio 2 058-59
36 107 33.8 732 6 US-09-230- Sequence 1, Applicatio 2 058-59
37 106 33.4 654 14 PCT-US96-1 Sequence 1, Applicatio 1 108-58
38 106 33.4 720 1 5455030-14 Patent No. 5455030 1 108-58
39 105 33.1 739 7 US-08-197- Sequence 6, Applicatio 5 898-58
40 104 32.8 330 6 US-08-318- Sequence 37, Applicati 3 158-57
41 104 32.8 335 6 US-08-318- Sequence 35, Applicati 3 158-57
42 104 32.8 354 6 US-08-318- Sequence 44, Applicati 3 158-57
43 104 32.8 384 6 US-08-259- Sequence 13, Applicati 3 158-57
44 104 32.8 417 6 US-08-318- Sequence 46, Applicati 3 158-57
45 104 32.8 438 6 US-08-318- Sequence 45, Applicati 3 158-57

ALIGNMENTS

RESULT 1
ID PCT-US95-11235-2 STANDARD: DNA: UNC: 646 BP.
AC xxxxxx
DT 01-JAN-1900
CC Sequence 2, Application PC/TUS9511235.
CC Sequence 2, Application PC/TUS9511235.
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGENIC LIGHT
CC CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10666 North Torrey Pines Road, TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11235
CC FILING DATE: 31-SEP-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/300,386
CC FILING DATE: 02-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/829,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993

RESULT 14

ID R41286 standard; Protein: 129 AA.
 AC R41286;
 DT 01-NOV-1993 (first entry)
 DE F105 rearranged variable region light chain.
 KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW Chain; epitope; immune deficiency.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..129
 FT /label= mat_protein
 FT W09J12232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1991: U10928.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 DR WPI: 93-214174/26.
 DR N-PSDB: Q49155.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Claim 10; Page 79; 109pp; English.
 CC mpNA from the known hybridoma F105 was converted to cDNA and this
 CC subjected to PCR amplification using primers corresp. to appropriate
 CC parts of the heavy or light chains and having restriction sites to
 CC permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (MAB) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The MAB may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.
 SQ Sequence 129 AA;

Query Match 87.5%; Score 561; DB 7; Length 129;

Best Local Similarity 90.5%; Pred. No. 6.47e-39;

Matches 95; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 24 ltqspgtlslsageratlscrasqsvsrylawyqkpgqaprillygassratgipdrf 83

QY 3 LTQSPGTLSLSPGPATLSCGASQSVPSNYLAWYQKPGQAPPLIYGVSSPATGIDPF 62

Db 84 ssgsgtdftltisrvepedfavyycqygdsvctfsggtkleik 128

QY 53 SSGSGTDFTLTISRIPEDFAVYVCQYGSSPRTFGGKTLEIK 107

RESULT 15

ID R38673 standard; Protein: 129 AA.
 AC R38673;
 DT 01-NOV-1993 (first entry)
 DE F105VK-F105JK.
 KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW Chain; epitope; immune deficiency.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT Protein 21..129
 FT /label= mat_protein
 FT Region 1..116
 FT /label= F105VK
 FT Region 117..129
 FT /label= F105JK
 FT Region 44..55
 FT /label= CDR1

FT Region 71..77

FT /label= CDR2

FT Region 110..117

FT /label= CDR3

FT Misc_difference 1

FT /note= "Met encoded by ATC (sic)"

FT Misc_difference 35

FT /note= "Pro encoded by GCA (sic)"

FT Misc_difference 99

FT /note= "Leu encoded by GTG (sic)"

FT Misc_difference 113

FT /note= "Gly encoded by GAT (sic)"

FT Misc_difference 114

FT /note= "Ser encoded by AAC (sic)"

FT Misc_difference 116

FT /note= "Pro encoded by GTT (sic)"

FN W09J12232-A.

PD 24-JUN-1993.

PF 10-DEC-1991: U10928.

PA (DAND) DANA FARBER CANCER INST INC.

PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.

PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;

DR WPI: 93-214174/26.

DR N-PSDB: Q42706.

PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection

PS Disclosure: Page 74-75; 109pp; English.

CC The nucleotide sequence of F105 V κ (Q42707 - sequence differs from
 CC other F105 V κ sequences given elsewhere in the specification) was
 CC compared with germline gene Humk325 (Q42706), showing 97.7%
 CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the V κ III subgroup gene family.

SQ Sequence 129 AA;

Query Match 87.2%; Score 658; DB 7; Length 129;

Best Local Similarity 89.5%; Pred. No. 1.07e-38;

Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Db 24 ltqspgtlslsageratlscrasqsvsrylawyqkpgqaprillygassratgipdrf 83

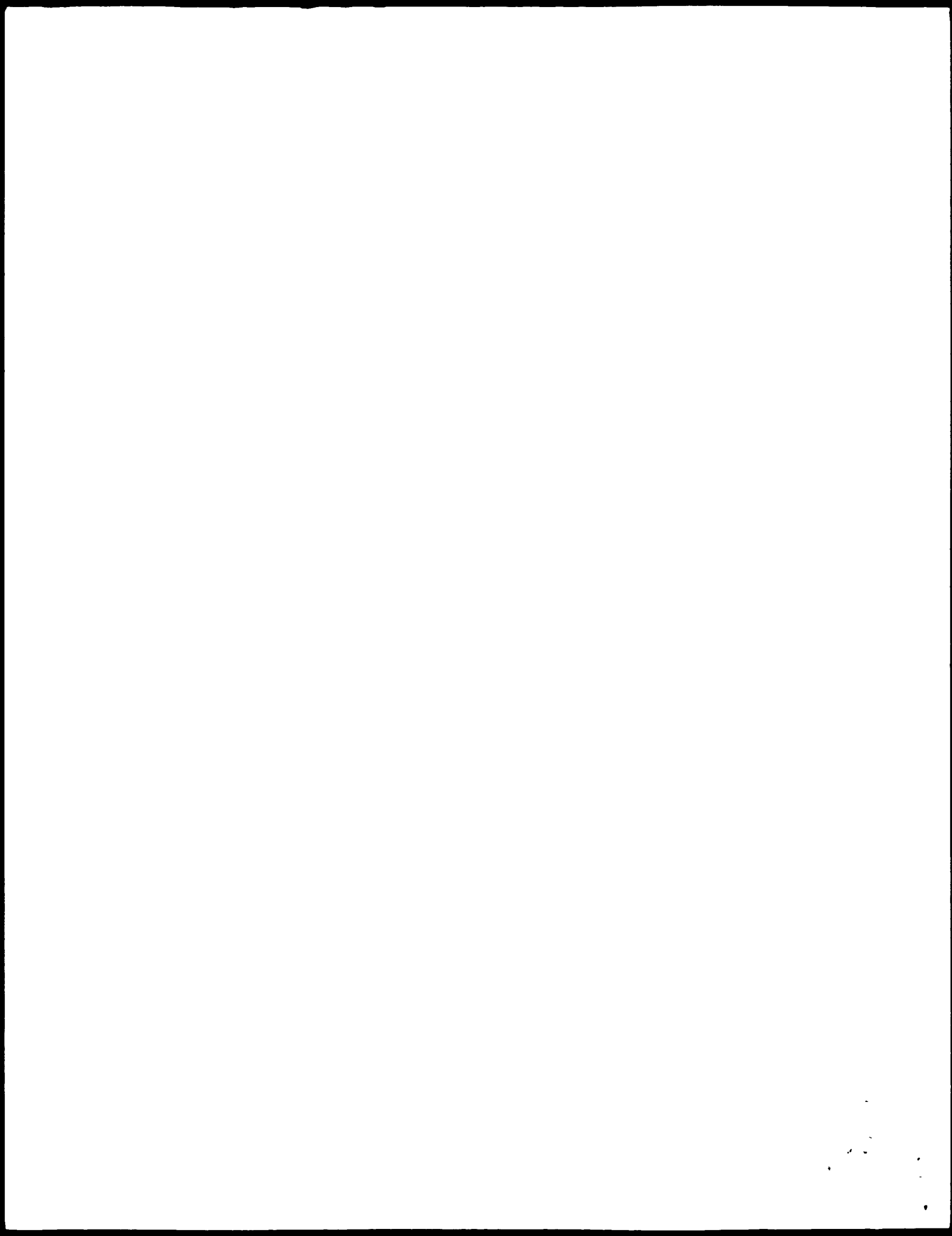
QY 3 LTQSPGTLSLSPGPATLSCGASQSVPSNYLAWYQKPGQAPPLIYGVSSRAIGIPDR 52

Db 84 ssgsgtdftltisrvepedfavyycqygdsvctfsggtkleik 128

QY 53 SSGSGTDFTLTISRIPEDFAVYVCQYGSSPRTFGGKTLEIK 107

Search completed: Tue Feb 24 07:22:39 1998

Job time : 29 secs.



CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/926,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: TSP1 409 1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 546 BP: 162 A: 187 C: 170 G: 127 T: 0 other:

Query Match 81.4% Score 258. DB 7: Length 546.
Best Local Similarity 90.8% Pred No 172e-172:
Matches 286: Conservative 0: Mismatches 29: Indels 0: Gaps 0:

Db 1 GAGCTCACCGAGTCTCCAGGACCGCTGTTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60
|||||
QY 4 GAGCTCACCGAGTCTCCAGGACCGCTGTTTGTCTCCAGGGGAAAGAGCCACCTCTCC 63
|||||

Db 61 TCGAGGGGAGTCAAGAGTGTAGAGAGAGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCT 120
|||||
QY 64 TCGAGGGGAGTCAAGAGTGTAGAGAGAGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCT 123
|||||

Db 121 CAGGCTCCAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
|||||
QY 124 CAGGCTCCAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
|||||

Db 181 TCGAGTGGAGTGGTGTGGGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
|||||
QY 184 TCGAGTGGAGTGGTGTGGGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
|||||

Db 241 GATTGTGAGTGTACTGCT 300
|||||
QY 244 GATTGTGAGTGTACTGCT 303
|||||

Db 301 AAGGTGGAACTCAA 315
|||||
QY 304 AAGGTGGAACTCAA 318
|||||

RESULT 4
ID US-08-053-131-182 STANDARD: DNA; UNC: 900 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 182, Application US/08053131
CC Sequence 182, Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 200

CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent-In Release #1 0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,850
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 182:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 900 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 301e(116 163 351 650)
CC Sequence 900 BP: 229 A: 241 C: 201 G: 238 T: 0 other:

Query Match 77.9% Score 247: DB 7: Length 900:
Best Local Similarity 95.2% Pred No 3.85e-154:
Matches 256: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

Db 375 AGCGAGTCTCCAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
|||||
QY 10 AGCGAGTCTCCAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
|||||

Db 435 GCAGTCTCAGTGTGTAGCAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
|||||
QY 70 GCAGTCTCAGTGTGTAGCAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
|||||

Db 495 CCAGGCTCCCTCACTATGCT 554
|||||
QY 130 CCAGGCTCCCTCACTATGCT 589
|||||

Db 555 GCAGTGTGTGTGTGGGACAGATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
|||||
QY 190 GCAGTGTGTGTGTGGGACAGATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
|||||

Db 615 GCAGTGTGTGTGTGGGACAGATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640
|||||
QY 250 GCAGTGTGTGTGTGGGACAGATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
|||||

RESULT 5
ID PCT-US93-12501-1 STANDARD: DNA; UNC: 325 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9312501.
CC Sequence 1, Application PC/TUS9312501
CC GENERAL INFORMATION:

CC APPLICANT: Chang, Tse Wen
 CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IgA MONOCLONAL ANTIBODIES AND
 CC TITLE OF INVENTION: RELATED PRODUCTS FOR ALLERGY TREATMENT
 CC NUMBER OF SEQUENCES: 10
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Tanox Biosystems, Inc
 CC STREET: 10101 Stella Link Rd.
 CC CITY: Houston
 CC STATE: Texas
 CC COUNTRY: USA
 CC ZIP: 77025
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5" Hi Density Diskette
 CC COMPUTER: IBM PS/2
 CC OPERATING SYSTEM: DOS, Version 3.30
 CC SOFTWARE: Wordperfect 5.1
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/12501
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Mirabel, Eric P
 CC REGISTRATION NUMBER: 31,211
 CC REFERENCE/DOCKET NUMBER: TXN92-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 713-664-2288
 CC TELEFAX: 713-664-8914
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 325 nucleotides
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double stranded
 CC TOPOLOGY: Linear
 CC Sequence 325 BP; 79 A; 93 C; 79 G; 74 T; 0 other;

Query Match 75.1%; Score 238; DB 11; Length 325;

Best Local Similarity 90.4%; Pred No. 257e-157; Indels 3; Gaps 3;

Matches 282; Conservative 0; Mismatches 27;

Db 13 AGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGAAAGAGCCACCCCTCTCTCCAGG 72

QY 10 AGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGAAAGAGCCACCCCTCTCTCCAGG 69

Db 73 GCAGTCAGACTGTAGCAGCAACTACTTAGCCTGGTACCAGCACAAACCTGGCCAGGCT 132

QY 70 GCAGTCAGAGTCTTAGCAGCAACTACTTAGCCTGGTACCAGCACAAACCTGGCCAGGCT 129

Db 133 CCAGGCTCTCATCTGCTACATCCATCCATGAGTTCATCGGCATCCAGACAGGTTCACT 192

QY 130 CCAGGCTCTCATCTGCTACATCCATCCATGAGTTCATCGGCATCCAGACAGGTTCACT 189

Db 193 GGCAGTGGTCTGGACAGACTTACTCTCACCATCAGCAGACTGGAGGCTGAAGATTTT 252

QY 190 GGCAGTGGTCTGGACAGACTTACTCTCACCATCAGCAGACTGGAGGCTGAAGATTTT 249

Db 253 GCAGTGTATTACTGTCAGCACTTCGTAACCTCAGAGTGGAGTTCGCGCCAGGACCAAG 312

QY 250 GCAGTGTATTACTGTCAGCACTTCGTAACCTCAGAGTGGAGTTCGCGCCAGGACCAAG 306

Db 313 GTTGAATCAAA 324

QY 307 GTTGAATCAAA 318

RESULT

ID US-08-053-131-178 STANDARD; DNA; UNC; 812 BP.

AC xxxxxx

DE 01-JAN-1900

DT Sequence 178, Application US/08053131

CC Sequence 178, Application US/08053131

CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: One Market Plaza, Steuart Tower, Suite 200
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/053,131
 CC FILING DATE: 26-APR-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/990,860
 CC FILING DATE: 16-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 178:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 812 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: join(199..246, 418..714)
 CC Sequence 812 BP; 201 A; 225 C; 187 G; 194 T; 0 other;

Query Match 67.8%; Score 215; DB 7; Length 812;
 Best Local Similarity 93.9%; Pred No. 6.48e-140;
 Matches 245; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

Db 442 ACACAGCTCCAGCAGCTCTCTTTTCTTCTCCAGGGAAAGAGCCACCCCTCTCTCCAGG 501

QY 10 AGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGAAAGAGCCACCCCTCTCTCCAGG 69

Db 502 GCCAGTCAGAGTCTTAGCAGCAACTACTTAGCCTGGTACCAGCACAAACCTGGCCAGGCT 558

QY 70 GCCAGTCAGAGTCTTAGCAGCAACTACTTAGCCTGGTACCAGCACAAACCTGGCCAGGCT 129

Db 559 CCCAGGCTCTCATCTGCTACATCCATCCATGAGTTCATCGGCATCCAGACAGGTTCACT 618

QY 130 CCCAGGCTCTCATCTGCTACATCCATCCATGAGTTCATCGGCATCCAGACAGGTTCACT 189

Db 619 GGCAGTGGGCTGGACAGACTTACTCTCACCATCAGCAGACTGGAGGCTGAAGATTTT 678

QY 190 GGCAGTGGGCTGGACAGACTTACTCTCACCATCAGCAGACTGGAGGCTGAAGATTTT 249

Db 679 GCAGTGTATTACTGTCAGCACTTCGTAACCTCAGAGTGGAGTTCGCGCCAGGACCAAG 699

Dh 78 CTCACGAGCTCTCCAGGACCGCTGTCTCTGCTCTCCAGGAAAGAGGACCTCTCTCTGT 137
|||||
Qy 7 CTCACGAGCTCTCCAGGACCGCTGTCTCTGCTCTCCAGGAAAGAGGACCGCTCTCTGT 66
|||||
Dh 138 AGTCTCAGTCAAGATTCGATGAGGCGCGGAGTCTCTGATGATCAAGATCAAGATGAG 197
|||||
Qy 67 AGGGCCAGTTCAGAGCTCTTACGACGAAATACCTAGCTGATGATGATGATGATGATG 126
|||||
Dh 198 GTCCCAAGGCTGTGATACATGCTGTTTCCCAATAGGGGCTCTGATCTCTCAGACAGTTC 257
|||||
Qy 127 GTCCCAAGGCTGTGATACATGCTGTTTCCCAATAGGGGCTCTGATCTCTCAGACAGTTC 186
|||||
Dh 258 AGGGCAGTGGTCTGGGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 317
|||||
Qy 187 AGTGGCAGTGGTCTGGGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246
|||||
Dh 318 TTTCAGCTGATCTACTGTCAGCTCTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 377
|||||
Qy 247 TTTCAGCTGATCTACTGTCAGCTCTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303
|||||
Dh 378 AAAGTGGAGAGGAAA 392
|||
Qy 304 AAGGTGGAATCAAA 318
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RESULT 9

ID PCT-US95-08743-152 STANDARD; DNA: UNC; 729 BP.
AC XXXXX
DE 01-JAN-1900
DE Sequence 152, Application PC/TUS9508743.
CC Sequence 152, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO. 152:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 729 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 9..715
CC Sequence 729 BP; 173 A; 208 C; 192 G; 156 T; 0 other;

Query Match 62.1%; Score 197; DB 13; Length 729;
Best Local Similarity 83.5%; Pred No 2.44e-156;
Matches 263; Conservative 0; Mismatches 49; Indels 3; Gaps 3;

Dh 78 CTCACGAGCTCTCCAGGACCGCTGTCTCTGCTCTCCAGGAAAGAGGACCTCTCTCTGT 137
|||||
Qy 7 CTCACGAGCTCTCCAGGACCGCTGTCTCTGCTCTCCAGGAAAGAGGACCGCTCTCTGT 66
|||||
Dh 138 AGTCTCAGTCAAGATTCGATGAGGCGCGGAGTCTCTGATGATCAAGATCAAGATGAG 197
|||||
Qy 67 AGGGCCAGTTCAGAGCTCTTACGACGAAATACCTAGCTGATGATGATGATGATGATG 126
|||||
Dh 198 GTCCCAAGGCTGTGATACATGCTGTTTCCCAATAGGGGCTCTGATCTCTCAGACAGTTC 257
|||||

Qy 127 GCTCCAGGCT 186
|||||
Dh 258 AGGGCAGTGGTCTGGGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 317
|||||
Qy 187 AGTGGCAGTGGTCTGGGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246
|||||
Dh 318 TTTCAGCTGATCTACTGTCAGGCTCTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 377
|||||
Qy 247 TTTCAGCTGATCTACTGTCAGGCTCTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 303
|||||
Dh 378 AAAGTGGAGAGGAAA 392
|||
Qy 304 AAGGTGGAATCAAA 318
|||

RESULT 10

ID PCT-US95-08743-168 STANDARD; DNA: UNC; 729 BP.
AC XXXXX
DE 01-JAN-1900
DE Sequence 168, Application PC/TUS9508743.
CC Sequence 168, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO. 168:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 729 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 729 BP; 156 A; 192 C; 208 G; 173 T; 0 other;

Query Match 62.1%; Score 197; DB 13; Length 729;
Best Local Similarity 83.5%; Pred No 2.44e-126;
Matches 263; Conservative 0; Mismatches 49; Indels 3; Gaps 3;

Dh 338 TTTCCTCTCCAGTGTGCT 397
|||||
Qy 318 TTTCCTCTCCAGTGTGCT 262
|||||
Dh 368 GTATACAGTCAAGATTCGATGAGGCGCGGAGTCTCTGATGATCAAGATCAAGATGAG 457
|||||
Qy 261 GTATACAGTCAAGATTCGATGAGGCGCGGAGTCTCTGATGATCAAGATCAAGATGAG 202
|||||
Dh 458 AGAGCCAGTGGCGTGGGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 517
|||||
Qy 261 AGAGCCAGTGGCGTGGGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142
|||||
Dh 518 GACGAGCTCTGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 577
|||||
Qy 141 GAAGAGCTGGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 82
|||||
Dh 578 GCTGTGACTGAGCTCAAGAGAGAGGCTGTGATGATGATGATGATGATGATGATGATGAT 637
|||||
Qy 81 ACTCTGACTGCTGAGGAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 22
|||||
Dh 638 TGGAGACTGCTGTGAG 652
|||||
Qy 21 TGGAGACTGCTGTGAG 7
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DR PIR: A01896; K3HUML.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11746 MW; 7D9F5D75 CRC32;
BY SIMILARITY.

Query Match 81.3%; Score 600; DB 5; Length 109;
Best Local Similarity 84.8%; Pred. No. 2.53e-110;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 ltqspgtlslspgeratlscrasqsvsflwyqgkqgqaprllyvassratgiparf 63
Qy 3 LTQSPATLSLSPGERATLSQASQSV-NKYLAWYQKQPGQAPPLIYDASNPATGIPARF 61
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Db 64 sgsgsgtdftltisrlepafavyqcgysqslrtfggktveik 108
Qy 62 SGSGSGTDFTLTISNLEPEDFAVYQCGQSDWV-TFGGKTVEIK 105
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
ID KV3D_HUMAN STANDARD: PPT: 109 AA
AC P01622:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE.
RX MEDLINE: 72188439.
RA SUTER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.:
PL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972)
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUTI.
DR HSSP: P01607; 2IMM.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DISULFID 23 89
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11788 MW; D0A7A8B1 CRC32;
BY SIMILARITY.

Query Match 80.8%; Score 596; DB 5; Length 109;
Best Local Similarity 84.8%; Pred. No. 2.16e-109;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 ltqspgtlslspgeratlscrasqsvsflwyqgkqgqaprllyvassratgiparf 63
Qy 3 LTQSPATLSLSPGERATLSQASQSV-NKYLAWYQKQPGQAPPLIYDASNPATGIPARF 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 sgsgsgtdftltisrlepafavyqcgysqslrtfggktveik 108
Qy 62 SGSGSGTDFTLTISNLEPEDFAVYQCGQSDWV-TFGGKTVEIK 105
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RESULT 7
ID KV3H_HUMAN STANDARD: PPT: 129 AA
AC P04207:
DT 20-MAR-1987 (REL. 04, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (CLL) (RHEUMATOID FACTOR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 86177570.
RA JIRIK F.P., SORCE J., FONG S., HEITZMANN J.G., CURD J.G., CHEN P.P.,
RA GOLDFEIN P., CARSON D.A.:
PL PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2199(1986)

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DR EMBL: M12740; G553436; -.
DR PIR: A01898; K3HDCU.
DR HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 59
FT DOMAIN 70 75
FT DOMAIN 77 108
FT DOMAIN 109 118
FT DOMAIN 119 129
FT DISULFID 43 108
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14275 MW; 2F344868 CRC32;
BY SIMILARITY.

Query Match 80.6%; Score 595; DB 5; Length 129;
Best Local Similarity 81.0%; Pred. No. 3.70e-109;
Matches 85; Conservative 11; Mismatches 7; Indels 2; Gaps 1;

Db 24 mtqspvtlslspgeratlscrasqsvsnlawyqgkqgqpprlllygastratgiparf 83
Qy 3 LTQSPATLSLSPGERATLSQASQSV-NKYLAWYQKQPGQAPPLIYDASNPATGIPARF 52
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Db 84 sgsgsgtdftltisrlepafavyqcgysqslrtfggktveik 128
Qy 63 SGSGSGTDFTLTISNLEPEDFAVYQCGQSDWV-TFGGKTVEIK 105
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RESULT 8
ID KV3E_HUMAN STANDARD: PPT: 109 AA
AC P01624:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE.
RX MEDLINE: 1376261-271(1976).
RA KLAPPER D.C., CAPRA J.D.:
PL ANN. INST. PASTEUR IMMUNOL. 1376:261-271(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01897; K3HUPM
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11922 MW; A0C42C88 CRC32;
BY SIMILARITY.

Query Match 80.2%; Score 592; DB 5; Length 109;
Best Local Similarity 79.0%; Pred. No. 1.85e-108;
Matches 83; Conservative 12; Mismatches 8; Indels 2; Gaps 2;

Db 4 mtqspvtlslspgeratlscrasqsvsnlawyqgkqgqpprlllygastratgiparf 63
Qy 3 LTQSPATLSLSPGERATLSQASQSV-NKYLAWYQKQPGQAPPLIYDASNPATGIPARF 51
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Db 64 sgsgsgtdftltisrlepafavyqcgysqslrtfggktveik 108
Qy 62 SGSGSGTDFTLTISNLEPEDFAVYQCGQSDWV-TFGGKTVEIK 105
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RESULT 9
ID KV3A_HUMAN STANDARD: PPT: 108 AA
AC P01619:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (B6)

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AC P18136;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CAPSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLOC22; K3HUH.
DR HSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 FRAMEWORK 3
FT DOMAIN 78 109 FRAMEWORK 4
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14070 MW: 20000366 CRC32.

Query Match 82.4%; Score 608; DB 5; Length 129;
Best Local Similarity 85.8%; Pred. No. 3.46e-112;
Matches 91; Conservative 3; Mismatches 8; Indels 4; Gaps 3;

Db 24 ltspgtlslsperatlscrasqssvssylawyqkqkqaprllygassratgipdrf 83
QY 3 LTSPGATLSLSPGERATLSGASQSVNK-YLAWYQKQKQAPRLLYDASNPATGIPAPF 61
Db 84 sqsgsgtdftltisrlepddfavvyqgqgsspw-tfgggtkveik 128
QY 62 SGSGSGTDTLTISNLEPDDFAVYVCQPSDWV-IFGSGTKEIK 105

RESULT 3
ID KV3B_HUMAN STANDARD; PRT: 109 AA.
AC P01620;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUSI.
DR HSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11775 MW: 00850050 CRC32.

Query Match 82.08; Score 605; DB 5; Length 109;
Best Local Similarity 84.8%; Pred. No. 1.73e-111;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

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Db 4 ltspgtlslsperatlscrasqssvssylawyqkqkqaprllygassratgipdrf 63
QY 3 LTSPGATLSLSPGERATLSGASQSVNK-YLAWYQKQKQAPRLLYDASNPATGIPAPF 61
Db 64 sqsgsgtdftltisrlepddfavvyqgqgsspw-tfgggtkveik 108
QY 62 SGSGSGTDTLTISNLEPDDFAVYVCQPSDWV-IFGSGTKEIK 105

RESULT 4
ID KV3L_HUMAN STANDARD; PRT: 129 AA.
AC P18135;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAI)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CAPSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLOC22; K3HUH.
DR HSP: P01607; IANG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAI)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 FRAMEWORK 3
FT DOMAIN 78 109 FRAMEWORK 4
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14073 MW: 20448856 CRC32.

Query Match 81.8%; Score 604; DB 5; Length 129;
Best Local Similarity 85.7%; Pred. No. 2.96e-111;
Matches 90; Conservative 4; Mismatches 9; Indels 2; Gaps 2;

Db 24 ltspgtlslsperatlscrasqssvssylawyqkqkqaprllygassratgipdrf 83
QY 3 LTSPGATLSLSPGERATLSGASQSVNK-YLAWYQKQKQAPRLLYDASNPATGIPAPF 61
Db 84 sqsgsgtdftltisrlepddfavvyqgqgsspw-tfgggtkveik 128
QY 62 SGSGSGTDTLTISNLEPDDFAVYVCQPSDWV-IFGSGTKEIK 105

RESULT 5
ID KV3E_HUMAN STANDARD; PRT: 109 AA.
AC P01623;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.

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WATERBURY

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSEARCH_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:19:05 1998: MasPar time 4.86 Seconds
Tabular output not generated. 458.034 Million cell updates/sec

Title: >US-08-844-215-9
Description: (1-105) from US08844215.pep
Perfect Score: 738
Sequence: 1 AELTQSPATLSLSPGERATL.....YQQQRSDWVTFGGTKVEIK 105

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 40.473; Variance 70.596; scale 0.573
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	626	84.8	115	5	KV3I_HUMAN	IG KAPPA CHAIN PRECUR 2.18e-116
2	608	82.4	129	5	KV3M_HUMAN	IG KAPPA CHAIN PRECUR 3.46e-111
3	605	82.0	109	5	KV3E_HUMAN	IG KAPPA CHAIN V-III 1.73e-111
4	604	81.8	129	5	KV3L_HUMAN	IG KAPPA CHAIN PRECUR 2.96e-111
5	600	81.3	109	5	KV3E_HUMAN	IG KAPPA CHAIN V-III 2.53e-110
6	596	80.8	109	5	KV3D_HUMAN	IG KAPPA CHAIN V-III 2.16e-109
7	595	80.6	129	5	KV3H_HUMAN	IG KAPPA CHAIN PRECUR 3.70e-109
8	592	80.2	109	5	KV3F_HUMAN	IG KAPPA CHAIN V-III 1.85e-108
9	577	78.2	108	5	KV3G_HUMAN	IG KAPPA CHAIN V-III 5.68e-105
10	572	77.5	109	5	KV3G_HUMAN	IG KAPPA CHAIN V-III 8.23e-104
11	554	75.1	100	5	KV3C_HUMAN	IG KAPPA CHAIN PRECUR 1.23e-99
12	554	75.1	128	5	KV3K_HUMAN	IG KAPPA CHAIN PRECUR 1.23e-99
13	548	74.3	116	5	KV3J_HUMAN	IG KAPPA CHAIN PRECUR 3.01e-98
14	543	73.6	108	5	KV1M_HUMAN	IG KAPPA CHAIN V-I RE 4.32e-97
15	525	71.1	107	5	KV1D_HUMAN	IG KAPPA CHAIN V-I RE 6.22e-93
16	522	70.7	108	5	KV1F_HUMAN	IG KAPPA CHAIN V-I RE 3.06e-92
17	520	70.5	108	5	KV1N_HUMAN	IG KAPPA CHAIN V-I RE 8.84e-92
18	516	69.9	108	5	KV1H_HUMAN	IG KAPPA CHAIN V-I RE 7.39e-91
19	514	69.6	129	5	KV1X_HUMAN	IG KAPPA CHAIN PRECUR 2.13e-90
20	514	69.6	129	5	KV1W_HUMAN	IG KAPPA CHAIN PRECUR 2.13e-90
21	509	69.0	108	5	KV1E_HUMAN	IG KAPPA CHAIN V-I RE 3.02e-89
22	507	68.7	108	5	KV1P_HUMAN	IG KAPPA CHAIN V-I RE 8.71e-89

23	506	68.6	109	5	KV1T_HUMAN	IG KAPPA CHAIN V-I RE 1.48e-88
24	505	68.4	108	5	KV1S_HUMAN	IG KAPPA CHAIN V-I RE 2.51e-88
25	504	68.3	108	5	KV1Y_HUMAN	IG KAPPA CHAIN V-I RE 4.27e-88
26	502	68.0	108	5	KV1V_HUMAN	IG KAPPA CHAIN V-I RE 1.23e-87
27	499	67.6	108	5	KV1B_HUMAN	IG KAPPA CHAIN V-I RE 6.02e-87
28	498	67.5	108	5	KV1K_HUMAN	IG KAPPA CHAIN V-I RE 1.02e-86
29	497	67.3	108	5	KV1L_HUMAN	IG KAPPA CHAIN V-I RE 1.73e-86
30	492	66.7	108	5	KV1G_HUMAN	IG KAPPA CHAIN V-I RE 2.43e-85
31	488	66.1	108	5	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE 2.01e-84
32	487	66.0	108	5	KV1R_HUMAN	IG KAPPA CHAIN V-I RE 3.41e-84
33	487	66.0	117	5	KV1J_HUMAN	IG KAPPA CHAIN V-I RE 3.41e-84
34	484	65.6	108	5	KV1O_HUMAN	IG KAPPA CHAIN V-I RE 1.66e-83
35	480	65.0	133	5	KV4B_HUMAN	IG KAPPA CHAIN V-I RE 1.37e-82
36	473	64.1	108	5	KV5J_MOUSE	IG KAPPA CHAIN V-V RE 5.48e-81
37	472	64.0	108	5	KV1A_HUMAN	IG KAPPA CHAIN V-I RE 9.28e-81
38	472	64.0	111	5	KV3A_MOUSE	IG KAPPA CHAIN V-I RE 9.28e-81
39	472	64.0	136	5	KV5B_MOUSE	IG KAPPA CHAIN V-I RE 9.28e-81
40	470	63.7	108	5	KV5P_MOUSE	IG KAPPA CHAIN V-V RE 2.66e-80
41	470	63.7	110	5	KV3P_MOUSE	IG KAPPA CHAIN V-I RE 2.66e-80
42	470	63.7	149	5	KV5A_MOUSE	IG KAPPA CHAIN V-I RE 2.66e-80
43	469	63.6	108	5	KV5Q_MOUSE	IG KAPPA CHAIN V-V RE 4.50e-80
44	469	63.6	111	5	KV3Q_MOUSE	IG KAPPA CHAIN V-I RE 4.50e-80
45	467	63.3	108	5	KV5N_MOUSE	IG KAPPA CHAIN V-V RE 1.29e-79

ALIGNMENTS

RESULT 1
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (V9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85087932.
RA PECH M., ZACHAU H.G.;
PL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL; X01668; -. NOT ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P01607; IAAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 77 108 FRAMEWORK 3
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA: 12575 MW: 375182PC QSC12;
Query Match 84.8%; Score 626; DB 5; Length 115;
Best Local Similarity 95.6%; Pred. No. 2.18e-116;
Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratlscrasgssvylawvqgkpggqprlllydasnratgiparls 83
|||||
Qy 3 LQTSIPATLSLSPGERATLSPPASVSUNKYLAWYQTFAPLAPPLLIYDASNRATGIPARIS 62
Db 84 gsgsgtdftltissslepedfavyvycqqrsw 114
|||||
Qy 63 GSGSGTDTFTLTISNIEPEDFAVYVYCCQQRSDW 93

RESULT 2
ID KV3M_HUMAN STANDARD; PRT; 129 AA.

DR WPI: 96-179601/18
 PI Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PI passive immunotherapy and detection of HIV infection.
 PS Example 3; Fig 19; 366pp; English.
 CC The sequences given in W01320-24 represent the light chain variable
 CC regions (VH) of a series of antibody fragments (Fab's) which are
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents
 CC the sequence of the clone, Dc 41.19. These sequences represent light
 CC chains which bind to the heavy light chain clones given in W01315-19. A
 CC monoclonal antibody containing one of these Fab sequences may have the
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
 CC The Mab may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 109 AA:

Query Match 88.7%; Score 670; DB 19; Length 109;
 Best Local Similarity 90.7%; Pred. No. 1.41e-39;
 Matches 97; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlylawyqgkpgqaprllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERATLSGASVSFNSNYLAWYQKPGQAPRLLYGVSSHAATGIPD 60

Db 62 rfsgsgsgdftltisrlepedfavyycqgysg-tfggqtkleik 107
 QY 61 RFSGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGQTKLEIK 107

RESULT 12
 ID W01322 standard; Protein: 111 AA.
 AC W01322:
 DE 29-JAN-1997 (first entry)
 DE VL of Fab, GL 41.1, binds to HIV gp41.
 KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
 KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..111
 FT /label= FR4
 PN W09407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U09328.
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 11; Page 217; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the Mab regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VL region sequence R54277 neutralises HIV;
 CC gp41.
 SQ Sequence 111 AA:

Query Match 88.5%; Score 668; DB 10; Length 111;
 Best Local Similarity 87.9%; Pred. No. 1.98e-39;
 Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlylawyqgkpgqaprllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERATLSGASVSFNSNYLAWYQKPGQAPRLLYGVSSHAATGIPD 60

Db 62 rfsgsgsgdftltisrlepedfavyycqgysg-tfggqtkleik 107
 QY 61 RFSGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGQTKLEIK 107

CC antibody and in the detection of HIV infection.
 SQ Sequence 111 AA:

Query Match 88.5%; Score 668; DB 19; Length 111;
 Best Local Similarity 87.9%; Pred. No. 1.98e-39;
 Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlylawyqgkpgqaprllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERATLSGASVSFNSNYLAWYQKPGQAPRLLYGVSSHAATGIPD 60

Db 62 rfsgsgsgdftltisrlepedfavyycqgysg-tfggqtkleik 107
 QY 61 RFSGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGQTKLEIK 107

RESULT 13
 ID R54277 standard; Protein: 111 AA.
 AC R54277:
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp41 immunoglobulin light chain V region clone GL 41.1.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
 KW neutralisation; monoclonal antibody; light chain; variable region;
 KW framework region; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..111
 FT /label= FR4
 PN W09407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U09328.
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 11; Page 217; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the Mab regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VL region sequence R54277 neutralises HIV;
 CC gp41.
 SQ Sequence 111 AA:

Query Match 88.5%; Score 668; DB 10; Length 111;
 Best Local Similarity 87.9%; Pred. No. 1.98e-39;
 Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgervivscrasvsnlylawyqgkpgqaprllygasmratgipd 61
 QY 1 AELTQSPGTLSLSPGERATLSGASVSFNSNYLAWYQKPGQAPRLLYGVSSHAATGIPD 60

Db 62 rfsgsgsgdftltisrlepedfavyycqgysg-tfggqtkleik 107
 QY 61 RFSGSGSGDFTLTISRLEPEDFAVYCYQYGSPPRTFGGQTKLEIK 107

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DT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
FT WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCR1 ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 180: 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence P54311 is from a gp120-
CC specific clone.
SQ Sequence 107 AA;

Query Match 88.7%; Score 670; DB 10; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.41e-39;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltqspgtlslspgeratlscrasglsennylawyqkpgqaprllygsstrgtgipdr 60
QY 2 ELTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQQKPGQAPRLLYGVSSRAIGIPDP 61
Db 61 fsgqsgtdftltisrlepedfavyvcchyanvyytfgggtkkleik 106
QY 62 FSGQSGTDFTLTISRLEPEDFAVYVCQYQSSPPTFGQGTKLEIK 107

RESULT 10
ID R54275 standard; protein; 109 AA.
AC R54275.
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW neutralisation; monoclonal antibody; light chain; variable region;
KW framework region; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..35
FT /label= CDR1
FT Region 36..50
FT /label= FR2
FT Region 51..57
FT /label= FR3
FT Region 58..89
FT /label= CDR3
FT Region 90..97
FT /label= FR4
FT WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCR1 ) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA;

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FT /label= CDR2
FT Region 58..89
FT /label= FR3
FT Region 90..97
FT /label= CDR3
FT Region 98..109
FT /label= FR4
FT WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCR1 ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Claim 11: Page 215-216: 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence P54275 neutralises HIV1
CC gp41.
SQ Sequence 109 AA;

Query Match 88.7%; Score 670; DB 10; Length 109;
Best Local Similarity 90.7%; Pred. No. 1.41e-39;
Matches 97; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Db 2 aeltqspgtlslspgeratlscrasglsennylawyqkpgqaprllygsstrgtgipdr 61
QY 1 AELTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQQKPGQAPRLLYGVSSPATGIPDP 60
Db 62 rfsgsgtdftltisrlepedfavyvcgysgsg-tfgggtkveik 107
QY 61 RFSGSGTDFTLTISRLEPEDFAVYVCYQSSPPTFGQGTKLEIK 107

RESULT 11
ID W01320 standard; Protein; 109 AA.
AC W01320.
DT 29-JAN-1997 (first entry)
DE VL of Fab, DL 41 19, binds to HIV gp41.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..35
FT /label= CDR1
FT Region 36..50
FT /label= FR2
FT Region 51..57
FT /label= CDR2
FT Region 58..89
FT /label= FR3
FT Region 90..97
FT /label= CDR3
FT Region 98..109
FT /label= FR4
FT WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCR1 ) SCRIpps RES INST.
PI Barbas CF, Burton DR, Lerner RA;

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PA (SCRI) SCRIPPS RES INST.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Barbas CF, Burton DR, Chanock RM, Crowe JE, Murphy RP;
 DP WPI: 94-118147/14.
 PT Human neutralising monoclonal antibodies to respiratory syncytial
 PT virus - for treatment prophylaxis and diagnosis of RSV and other
 PT diseases of the respiratory tract.
 PS Disclosure; Fig 4: 104pp; English.
 CC The sequences given in R50215-19 represent the heavy and light chain
 CC variable domains of various clones of a human monoclonal antibody
 CC which binds to an epitope on glycoprotein F of respiratory syncytial
 CC virus (RSV). These antibodies may be used as a reagent for the
 CC diagnosis of RSV disease and other viral mucosal diseases, eg
 CC influenza virus, rhinovirus and coronavirus. They are particularly
 CC useful in ameliorating RSV when delivered directly to the lungs, and
 CC may also be used for treating pneumonia and bronchiolitis.
 SQ Sequence 109 AA;
 Query Match 89.3%; Score 674; DB 9; Length 109;
 Best Local Similarity 88.8%; Pred. No. 7.15e-40;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 Db 2 aeltqspgtlslsperatlscratssnnylawyqgqprlllygasnratdipd 61
 Qy 1 AELTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPD 60
 Db 62 rfsqsgsgtdftltisrlepdmfavyvcqygsspxtfgqgtdveik 108
 Qy 61 PFGSGSGCTDFTLTISRLPEDFAVYVCQYGGSPRTFGGKLEIK 107
 RESULT 7
 ID R38593 standard; peptide: 107 AA.
 AC R38593;
 DT 28-OCT-1993 (first entry)
 DE Human lambda light chain subgroup 3 (HL3).
 KW Antibody: variable domain: light; L; heavy: H; consensus:
 KW affinity: antigen: immunogenicity; humanisation: framework.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 96
 FT /note- "residue conserved in less than 50% of the
 FT known sequences of HL3"
 FN W09311794-A.
 PD 24-JUN-1993.
 PF 14-DEC-1992; U10905.
 PR 13-DEC-1991; US-808464.
 PA (XOMA) XOMA CORP.
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 DR WPI: 93-213827/25.
 CC Antibodies prepn. used for treatment of auto-immune diseases - by
 CC replacement of critical residues to reduce immunogenicity but
 CC retain binding affinity, etc.
 PS Claim 2: Page 93-94: 160pp; English.
 CC The consensus amino acid sequences for the subgroups of light
 CC chains (HL1 - R38590, HK3 - NGK, HK2 - GST, HL2 - R38591, HL2 -
 CC R48592, HL3 - R38593, HL6 - R48594, HK4 - R38595, HL4 - R38596,
 CC and HL5 - R38597) and heavy chains (HH3 - R38598, HH1 - R38599 and
 CC HH2 - R38600) of human variable domains may be used to prepare, for
 CC example, a modified mouse antibody variable domain that retains the
 CC affinity of the natural domain for antigen while exhibiting reduced
 CC immunogenicity in humans.
 CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.
 SQ Sequence 107 AA;
 Query Match 88.9%; Score 671; DB 7; Length 107;
 Best Local Similarity 92.4%; Pred. No. 1.19e-39;
 Matches 97; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 4 ltqspgtlslsperatlscratssnnylawyqgqprlllygasnratdipd 62
 Qy 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDR 62
 Db 63 sqsgsgtdftltisrlepdmfavyvcqygsspxtfgqgtdveik 107
 Qy 63 SSGSGGTDFTLTISRLPEDFAVYVCQYGGSPRTFGGKLEIK 107
 RESULT 8
 ID W01269 standard; Protein: 107 AA.
 AC W01269;
 DT 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAb, clone B20.
 KW Heavy chain: light chain: variable region; VH: monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 98..107
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example; Fig 11: 366pp; English.
 CC The sequences given in W01361-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of the
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, B20. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 107 AA;
 Query Match 88.7%; Score 670; DB 19; Length 107;
 Best Local Similarity 88.7%; Pred. No. 1.41e-39;
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 Db 1 eltqspgtlslsperatlscratssnnylawyqgqprlllygasnratdipdr 60
 Qy 2 ELTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDR 61
 Db 61 fsgsgsgtdftltisrlepdmfavyvcqygsspxtfgqgtdveik 106
 Qy 62 FSGSGGTDFTLTISRLPEDFAVYVCQYGGSPRTFGGKLEIK 107
 RESULT 9
 ID R54311 standard; protein: 107 AA.
 AC R54311;

AC R54316;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region b6.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region
 OS Homo sapiens.
 FH Key
 FT Region Location/Qualifiers
 FT /label= FR1 1..21
 FT /label= FR1 22..33
 FT /label= CDR1 34..48
 FT /label= FR2 49..55
 FT /label= CDR2 56..87
 FT /label= FR3 88..96
 FT /label= CDR3 97..108
 FT /label= FR4 109..119
 PN WO9407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U09328
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCRIpps RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example; Page 186; 248pp; English
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli X11
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAb regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence R54316 neutralises HIV1
 CC gp120.
 SQ Sequence 108 AA;

Query Match 90.7%; Score 685; DB 9; Length 108;
 Best Local Similarity 89.6%; Pred No. 1,11e-40; Indels 0; Gaps 0;
 Matches 95; Conservative 6; Mismatches 5;
 Db 1 eltsqsgtltslpgeratlscragssnylawyqgkpgqaprllygasnratgipdr 60
 QY 2 ELTQSPGTLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLIYGVSSPATGIPDP 61
 Db 61 fsgsgsgtdftlsrlpepfavvyccqyqtsptfsggtqldik 106
 QY 62 FSGSGSGTDFLTLSRLEPEDFAVYCCQYQGSPPRTFGGQTKLEIK 107

RESULT 5
 ID W01278 standard; Protein; 108 AA.
 AC W01278.
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b6.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV, human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1 21
 FT /label= FR1 22 33
 FT /label= CDR1 34..48
 FT Region

FT /label= FR2 49..55
 FT /label= CDR2 56..87
 FT /label= FR3 88 96
 FT /label= CDR3 97..108
 FT /label= FR4 109..119
 PN WO9602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U09743
 PR 14-JUL-1994; US-276852.
 PA (SCRI) SCRIpps RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, b6. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 90.7%; Score 685; DB 19; Length 108;
 Best Local Similarity 89.6%; Pred No. 1,11e-40; Indels 0; Gaps 0;
 Matches 95; Conservative 6; Mismatches 5;
 Db 1 eltsqsgtltslpgeratlscragssnylawyqgkpgqaprllygasnratgipdr 60
 QY 2 ELTQSPGTLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLIYGVSSPATGIPDP 61
 Db 61 fsgsgsgtdftlsrlpepfavvyccqyqtsptfsggtqldik 106
 QY 62 FSGSGSGTDFLTLSRLEPEDFAVYCCQYQGSPPRTFGGQTKLEIK 107

RESULT 6
 ID R50217 standard; Protein; 109 AA.
 AC R50217.
 DT 31-OCT-1994 (first entry)
 DE HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.
 KW Complementarity determination region; CDR1; human; bronchiolitis;
 KW monoclonal antibody; epitope; glycoprotein F; influenza virus;
 KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1 24..35
 FT /label= CDR1 36..50
 FT /label= FR2 51..57
 FT /label= CDR2 58..89
 FT /label= FR3 90..98
 FT /label= CDR3 99..109
 FT /label= FR4 110..119
 PN WO9406448-A.
 PD 31-MAR-1994.
 PF 16-SEP-1993; U08786.
 PR 16-SEP-1992; US-945515.

Matches	99:	Conservative	4:	Mismatches	3:	Indels	0:	Gaps
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Db	1	eltqspgtlslspgeratlscrasqvisnlyawgqkpaqaprlliyavsnratpdr	60
QY	2	ELTQSPGTLSPGERATLSGASVSRSNYLAWYQKPAQAPRLIIYGVSSKATSPDR	61
Db	61	fsqssgtdftltlsrlepafavyscqygtspwffggatkveik	106
QY	62	FSQSSGTDFTLTISRLEPEDFAVYQCQYGSSPRTFGGQTKLEIK	107

RESULT	3
ID	W01265, standard, Protein; 108 AA.
AC	W01365.
DC	28-JAN-1997 (first entry)
DE	VL region of HIV neutralising MAb, clone b24.
KW	Heavy chain; light chain; variable region; VH; monoclonal antibody;
KE	MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW	virus infectivity assay; precursor gp150; immunocompetence; human;
KW	anti-HIV antibody; detection; HIV infection.
OS	Homo sapiens.
FS	Key
FT	Location/Qualifiers
FT	/Region 1..21
FT	/Label- FR1
FT	/Region 22..33
FT	/Label- CDR1
FT	/Region 34..48
FT	/Label- FR2
FT	/Region 49..55
FT	/Label- CDR2
FT	/Region 56..87
FT	/Label- FR3
FT	/Region 88..96
FT	/Label- CDR3
FT	/Region 97..108
FT	/Label- FR4
PN	WC9502273-A1.
PD	01-FEB-1996.
PF	11-JUL-1995; U08743.
PF	18-JUL-1994; JS:276852.
PI	(SCRI) SCRIPPS RES INST.
PI	Barbas CF, Burton DR, Lerner RA;
DR	WPI: 96-179601/18.
PT	Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT	passive immuno:therapy and detection of HIV infection.
PS	Example; Fig 11, 366pp, English.
CC	The sequences given in W01261-92 represent the light chain variable
CC	regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC	immunoreactive with HIV glycoprotein gp120 and are capable of
CC	neutralising HIV. This sequence represents the sequence of the JK1
CC	gene clone, b24. A MAB containing this VL sequence has the capacity
CC	to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC	by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC	binds mature gp120 preferentially over the precursor gp150. The MAB
CC	may be used for determining immunocompetence of a human anti-HIV
CC	antibody and in the detection of HIV infection.
SQ	Sequence 108 AA;

Query Match	91.7%;	Score	692;	DB	19;	Length	108;	
Best Local Similarity	93.4%;	Pred.	No. 3,38e-41;					
Matches	99:	Conservative	4:	Mismatches	3:	Indels	0:	Gaps

Db	1	eltqspgtlslspgeratlscrasqvisnlyawgqkpaqaprlliyavsnratpdr	60
QY	2	ELTQSPGTLSPGERATLSGASQVSRSNYLAWYQKPAQAPRLIIYGVSSPAISIPDR	61
Db	61	fsqssgtdftltlsrlepafavyscqygtspwffggatkveik	106
QY	62	FSQSSGTDFTLTISRLEPEDFAVYQCQYGSSPRTFGGQTKLEIK	107

RESULT	4
DB	F54316, standard; protein; 108 AA.

WIRE (TM)

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Mbsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:22:10 1998; MasPar time 6.74 Seconds
Tabular output not generated. 220,599 Million cell updates/sec

Title: >US-08-844-215-10
Description: (1-107) from US08844.215.pep
Perfect Score: 755
Sequence: 1 AELTQSPGTLSPGERATL CQQYGSPPRTFGGKLEIK 107

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 29.661; Variance 168.850; scale 0.176
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No	Score	Query Match Length	ID	Description
1	696	92.2	129 7 R38672	vk325-Jk2.
2	692	91.7	108 10 R54307	Anti-HIV gp120 immuno
3	692	91.7	108 19 W01265	VL region of HIV neut
4	685	90.7	108 9 R54316	Anti-HIV gp120 immuno
5	685	90.7	108 9 R54316	VL region of HIV neut
6	674	89.3	109 9 R50217	HSV glycoprotein F bi
7	671	88.9	107 7 R38593	Human lambda light ch
8	670	88.7	107 14 W01264	VL region of HIV neut
9	670	88.7	107 10 R54311	Anti-HIV gp120 immuno
10	670	88.7	109 10 R54275	Anti-HIV gp120 immuno
11	670	88.7	109 19 W01320	VL of Fab, DL 41 19.
12	668	88.5	111 19 W01322	VL of Fab, GL 41 1, b
13	668	88.5	111 10 R54277	Anti-HIV gp41 immuno
14	661	87.5	129 7 R41286	F105vk-F105JK.
15	658	87.2	129 7 R39672	F105vk-F105JK.
16	657	87.0	104 9 R54317	Anti-HIV gp120 immuno
17	657	87.0	104 19 W01279	VL region of HIV neut
18	657	87.0	134 20 W11155	Anti-lung tumour anti
19	653	86.5	108 19 W01289	VL region of HIV neut
20	650	86.1	107 19 W01266	VL region of HIV neut

21	650	86.1	107 10 R54308	Anti-HIV gp120 immuno
22	650	86.1	108 10 R54355	Anti-HIV gp120 immuno
23	650	86.1	108 19 W01275	VL region of HIV neut
24	650	86.1	109 9 R50218	HSV glycoprotein F bi
25	649	86.0	109 10 R56286	Light chain of Amb al
26	646	85.4	109 10 R54353	Anti-HIV gp120 immuno
27	638	84.5	124 22 W24339	Immunoglobulin F101-2
28	637	84.4	108 19 W01267	VL region of HIV neut
29	636	84.2	214 19 W07615	Ulcerative colitis-as
30	633	83.8	215 19 W07616	Ulcerative colitis-as
31	628	83.2	112 10 R54379	Anti-HIV gp41 immuno
32	628	83.2	112 10 W01324	VL of Fab, SS 41 8, E
33	626	82.9	115 11 R62930	Human V-kappa vk55.8
34	626	82.9	116 22 W03949	DNA fragment vk55.8
35	625	82.6	116 7 R38550	Human V-kappa fragment
36	624	82.6	108 10 R54309	Anti-HIV gp120 immuno
37	619	82.0	100 5 P25324	VL region of human rh
38	615	81.5	107 9 R54328	Anti-HIV gp120 immuno
39	615	81.5	107 19 W01299	VL region of HIV neut
40	614	81.3	105 9 R54314	Anti-HIV gp120 immuno
41	614	81.3	105 19 W01272	VL region of HIV neut
42	614	81.3	107 9 R54327	Anti-HIV gp120 immuno
43	614	81.3	107 19 W01298	VL region of HIV neut
44	611	80.9	104 9 R54315	Anti-HIV gp120 immuno
45	611	80.9	104 19 W01273	VL region of HIV neut

ALIGNMENTS

RESULT 1
ID R38672 standard; Protein: 129 AA.
AC R38672:
DI 01-NOV-1993 (first entry)
DE vk325-Jk2.
KW Monoclonal antibody; MAB; envelope: glycoprotein; gp120; HIV; AIDS;
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Protein 21..129
FT /label= mat_protein
FT Region 1..116
FT /label= vk325
FT /label= Jk2
FT /label= Jk2
FT /label= CDR1
FT /label= CDR2
FT /label= CDR3
FT /label= CDR3
FT Misc_difference 1
FT /note= "Met encoded by ATC (sic)"
FT Misc_difference 35
FT /note= "Pro encoded by GCA (sic)"
FT Misc_difference 99
FT /note= "Leu encoded by GTG (sic)"
FT Misc_difference 113
FT /note= "Gly encoded by GAR (sic)"
FT Misc_difference 114
FT /note= "Ser encoded by AAC (sic)"
FT /note= "Pro encoded by GTT (sic)"
FN W03912235-A.
PD 24-JUN-1993
PF 10-DEC-1992; U10928.
PP 10-DEC-1991; US-804652.
PA (DAND) DANA FABER CANCER INST INC.
PA (NEMO-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JC;
DR WP1: 93-214174/26.

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Db 4 ltqspdtlspgertatlsrscasqvssylawygkqgqaprrlllygassratgipdrf 63
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QY 3 LTQSPGTLSPGERTATLSGASQSVPSNYLAWYQCKPQCAPRLIYGVSSPATGIPDPF 62
|||||

Db 64 sgsasgtdftltisrlepedfavyycqygssppafgqgatkveik 108
|||||
QY 63 SGSGSGTDFLTISPLEPEDFAVYVCQYGSPPPTFGWTKLEIK 107
|||||

RESULT 10
ENTRY K3HUHI *type complete
TITLE Ig kappa chain precursor V-III region (Hic) - human
ORGANISM *formal_name Homo sapiens *common_name man
DATE 30-Jun-1990 *sequence_revision 30-Jun-1990 *text_change
ACCESSIONS PLO021
REFERENCE Kipps, T.J.; Tomhave, E.; Chen, P. P.; Carson, D.A.
*journal J. Exp. Med. (1988) 167:840-852
*title Autoantibody-associated kappa light chain variable region
gene expressed in chronic lymphocytic leukemia with little
or no somatic mutation. Implications for etiology and
immunotherapy.
*cross-references MUID:88171307
*accession PLO021
**molecule_type mRNA
**residues 1-129 **label KIP
COMMENT The protein is one of the surface immunoglobulin M autoantibodies
expressed in patients with chronic lymphocytic leukemia.
GENETICS
*gene GDB:IGKV3
**cross-references GDB:136266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS autoantibody; chronic lymphocytic leukemia; heterotetramer;
immunoglobulin
FEATURE
1-20 *domain signal sequence *status predicted *label SIG\
21-129 *product Ig kappa chain V-III region (Hic) *status
predicted *label KAP\
21-117 *region V segment\
44-55 *region complementarity-determining 1\
71-77 *region complementarity-determining 2\
110-117 *region complementarity-determining 3\
118-129 *region J segment (JK1)\
43-109 *disulfide_bonds *status predicted
SUMMARY *length 129 *molecular_weight 14070 *checksum 8174
Query Match 91.78; Score 692; DB 2; Length 129;
Best Local Similarity 91.78; Pred. No. 8,576;66;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltqspdtlspgertatlsrscasqvssylawygkqgqaprrlllygassratgipdrf 83
|||||
QY 3 LTQSPGTLSPGERTATLSGASQSVPSNYLAWYQCKPQCAPRLIYGVSSPATGIPDPF 62
|||||

Db 84 sgsasgtdftltisrlepedfavyycqygssppafgqgatkveik 128
|||||
QY 63 SGSGSGTDFLTISPLEPEDFAVYVCQYGSPPPTFGWTKLEIK 107
|||||

RESULT 11
ENTRY R30601 *type fragment
TITLE Ig kappa chain V-III region (Glo) - human (fragment)
ORGANISM *formal_name Homo sapiens *common_name man
DATE 29-Jun-1989 *sequence_revision 29-Jun-1989 *text_change
16-Aug-1996

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ACCESSIONS B30601
REFERENCE A30601
*authors Goni, F. R.; Chen, P. P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
*journal J. Immunol. (1989) 142:3158-3163
*title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
*cross-references MUID:89215279
*accession B30601
**status preliminary
**molecule_type protein
**residues 1-109 **label GON
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY *length 109 *checksum 5911
Query Match 91.5%; Score 691; DB 7; Length 109;
Best Local Similarity 94.3%; Pred. No. 1,136;65;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltqspdtlspgertatlsrscasqvssylawygkqgqaprrlllygassratgipdrf 63
|||||
QY 3 LTQSPGTLSPGERTATLSGASQSVPSNYLAWYQCKPQCAPRLIYGVSSPATGIPDPF 62
|||||

Db 64 sgsasgtdftltisrlepedfavyycqygssppafgqgatkveik 108
|||||
QY 63 SGSGSGTDFLTISPLEPEDFAVYVCQYGSPPPTFGWTKLEIK 107
|||||

RESULT 12
ENTRY S47181 *type complete
TITLE Ig kappa chain - human
ORGANISM *formal_name Homo sapiens *common_name man
DATE 09-Jan-1995 *sequence_revision 06-Jan-1995 *text_change
16-Aug-1996
ACCESSIONS S47181
REFERENCE McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
*authors
*submission submitted to the EMBL Data Library, June 1994
*description Cloning and analysis of IgM anti-thyroglobulin autoantibodies
from patients with Hashimoto's thyroiditis.
*accession S47181
**status preliminary
**molecule_type mRNA
**residues 1-109 **label MCI
**cross-references EMBL:X79784
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY *length 109 *molecular_weight 11982 *checksum 4729
Query Match 91.5%; Score 691; DB 7; Length 109;
Best Local Similarity 91.5%; Pred. No. 1,136;65;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 3 eltqspdtlspgertatlsrscasqvssylawygkqgqaprrlllygassratgipdrf 62
|||||
QY 2 ELTQSPGTLSPGERTATLSGASQSVPSNYLAWYQCKPQCAPRLIYGVSSPATGIPDPF 61
|||||

Db 63 fsgsgsgtdftltisrlepedfavyycqygssppafgqgatkveik 108
|||||
QY 62 FSGSGSGTDFLTISPLEPEDFAVYVCQYGSPPPTFGWTKLEIK 107
|||||

RESULT 13
ENTRY F30607 *type fragment
TITLE Ig kappa chain V-III region (Bor) - human (fragment)
ORGANISM *formal_name Homo sapiens *common_name man
DATE 29-Jun-1989 *sequence_revision 29-Jun-1989 *text_change
16-Aug-1996
ACCESSIONS F30607
REFERENCE A30601
*authors Goni, F. R.; Chen, P. P.; McGinnis, D.; Arjonilla, M.L.;

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SUMMARY      #length 109 #checksum 5951
Query Match      92.2%; Score 696; DB 7; Length 109;
Best Local Similarity 95.2%; Pred. No. 2,85e-66;
Matches 100; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltqspgtlslsperatlscrasqsvssylawyqkpgqaprllygassratgipdrf 63
|||||
QY 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 62
|||||

Db 64 sqsgsgtdftltisrlepedfavyycqygsspytfgqgkkleik 108
|||||
QY 63 SGSGSGTDTLTLSRLEPEDFAVYCYQYQYGSPPRTFGQGTKLEIK 107
|||||

RESULT 6
ENTRY S20636 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
16-Aug-1996
ACCESSIONS S20636
REFERENCE Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
#authors submitted to the EMBL Data Library, April 1992
#accession S20636
#molecule_type preliminary
#residues 1-128 #label LEE
#cross-references EMBL:211894
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 128 #molecular_weight 13915 #checksum 4511

Query Match      91.9%; Score 694; DB 7; Length 128;
Best Local Similarity 93.3%; Pred. No. 4,94e-66;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 24 ltqspgtlslsperatlscrasqsvssylawyqkpgqaprllygassratgipdrf 83
|||||
QY 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 62
|||||

Db 84 sqsgsgtdftltisrlepedfavyycqygsspytfgqgkkleik 128
|||||
QY 63 SGSGSGTDTLTLSRLEPEDFAVYCYQYQYGSPPRTFGQGTKLEIK 107
|||||

RESULT 7
ENTRY S49532 #type complete
TITLE anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Feb-1995 #sequence_revision 12-May-1995 #text_change
02-Jun-1995
ACCESSIONS S49532
REFERENCE Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
#authors submitted to the EMBL Data Library, October 1994
#accession Molecular characterization of natural human anti-Sm
autoantibodies.
#status preliminary
#molecule_type mRNA
#residues 1-129 #label MAH
#cross-references EMBL:246345
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 129 #molecular_weight 14093 #checksum 5407

Query Match      91.9%; Score 694; DB 7; Length 129;
Best Local Similarity 94.3%; Pred. No. 4,94e-66;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltqspgtlslsperatlscrasqsvssylawyqkpgqaprllygassratgipdrf 83
|||||

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QY 3 LTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDRF 62
Db 84 sqsgsgtdftltisrlepedfavyycqygsspytfgqgkkleik 128
|||||
QY 63 SGSGSGTDTLTLSRLEPEDFAVYCYQYQYGSPPRTFGQGTKLEIK 107
|||||

RESULT 8
ENTRY F44151 #type fragment
TITLE Ig kappa chain V region (JM-01) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS F44151
REFERENCE Zebadee, S.L.; Barbas III, C.F.; Hong, Y.L.; Caethien, R.H.;
#authors Graff, P.; Degraw, J.; Pyatt, J.; Lapolla, P.; Burton,
D.R.; Lerner, R.A.; Thornton, G.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface
antigen.
#accession F44151
#status preliminary: not compared with conceptual translation
#molecule_type mRNA
#residues 1-109 #label ZEB
#note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5518

Query Match      91.8%; Score 693; DB 7; Length 109;
Best Local Similarity 92.5%; Pred. No. 6,51e-66;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 1 aeltqspgtlslsperatlscrasqsvsfnylawyqkpgqaprllygassratgipdr 60
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QY 1 AELTQSPGTLSLSPGERATLSGASQSVRSNYLAWYQKPGQAPRLLYGVSSRATGIPDR 60
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Db 61 rfsqsgsgtdftltisrlepedfavyycqygsspytfgqgkkleik 107
|||||
QY 61 RFSQSGSGTDTLTLSRLEPEDFAVYCYQYQYGSPPRTFGQGTKLEIK 107
|||||

RESULT 9
ENTRY PH0963 #type fragment
TITLE Ig kappa chain V region (G6+ CLL-SM1) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0963
REFERENCE Martin, T.; Duff, S.F.; Carson, D.A.; Kipps, T.J.
#authors J. Exp. Med. (1992) 175:983-991
#journal Evidence for somatic selection of natural autoantibodies.
#title #cross-references MIMD-92202880
#accession PH0963
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-109 #label MAR
#note heterotetramer; immunoglobulin
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-50 #region framework 2\
51-56 #region complementarity-determining 2\
57-89 #region framework 3\
90-97 #region complementarity-determining 3\
SUMMARY #length 109 #checksum 5292

Query Match      91.7%; Score 692; DB 7; Length 109;
Best Local Similarity 93.3%; Pred. No. 8,57e-66;
Matches 96; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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#authors      Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
               Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal      J. Immunol. (1989) 142:3158-3163
#title       Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession   C30608
#status      preliminary
#molecule_type protein
#residues    1-108 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
#length 108 #checksum 1607
SUMMARY

Query Match      93.4%; Score 705; DB 7; Length 108;
Best Local Similarity 95.2%; Pred. No. 2,39e-67;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspatllspgeratlsrscasvssvylawygqkpgqaprllygssratgipdrf 63
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Qy 3 ltqspgtllspgeratllscasvssvsnlyawyyqkpgqaprllygssratgipdrf 62
    |||||

Db 64 sgsqsgtdftltisrlepdefavvyccqygsspwtfqggtkkleik 108
    |||||
Qy 63 sgsqsgtdftltisrlepdefavvyccqygsspwtfqggtkkleik 107
    |||||

RESULT 3
ENTRY   D30601
TITLE   Ig kappa chain V-III region (Cur) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS D30601
REFERENCE  A30601
#authors   Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
               Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal   J. Immunol. (1989) 142:3158-3163
#title     Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities
#cross-references MUID:89215279
#accession D30601
#status    preliminary
#molecule_type protein
#residues  1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
#length 109 #checksum 6151
SUMMARY

Query Match      93.4%; Score 705; DB 7; Length 109;
Best Local Similarity 95.2%; Pred. No. 2,39e-67;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltqspatllspgeratlsrscasvssvylawygqkpgqaprllygssratgipdrf 63
Qy 3 ltqspgtllspgeratllscasvssvsnlyawyyqkpgqaprllygssratgipdrf 62

Db 64 sgsqsgtdftltisrlepdefavvyccqygsspwtfqggtkkleik 108
Qy 63 sgsqsgtdftltisrlepdefavvyccqygsspwtfqggtkkleik 107

RESULT 4
ENTRY   K3HURA
TITLE   Ig kappa chain precursor V-III region (Hah) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
30-May-1997
ACCESSIONS PL0022
REFERENCE  Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
#authors

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#journal      J. Exp. Med. (1988) 167:840-852
#title       Autoantibody-associated kappa light chain variable region
               gene expressed in chronic lymphocytic leukemia with little
               or no somatic mutation. Implications for etiology and
               immunotherapy.
#cross-references MUID:88171307
#accession   FL0022
#molecule_type mRNA
#residues    1-129 ##label KIP
COMMENT      The protein is one of the surface immunoglobulin M autoantibodies
               expressed in patients with chronic lymphocytic leukemia.
GENETICS
#gene        GDB:IGKV3
#cross-references GDB:136266
               An immunoglobulin heterotetramer subunit consists of two
               identical light (kappa or lambda) and two identical heavy
               (alpha, delta, epsilon, gamma, or mu) chains usually
               stabilized by interchain disulfide bonds. In some cases,
               such as IgA and IgM, the subunits associate into larger
               oligomers.
               #superfamily immunoglobulin V region: immunoglobulin homology
               autobody: chronic lymphocytic leukemia; heterotetramer;
               immunoglobulin
CLASSIFICATION #domain signal sequence #status predicted #label SIGN
KEYWORDS      #product Ig kappa chain V-III region (Hah) #status
               predicted #label MATN
               #region V segment
               #region complementarity-determining 1\
               #region complementarity-determining 2\
               #region complementarity-determining 3\
               #region J segment (JK1)\
               #disulfide_bonds #status predicted
               #length 129 #molecular_weight 14073 #checksum 7361
SUMMARY

Query Match      93.1%; Score 703; DB 2; Length 129;
Best Local Similarity 94.3%; Pred. No. 4,13e-67;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltqspatllspgeratlsrscasvssvylawygqkpgqaprllygssratgipdrf 83
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Qy 3 ltqspgtllspgeratllscasvssvsnlyawyyqkpgqaprllygssratgipdrf 62

Db 84 sgsqsgtdftltisrlepdefavvyccqygsspwtfqggtkkleik 128
    |||||
Qy 63 sgsqsgtdftltisrlepdefavvyccqygsspwtfqggtkkleik 107

RESULT 5
ENTRY   H30601
TITLE   Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS H30601; E30601
REFERENCE  A30601
#authors   Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
               Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
#journal   J. Immunol. (1989) 142:3158-3163
#title     Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession H30601
#status    preliminary
#molecule_type protein
#residues  1-109 ##label GON1
#accession E30601
#status    preliminary
#molecule_type protein
#residues  1-109 ##label GON2
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin

```

WIREA

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:23:29 1998. MasPar time 7.55 Seconds
Tabular output not generated.
431.742 Million cell updates/sec

Title: >US-08-844-215-10
Perfect Score: 755
Sequence: 1 AELTQSPGTLTSLSPGERATL.....CQYGSPPRTFGQTKLEIK 107

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir53
1:ann1 2:ann2 3:ann3 4:ann4 5:ann5 6:ann6 7:ann7 8:ann8
8:ann9 9:ann10 10:ann11 11:ann12 12:ann13
13:ann14 14:ann15 15:ann16 16:ann17 17:ann18:unrev

Statistics: Mean 40.248; Variance 138.316; scale 0.291

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	722	95.6	109	7	G30601	Ig kappa chain V-III	2.18e-69
2	705	93.4	108	7	K30609	Ig kappa chain V-III	2.38e-67
3	705	93.4	109	7	D30601	Ig kappa chain V-III	2.38e-67
4	703	93.1	126	7	K30H0A	Ig kappa chain V-III	4.13e-67
5	696	92.2	109	7	H30601	Ig kappa chain V-III	2.85e-66
6	694	91.9	128	7	S20635	Ig kappa chain V reg	4.94e-66
7	694	91.9	129	7	S49532	anti-Sm antibody VL	4.94e-66
8	693	91.8	109	7	F44151	Ig kappa chain V reg	6.51e-66
9	692	91.7	109	7	PH0963	Ig kappa chain V reg	8.57e-66
10	692	91.7	129	7	K30H01	Ig kappa chain V reg	8.57e-66
11	691	91.5	109	7	D30601	Ig kappa chain V-III	1.13e-65
12	691	91.5	109	7	S47181	Ig kappa chain - hum	1.13e-65
13	690	91.4	109	7	F30507	Ig kappa chain V-III	1.49e-65
14	690	91.4	109	7	K3H051	Ig kappa chain V-III	1.49e-65
15	690	91.4	109	7	S30601	Ig kappa chain V-III	1.49e-65
16	689	91.3	114	7	S46375	Ig kappa chain V-J r	1.96e-65
17	689	91.3	129	7	S46369	Ig light chain varia	1.96e-65
18	689	91.3	134	7	S86643	Ig kappa chain V reg	1.96e-65
19	688	91.1	109	7	G30601	Ig kappa chain V-III	2.58e-65
20	687	91.0	110	7	S20635	Ig kappa chain V reg	3.40e-65

21	685	90.7	108	2	K3HUB6	Ig kappa chain V-III	5.90e-65
22	682	90.3	109	2	K3HUB6	Ig kappa chain V-III	1.35e-64
23	682	90.3	130	7	S20637	Ig kappa chain V-III	1.35e-64
24	680	90.1	107	7	P0965	Ig kappa chain V-III	2.34e-64
25	680	90.1	108	7	H44151	Ig kappa chain V-III	2.34e-64
26	680	90.1	110	7	E30607	Ig kappa chain V-III	2.34e-64
27	676	89.5	109	7	E30608	Ig kappa chain V-III	7.03e-64
28	672	89.0	109	2	K3HUB6	Ig kappa chain V-III	2.11e-63
29	671	88.9	109	7	G30607	Ig kappa chain V-III	2.78e-63
30	669	88.6	108	7	B30608	Ig kappa chain V-III	4.82e-63
31	664	87.9	121	7	S40327	Ig kappa chain - hum	1.91e-62
32	663	87.8	129	7	A32274	Ig kappa chain - hum	2.51e-62
33	661	87.5	109	2	K3HUB6	Ig kappa chain V-III	4.35e-62
34	659	87.3	108	7	E30609	Ig kappa chain V-III	7.54e-62
35	659	87.3	124	7	S20633	Ig kappa chain - hum	7.54e-62
36	653	86.5	110	7	S44120	Ig kappa chain V-J	3.92e-61
37	647	85.7	129	7	S40325	Ig kappa chain - hum	2.04e-60
38	646	85.6	215	15	A23746	Ig kappa chain V-III	2.88e-60
39	644	85.3	108	7	S33988	Ig kappa chain V-III	4.64e-60
40	642	85.0	145	7	S20631	Ig kappa chain - hum	8.80e-60
41	635	84.1	104	7	PH0964	Ig kappa chain V-III	5.48e-59
42	628	83.2	127	7	S40380	Ig kappa light chain	3.73e-58
43	625	82.9	96	7	A30601	Ig kappa chain V-III	6.45e-58
44	626	82.9	116	7	R27594	Ig kappa chain - hum	6.45e-58
45	626	82.9	130	7	S40360	Ig kappa chain - hum	6.45e-58

ALIGNMENTS

RESULT 1
ENTRY G30601 #type fragment
TITLE Ig kappa chain V-III region (Got) - human (fragment)
ORGANISM Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS G30601
REFERENCE A30601
#authors Geni, F.P.; Chen, P.N.; McGinnis, B.; Arizono, M.L.; Fernandez, J.; Carlson, D.; Solomon, A.; Mende, F.; Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotype characterization of the L chains of human IgM autoantibodies with different specificities.
#cross-references MIM:89215279
#accession G30601
#status Preliminary
#molecule_type Protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology heterotetramer: immunoglobulin
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 5641

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Best Local Similarity 97.1%, Fred. No. 2.18e-69;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 3 17sgsgtdftlislslpdlfayvycggysprrfaggtkleik 108
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Db 64 17sgsgtdftlislslpdlfayvycggysprrfaggtkleik 108
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QY 63 17sgsgtdftlislslpdlfayvycggysprrfaggtkleik 108
||||| 17sgsgtdftlislslpdlfayvycggysprrfaggtkleik 108

RESULT 2
ENTRY G30608 #type fragment
TITLE Ig kappa chain V-III region (Pie) - human (fragment)
ORGANISM Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS G30608
REFERENCE A30601


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Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
J. Immunol. (1989) 142:3158-3163
#journal
#title Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MIMD:89215279
#accession F30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 6514

Query Match 91.4%; Score 690; DB 7; Length 109;
Best Local Similarity 92.4%; Pred. No. 1.49e-65;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 Ltqspgtlslsperatlsctasqsvssylawyqkqgqprlliyqasratgipdrf 63
QY 3 LTQSPGTLSLSPERATLSCTASQSVSSYLA WYQKQGPRLLIYQASRATGIPDRF 62

Db 54 sqsqsatdflltislrlepedfavyvqgqyqnsqptfgggtkveik 108
QY 63 SGSGSGTDFLLTISLPEDEFAVYVQYQYVSSSPRTFGGKTLEIK 107

RESULT 14
ENTRY K3HUSI #type complete
TITLE Ig kappa chain V-II region (Sie) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jul-1982 #sequence_revision 06-Jul-1982 #ext_change
06-Sep-1996
ACCESSION A01892
REFERENCE A90450
#authors Andrews, D. W.; Capra, J. D
#journal Biochemistry (1981) 20:5816-5822
#title Amino acid sequence of the variable regions of light chains
from two idiotypically cross-reactive human IgM
anti-gamma-globulins of the Wa group.
#cross-references MIMD:82046598
#accession A01892
#molecule_type protein
#residues 1-109 #label AND
COMMENT This chain was isolated from an IgM with anti-gamma globulin
activity.
GENETICS
#gene GDB:IGKV3
#cross-references GDB:I36266
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer
FEATURE
16-91 #domain immunoglobulin homology #label IMM
23-89 #disulfide_bonds #status predicted
SUMMARY #length 109 #molecular_weight 11775 #checksum 5885

Query Match 91.4%; Score 690; DB 2; Length 109;
Best Local Similarity 91.4%; Pred. No. 1.49e-65;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 4 Ltqspgtlslsperatlsctasqsvssylawyqkqgqprlliyqasratgipdrf 63
QY 3 LTQSPGTLSLSPERATLSCTASQSVSSYLA WYQKQGPRLLIYQASRATGIPDRF 62

Db 54 sqsqsatdflltislrlepedfavyvqgqyqnsqptfgggtkveik 108
QY 63 SGSGSGTDFLLTISLPEDEFAVYVQYQYVSSSPRTFGGKTLEIK 107

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RESULT 15

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ENTRY F30601 #type fragment
TITLE Ig kappa chain V-III region (Neu) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 26-Jun-1989 #sequence_revision 26-Jun-1989 #ext_change
16-Aug-1996
ACCESSION F30601
REFERENCE A30601
#authors Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of:
human IgM autoantibodies with different specificities.
#cross-references MIMD:89215279
#accession F30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer: immunoglobulin
SUMMARY #length 109 #checksum 4627

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Best Local Similarity 92.4%; Pred. No. 1.49e-65;
Matches 97; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 4 Ltqspgtlslsperatlsctasqsvssylawyqkqgqprlliyqasratgipdrf 63
QY 3 LTQSPGTLSLSPERATLSCTASQSVSSYLA WYQKQGPRLLIYQASRATGIPDRF 62

Db 64 tsgsgtdftltislrlepedfavyvqgqyqnsqptfgggtkveik 108
QY 63 SGSGSGTDFLLTISLPEDEFAVYVQYQYVSSSPRTFGGKTLEIK 107

Search completed: Tue Feb 24 07:21:53 1998
Job time : 24 secs.

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CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA: 11956 MW: 63169 GN:

Query Match      88.58: Score 668; DB 7; Length 111;
Best Local Similarity 87.98: Pred.No. 4.06e-44;
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

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QY 1 AELTQSPGTLTSLSPGERATLSGGASQSVRSNYLAWYQKPGAPRLIIYGVSSRATGIPD 60
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Db 62 RFGSGSGADFTLAIISLEPEDEFAVYCCQYAGS-HTFGGQTKLEIK 107
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QY 61 RFGSGSGIDFTITISLEPEDEFAVYCCQYGSPPFTFGGQTKLEIK 107
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Search completed: Tue Feb 24 07:48:37 1998
Job time : 12 secs.

CC INFORMATION FOR SEQ ID NO: 90:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11705 MW: 62938 CN:

Query Match 88.7% Score 670; DB 13; Length 107;
Best Local Similarity 88.7% Pred No 2 80e-44;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGCAPPLLIYGSSTGTGIPDR 60

QY 2 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGCAPPLLIYGVSSATGIPDR 61

Db 61 FSGSGSGTDFLTISRLEPEDFAVYCOHYGNSVYTFGGTKLEIK 106

QY 62 FSGSGSGTDFLTISRLEPEDFAVYCOHYGNSVYTFGGTKLEIK 107

RESULT 11
ID US-08-276-852-90 STANDARD: PRT: 107 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 90, Application US/08276852.

CC Sequence 90, Application US/08276852

CC Patent No. 5652138

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F

CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of

CC ADDRESSEE: Patent Counsel

CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCPI452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 90.

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 107 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11705 MW: 62938 CN:

Query Match 88.7% Score 670; DB 7; Length 107;
Best Local Similarity 88.7% Pred No 2 80e-44;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGCAPPLLIYGSSTGTGIPDR 60

QY 2 ELTQSPGTLSPGEPATLSCPASQSLNNYLAWYQKPGCAPPLLIYGVSSATGIPDR 61

Db 61 FSGSGSGTDFLTISRLEPEDFAVYCOHYGNSVYTFGGTKLEIK 106

QY 62 FSGSGSGTDFLTISRLEPEDFAVYCOHYGNSVYTFGGTKLEIK 107

RESULT 12
ID US-08-276-852-147 STANDARD: PRT: 109 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 147, Application US/08276852.

CC Sequence 147, Application US/08276852

CC Patent No. 5652138

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F

CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

CC NUMBER OF SEQUENCES: 170

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of

CC ADDRESSEE: Patent Counsel

CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCPI452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 147:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 109 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/487,200
 CC FILING DATE: 7-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/390,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002610
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: rsv 6L; 11L; 21L; anad 22L
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..109
 CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 90.3%; Score 682; DB 7; Length 108;
 Best Local Similarity 92.4%; Pred. No. 3,04e-45;
 Matches 97; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

D6 4 LTSPGTLSPGERATLSCRASQSSVSLGWYQKPGQAPPLLIYGRASSRATGIPDPF 63
 QY 3 LTSPGTLSPGERATLSCRASQSSVSLGWYQKPGQAPPLLIYGVSSRATGIPDPF 62

D6 64 SGSSGSGDTFTLTISRLPEPFAMVYQQYQGLRTEFGQGTKEIK 108
 QY 63 SGSSGSGDTFTLTISRLPEPFAMVYQQYQGLRTEFGQGTKEIK 107

RESULT 9
 ID PCT-US93-08786-23 STANDARD: PRT: 109 AA.
 XX xxxxxx
 XX 01-JAN-1900
 DE Sequence 23, Application PC/TUS9308786.
 XX Sequence 23, Application PC/TUS9308786
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis F
 CC APPLICANT: Barbas, III, Carlos F.
 CC APPLICANT: Chanock, Robert M.
 CC APPLICANT: Murphy, Brian R.
 CC APPLICANT: Crowe, Jr., James E.
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn, Jubas & Lubitz
 CC STREET: 1890 Century Park East, Suite 500

CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08786
 CC FILING DATE: 16-SEP-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Wetherell, Jr., Ph.D., John R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD-2791
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 23:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 109 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: rsv 6L; 11L; 21L; anad 22L
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..109
 CC SEQUENCE 109 AA; 12099 MW; 62556 CN;

Query Match 89.3%; Score 674; DB 11; Length 109;
 Best Local Similarity 88.8%; Pred. No. 1.34e-44;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

D6 2 AELTSPGTLSPGERATLSCRASQSSVSLGWYQKPGQAPPLLIYGRASSRATGIPDP 61
 QY 1 AELTSPGTLSPGERATLSCRASQSSVSLGWYQKPGQAPPLLIYGVSSRATGIPDP 60

D6 62 PFSSGSGDTFTLTISRLPEPFAMVYQQYQGLRTEFGQGTKEIK 108
 QY 61 PFSSGSGDTFTLTISRLPEPFAMVYQQYQGLRTEFGQGTKEIK 107

RESULT 10
 ID PCT-US95-08743-90 STANDARD: PRT: 107 AA.
 XX xxxxxx
 XX 01-JAN-1900
 DE Sequence 90, Application PC/TUS9508743.
 XX Sequence 90, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 90.3% Score 682; DB 6; Length 108;
Best Local Similarity 92.4% Pred No. 3 04e-45;
Matches 97; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQAPPLLIYGASSPATGIPDPF 63
QY 3 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQAPPLLIYGASSPATGIPDPF 62
Db 64 SGSGSGTDFTLTISRLEPEDEFAVYVCOQYQSGSLGRFTFGGQTKVEIK 108
QY 63 SGSGSGTDFTLTISRLEPEDEFAVYVCOQYQSGSLGRFTFGGQTKLEIK 107

RESULT 7
ID US-08-474-040-86 STANDARD: PRT: 108 AA.

XX XXXXXX
XX 01-JAN-1900
XX Sequence 86, Application US/08474040.
XX Sequence 86, Application US/08474040
XX Patent No. 5693761
XX GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELLINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend & Hourie and Crew
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN;

Query Match 90.3% Score 682; DB 7; Length 108;
Best Local Similarity 92.4% Pred No. 3 04e-45;

Matches 97; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQAPPLLIYGASSPATGIPDPF 63
QY 3 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQAPPLLIYGASSPATGIPDPF 62
Db 64 SGSGSGTDFTLTISRLEPEDEFAVYVCOQYQSGSLGRFTFGGQTKVEIK 108
QY 63 SGSGSGTDFTLTISRLEPEDEFAVYVCOQYQSGSLGRFTFGGQTKLEIK 107

RESULT 8
ID US-08-487-200-86 STANDARD: PRT: 108 AA.

XX XXXXXX
XX 01-JAN-1900
XX Sequence 86, Application US/08487200.
XX Sequence 86, Application US/08487200
XX Patent No. 5693762
XX GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELLINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US

RESULT 2
ID US-08-276-852-86 STANDARD: PRT: 108 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE
XX
Sequence 86, Application US/08276852.
XX
Sequence 86, Application US/08276852
CC
Patent No. 5652138
CC
GENERAL INFORMATION:
CC
APPLICANT: Burton, Dennis R
CC
APPLICANT: Barbas, Carlos F
CC
APPLICANT: Lerner, Richard A
CC
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC
NUMBER OF SEQUENCES: 170
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: The Scripps Research Institute, Office of
CC
ADDRESSEE: Patent Counsel
CC
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC
STREET: Mail Drop TPC8
CC
CITY: La Jolla
CC
STATE: CA
CC
COUNTRY: USA
CC
ZIP: 92037
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: Floppy disk
CC
OPERATING SYSTEM: IBM PC compatible
CC
SOFTWARE: Patent In Release #1.0, Version #1.25
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/276.852
CC
FILING DATE: 18-JUL-1994
CC
CLASSIFICATION: 514
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 08/178,302
CC
FILING DATE: 30-SEP-1993
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 07/954,148
CC
FILING DATE: 30-SEP-1993
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Fitting, Thomas
CC
REGISTRATION NUMBER: 34,163
CC
REFERENCE/DOCKET NUMBER: SCR1452P
CC
TELEPHONE: 619-554-2937
CC
TELEFAX: 619-554-6312
CC
INFORMATION FOR SEQ ID NO: 86:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 108 amino acids
CC
TYPE: amino acid
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: protein
CC
SEQUENCE 108 AA: 11769 MW: 65957 CN:
Query Match 91.7%: Score 692; DB 7; Length 108;
Best Local Similarity 93.4%: Pred No. 4 78e-46.
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGPERATLSCAGSQSVISNYLAWYQCKPGCAPRLIYGVSNPATGIPDR 60
QY 2 ELTQSPGTLSPGPERATLSCAGSQSVISNYLAWYQCKPGCAPRLIYGVSNPATGIPDR 61
Db 61 FSGSGSGTDFLTLSRLEPEDFAVYCCQYVGSISHWTFEGGKVEIK 106
QY 62 FSGSGSGTDFLTLSRLEPEDFAVYCCQYVGSISHWTFEGGKVEIK 107
RESULT 3
ID US-08-276-852-99 STANDARD: PRT: 108 AA.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE
XX
Sequence 99, Application US/08276852.
XX
Sequence 99, Application US/08276852
CC
Patent No. 5652138
CC
GENERAL INFORMATION:
CC
APPLICANT: Burton, Dennis R
CC
APPLICANT: Barbas, Carlos F
CC
APPLICANT: Lerner, Richard A
CC
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC
NUMBER OF SEQUENCES: 170
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: The Scripps Research Institute, Office of
CC
ADDRESSEE: Patent Counsel
CC
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC
STREET: Mail Drop TPC8
CC
CITY: La Jolla
CC
STATE: CA
CC
COUNTRY: USA
CC
ZIP: 92037
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: Floppy disk
CC
OPERATING SYSTEM: IBM PC compatible
CC
SOFTWARE: Patent In Release #1.0, Version #1.25
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/276.852
CC
FILING DATE: 18-JUL-1994
CC
CLASSIFICATION: 514
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 08/178,302
CC
FILING DATE: 30-SEP-1993
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 07/954,148
CC
FILING DATE: 30-SEP-1992
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Fitting, Thomas
CC
REGISTRATION NUMBER: 34,163
CC
REFERENCE/DOCKET NUMBER: SCR1452P
CC
TELEPHONE: 619-554-2937
CC
TELEFAX: 619-554-6312
CC
INFORMATION FOR SEQ ID NO: 99:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 108 amino acids
CC
TYPE: amino acid
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: protein
CC
SEQUENCE 108 AA: 11738 MW: 63142 CN:
Query Match 90.7%: Score 685; DB 7; Length 109;
Best Local Similarity 89.6%: Pred. No. 1.75e-45;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGPERATLSCAGSQSVISNYLAWYQCKPGCAPRLIYGVSNPATGIPDR 60
QY 2 ELTQSPGTLSPGPERATLSCAGSQSVISNYLAWYQCKPGCAPRLIYGVSNPATGIPDR 61
Db 61 FSGSGSGTDFLTLSRLEPEDFAVYCCQYVGSISHWTFEGGKVEIK 106
QY 62 FSGSGSGTDFLTLSRLEPEDFAVYCCQYVGSISHWTFEGGKVEIK 107
RESULT 4
ID PCT-US95-08743-99 STANDARD: PRT: 108 AA.
XX
AC xxxxxx
XX



US-08-844-215-10.rsp

Thu, Feb 26 07:03:43 1998

RESULT 13
ID KVM_HUMAN STANDARD; PRT: 108 AA.
AC P01605;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP MEDLINE: 77038198
RX CAPRA J.D., KLAPPER D.G.;
RA SCAND. J. IMMUNOL. 5:677-684(1976).
CC -!- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
CC PIR: A01871; KIHULY.
DR HSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 2222880C CPC32;

Query Match 72.5%; Score 547; DB 5; Length 108;
Best Local Similarity 67.0%; Pred. No. 3,28e-99;
Matches 71; Conservative 20; Mismatches 14; Indels 1; Gaps 1;
Db 3 qmtqpsstlsysvqdrvtlscrasqsvrsnylwyqkqaprllygastreatgvspr 61
QY 2 ELTQSPGTLSPGERATLSGASQSVRSNYLWYQKQAPRLLYGVSSRATGIDPR 61
Db 62 fsgsgsgtdfttlisrlpeditatycqynwptfgqtkvevk 107
QY 62 FSGSGSGTDTLTISRLEPEDFAVYICQYGGSPRTFGQTKLEIK 107

RESULT 14
ID KVM_HUMAN STANDARD; PRT: 116 AA.
AC P04434; 1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECIPFOR V-III REGION (VH) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP MEDLINE: 85087932.
RX PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL: X07225; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HCVH.
DR HSP: P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH).
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 77 77

Query Match 71.0%; Score 536; DB 5; Length 108;
Best Local Similarity 64.2%; Pred. No. 1,22e-96;
Matches 68; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
Db 3 qmtqpsstlsysvqdrvtlscrasqsvrsnylwyqkqaprllygastreatgvspr 61
QY 2 ELTQSPGTLSPGERATLSGASQSVRSNYLWYQKQAPRLLYGVSSRATGIDPR 61
Db 62 fsgsgsgtdfttlisrlpeditatycqynwptfgqtkvevk 107
QY 62 FSGSGSGTDTLTISRLEPEDFAVYICQYGGSPRTFGQTKLEIK 107

Search completed: Tue Feb 24 07:21:11 1998
Job time : 15 secs.

FT DOMAIN 78 109
FT DOMAIN 110 116
FT DISULFID 43 109
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 27FA19CE CRC32;
Query Match 72.3%; Score 545; DB 5; Length 116;
Best Local Similarity 85.3%; Pred. No. 9,63e-99;
Matches 75; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Db 24 mtqpsstlsysvqdrvtlscrasqsvrsnylwyqkqaprllygastreatgvspr 83
QY 3 LTQSPGTLSPGERATLSGASQSVRSNYLWYQKQAPRLLYGVSSRATGIDPR 62
Db 84 sgsqsgtdfttlisrlpeditatycqynwptfgqtkvevk 111
QY 63 SSGSGSGTDTLTISRLEPEDFAVYICQY 90

RESULT 15
ID KVM_HUMAN STANDARD; PRT: 108 AA.
AC P01603; 1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (KA).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP MEDLINE: 76189985.
RX SHINODA T.; 77:1277-1296(1975)
RL J. BIOCHEM. -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01869; KIHURA.
DR HSP: P01607; 11GM.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 98 107
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 41BC730E CRC32;

Query Match 71.0%; Score 536; DB 5; Length 108;
Best Local Similarity 64.2%; Pred. No. 1,22e-96;
Matches 68; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
Db 3 qmtqpsstlsysvqdrvtlscrasqsvrsnylwyqkqaprllygastreatgvspr 61
QY 2 ELTQSPGTLSPGERATLSGASQSVRSNYLWYQKQAPRLLYGVSSRATGIDPR 61
Db 62 fsgsgsgtdfttlisrlpeditatycqynwptfgqtkvevk 107
QY 62 FSGSGSGTDTLTISRLEPEDFAVYICQYGGSPRTFGQTKLEIK 107

```

DR HSSP: P01607: IAAG
KW IMMUNOGLOBULIN V REGION: SIGNAL
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (CLL).
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14275 MW: 2F344658 CRC32.

Query Match 81.1% Score 612, DB 5, Length 129.
Best Local Similarity 81.1% Pred. No. 1.74e-114;
Matches 85: Conservative 13; Mismatches 55; Indels 2; Gaps 2;

Db 24 mtqspatlsvsggeratlsrsgsv:snrlawyqgkpgqpprlllygastratgiparf 82
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGAPRLLIYGVSSPATGIPDRF 62
Db 83 sgsqsgtftltisslqsedfavyycqgynnwppwtfgqtrveik 128
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS-SPRTSGGTGLEIK 107

RESULT 10
ID KV3C_HUMAN STANDARD: PRT: 100 AA.
AC P01621;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84093600.
RA BENTLEY D.L.;
PI NATURE 307:77-80(1984)
CC -!- THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIP: A01944: K3HUNG
DR HSSP: P01607: IAAG
KW IMMUNOGLOBULIN V REGION: SIGNAL: HYBRIDOMA
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NG9).
FT DISULFID 27 93 BY SIMILARITY
FT NON_TER 100 100
SQ SEQUENCE 100 AA: 10729 MW: 99A75223 CRC32.

Query Match 80.4% Score 607, DB 5, Length 100.
Best Local Similarity 92.4% Pred. No. 2.63e-113;
Matches 85: Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 8 ltqspatlsvsggeratlsrsgsvssslawyqgkpgqpprlllygastratgipdrf 67
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGAPRLLIYGVSSPATGIPDRF 62
Db 68 sgsasgtftltisslqsedfavyycqgyns 99
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS 94

RESULT 11
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RA KLAPPER D.G., CAPPA J.D.;
AL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976).
CC -!- THIS CHAIN WAS ISOLATED FROM AN ICM WITH ANTI-GAMMA GLOBULIN
ACTIVITY.
DR PIP: A01897: K3HUPM
DR HSSP: P01607: IDFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11922 MW: A0C42C88 CRC32.

Query Match 79.7% Score 602, DB 5, Length 109.
Best Local Similarity 77.1% Pred. No. 3.96e-112;
Matches 81: Conservative 14; Mismatches 10; Indels 0; Gaps 0;

Db 4 mtqspatlsvsggeratlsrsgsv:snrlawyqgkpgqpprlllygastratgiparf 63
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGAPRLLIYGVSSPATGIPDRF 62
Db 64 sgsqsgtftltisslqsedfavyycqgynnwppwtfgqtrveik 108
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQYGS-SPRTSGGTGLEIK 107

RESULT 12
ID KV3I_HUMAN STANDARD: PRT: 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932.
RA PECH M., ZACHAU H.G.;
PI NUCLEIC ACIDS RES. 12:9239-9234(1984)
DR EMBL: X01668; -; NOT_ANNOTATED_CDS.
DR PIP: A01900: K3HUVG.
DR HSSP: P01607: IAAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA: 12575 MW: 37E182FC CRC32.

Query Match 72.7% Score 549, DB 5, Length 115.
Best Local Similarity 89.8% Pred. No. 1.12e-99;
Matches 79: Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Db 24 ltqspatlsvsggeratlsrsgsv:snrlawyqgkpgqpprlllygastratgiparf 82
QY 3 LTQSPGTLSLSPGERATLSGASQSVPSNYLAWYQKPGAPRLLIYGVSSPATGIPDRF 62
Db 83 sgsqsgtftltisslqsedfavyycqg 110
QY 63 SGSGSGTDFLTISRLEPEDFAVYCYQY 90

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Matches 97: Conservative 2: Mismatches 6: Indels 0: Gaps 0:

Db 4 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 63
 QY 3 LTQSPGTLSLSPGERATLSGASQSVSNYLAWYQKQPGQAPPLLYGVSSPATGIPDRF 62
 Db 64 ssgsgtdftltisrlepedfavyycqygsgrtfggatkveik 108
 QY 63 SSGSGTDFTLTISRLEPEDFAVYCCQYGSSTPFGGATKLEIK 107

RESULT 6 STANDARD: PRT: 109 AA.

ID KV3D_HUMAN
 AC P01522:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (TI)
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 72188439
 RA SUTER L., RABINIKOL H.U., WATANABE S., HILSCHMANN N.:
 RL HOPPE-SEYLER'S 2. PHYSIC. CHEM. 353:183-238(1972).
 CC -/- THE C REGION OF THIS CHAIN HAS THE INV (3) MAPKER.
 CC -/- THIS IS A BENCE-JONES PROTEIN
 DR PIR: A01895; K3HUT1.
 DR HSSP: P01607; 2IMM.
 KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN
 FT DISULFID 23 89 BY SIMILARITY
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11788 MW; D03795R1 CPC32:

Query Match 89.0%; Score 672; DR 5; Length 109;
 Best Local Similarity 90.5%; Pred. No. 1.10e-129;
 Matches 95: Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 63
 QY 3 LTQSPGTLSLSPGERATLSGASQSVSNYLAWYQKQPGQAPPLLYGVSSPATGIPDRF 62
 Db 64 ssgsgtdftltisrlepedfavyycqygsgrtfggatkveik 108
 QY 63 SSGSGTDFTLTISRLEPEDFAVYCCQYGSSTPFGGATKLEIK 107

RESULT 7 STANDARD: PRT: 109 AA.

ID KV3G_HUMAN
 AC P04206:
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (GOL) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE
 RX MEDLINE: 86230578.
 RA NEWKIRK M., CHEN P.P., CARSON D.A., POSNETT D., CAPPA J.D.:
 RL MOL IMMUNOL 23:239-244(1986).
 DP PIR: A01893; K3HUGO
 DR HSSP: P01607; 1DPR
 KW IMMUNOGLOBULIN V REGION
 FT DISULFID 23 89 BY SIMILARITY
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 11840 MW; 893DCC4A CPC32:

Query Match 87.5%; Score 661; DR 5; Length 109;
 Best Local Similarity 88.6%; Pred. No. 4.48e-126;
 Matches 93: Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscraallsgyiaawqkqgqaprllygassratgipdrf 63
 QY 3 LTQSPGTLSLSPGERATLSGASQSVSNYLAWYQKQPGQAPPLLYGVSSPATGIPDRF 62
 Db 64 ssgsgtdftltisrlepedfavyycqygsgrtfggatkveik 108
 QY 63 SSGSGTDFTLTISRLEPEDFAVYCCQYGSSTPFGGATKLEIK 107

RESULT 8

ID KV3K_HUMAN STANDARD: PPT: 128 AA.

AC P06311:
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECIP SOP V-III REGION (IAPC/BL41).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA KLOECK H.G., MEINEL A., COMBIATO G., SOLOMON A., ZACHAU H.G.:
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: 200021, G33179.
 DR PIR: A01899; K3HU04
 DR HSSP: P01607; 3HEM.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IAPC/BL41).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA: 14070 MW; 318E08AF CRC32:

Query Match 81.1%; Score 612; DR 5; Length 128;
 Best Local Similarity 86.7%; Pred. No. 1.74e-114;
 Matches 91: Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Db 24 ltspgtlslspgeratlscrasqvsnylawyqkqgqaprllygassratgipdrf 82
 QY 3 LTQSPGTLSLSPGERATLSGASQSVSNYLAWYQKQPGQAPPLLYGVSSPATGIPDRF 62
 Db 83 ssgsgtdftltisrlepedfavyycqygsgrtfggatkveik 127
 QY 63 SSGSGTDFTLTISRLEPEDFAVYCCQYGSSTPFGGATKLEIK 107

RESULT 9

ID KV3H_HUMAN STANDARD: PPT: 129 AA.

AC P04207:
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECIP SOP V-III REGION (CII) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUTHERIA: PRIMATES
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86177579.
 RA TITIK F.P., SORGE J., PONG S., HEITZMANN J.G., CHUO T.G., CHEN P.P.,
 RA GOLDFIEN R., CARSON D.A.:
 PL PROC. NATL. ACAD. SCI. U.S.A. 84:2195-2199(1986).
 DR EMBL: M12740; G553486;
 DR PIR: A01898; K3HUCL.

Query Match 86.7%; Score 612; DR 5; Length 128;
 Best Local Similarity 86.7%; Pred. No. 1.74e-114;
 Matches 91: Conservative 3; Mismatches 10; Indels 1; Gaps 1;

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RESULT 2
ID KV3M_HUMAN STANDARD: PRT: 129 AA.
AC P18136;
DT 01-NOV-1990 (REL 16, CREATED)
DT 01-NOV-1990 (REL 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
PL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P10021; K3HUB1.
DR HSP: P01607; IDPB.
KW IMMUNOGLOBULIN V REGION; SIGNAL
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 119 129 JK1 SEGMENT
FT DISULFID 43 109 BY SIMILARITY
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; DD00C369 CRC32;

Query Match 91.7%; Score 592; DB 5; Length 129;
Best Local Similarity 91.3%; Pred. No. 1.96e-133;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 24 ltspgtlslspgeratlscrasqsvssnylawyqgkpgqaprllygssratgipdrf 83
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVFNSNYLAWYQKPKQAPRLLYGVSSPATGIPDRF 62
|||||

Db 84 sqsqsqtdftltisrlpepddfavyyccqygsspwtfqgskveik 128
|||||
QY 63 SGSSGSDTFTLTISRLPEPDDFAVYYCQYGVSSPRTFGQTKLEIK 107
|||||

RESULT 3
ID KV3B_HUMAN STANDARD: PRT: 109 AA.
AC P01620;
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598
RA ANDREWS D.W., CAPPA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981)
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUS1
DR HSP: P01607; IDPB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 00B5DD5D CRC32;

Query Match 91.4%; Score 690; DB 5; Length 109;
Best Local Similarity 92.4%; Pred. No. 4.65e-131;

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Best Local Similarity 91.4%; Pred. No. 5.84e-133;
Matches 96; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltspgtlslspgeratlscrasqsvssnylawyqgkpgqaprllygssratgipdrf 63
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVFNSNYLAWYQKPKQAPRLLYGVSSPATGIPDRF 62
|||||

Db 64 sqsqsqtdftltisrlpepddfavyyccqygsspwtfqgskveik 108
|||||
QY 63 SGSSGSDTFTLTISRLPEPDDFAVYYCQYGVSSPRTFGQTKLEIK 107
|||||

RESULT 4
ID KV3A_HUMAN STANDARD: PRT: 108 AA.
AC P01619;
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (B6)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 2-301-304(1969).
RA MILSTEIN C.;
PL FEBS LETT. 2-301-304(1969).
CC -1- THIS IS A BENICE-JONES PROTEIN.
DR PIR: A01891; K3HUB6.
DR HSP: P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 46D6B68E CRC32;

Query Match 90.7%; Score 685; DB 5; Length 108;
Best Local Similarity 88.8%; Pred. No. 9.01e-132;
Matches 93; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

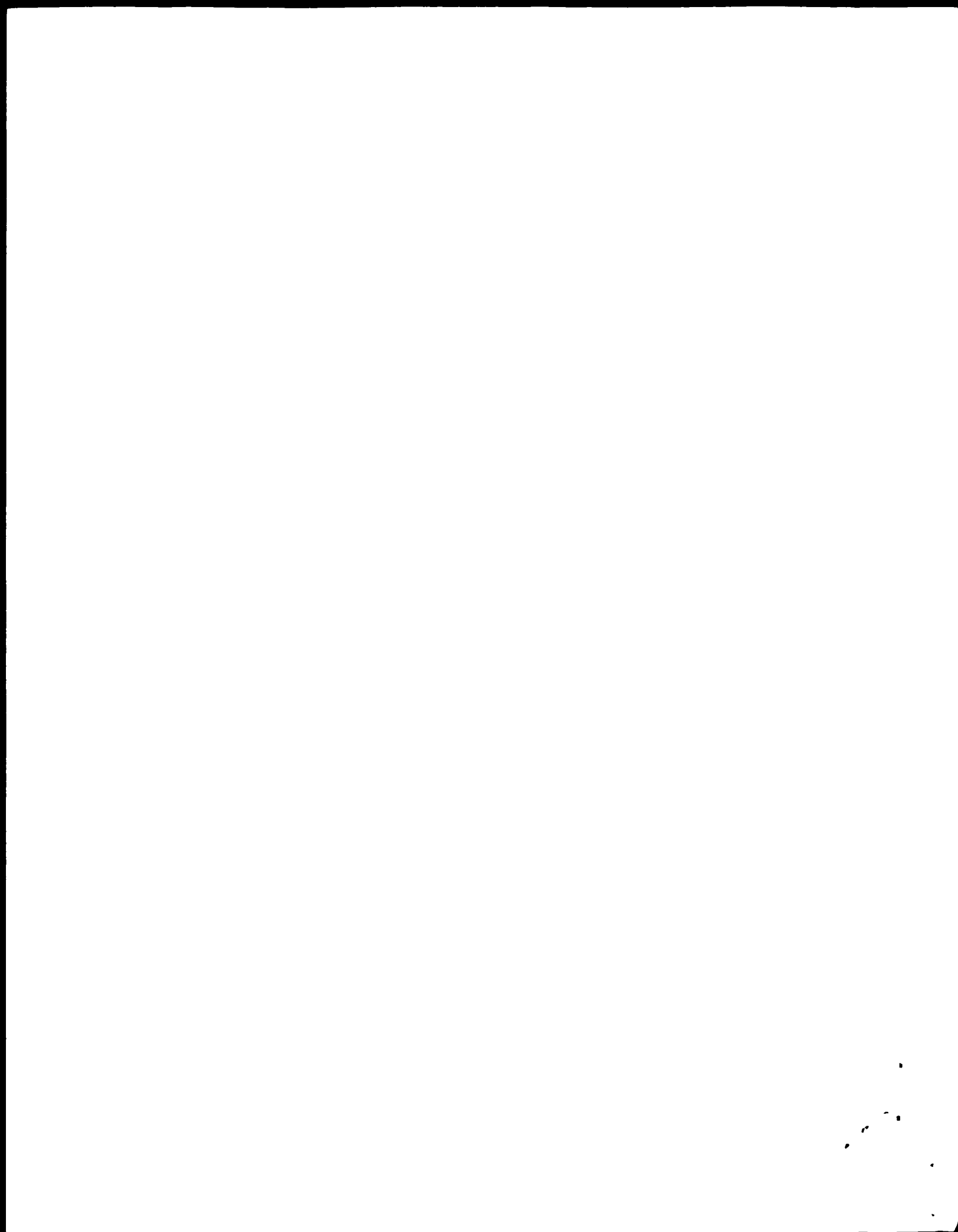
Db 4 ltspgtlslspgeratlscrasqsvssnylawyqgkpgqaprllygssratgipdrf 63
|||||
QY 3 LTQSPGTLSPGERATLSGASQSVFNSNYLAWYQKPKQAPRLLYGVSSPATGIPDRF 62
|||||

Db 64 sqsqsqtdftltisrlpepddfavyyccqygsspwtfqgskveik 108
|||||
QY 63 SGSSGSDTFTLTISRLPEPDDFAVYYCQYGVSSPRTFGQTKLEIK 107
|||||

RESULT 5
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01623;
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598
RA ANDREWS D.W., CAPPA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981)
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01896; K3HUBL.
DR HSP: P01607; IDPB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 7D8F5D75 CRC32;

Query Match 90.3%; Score 682; DB 5; Length 109;
Best Local Similarity 92.4%; Pred. No. 4.65e-131;

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PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB: Q11879
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 4; Fig 16; 104pp; English.
CC This sequence is derived from the nucleotide sequence encoding the
CC light chain variable region. The "x" residues represent nonsense
CC codons. The coding sequence has been translated in all 3 reading
CC frames (see also P13130 and P13131). The L'V region is duplicated
CC in so-called "aberrant" light chains (see Q11878), conferring
CC increased avidity on antibodies comprising such aberrant chains.
CC See also Q11880.
SQ Sequence 401 AA:

Query Match 79.0%; Score 589; DB 2; Length 401;
Best Local Similarity 79.2%; Pred. No. 2.27e-32;
Matches 84; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Db 230 ltqspatlsppgeratlsccrassgsy:lawyggkpgqgprplydasnratgiparfs 289
QY 3 LTQSPATLSVSPGERASLSCFASQSVGNLAWYQKPKQAPPLLIYGGNTPATGIPDPFS 62

Db 290 gsgsgtdftltisslepedfavyvqcdrndwppgatfgggtkveik 335
QY 63 GSGSGTEFTLTISLSQSEDFAVYFCQHYSTWP--LTFGGGTKVEFK 106

RESULT 15
ID R13111 standard; Protein: 414 AA.
AC R13111;
DT 10-MAR-1993 (revised)
DE 01-AUG-1991 (first entry)
DE 1B1 IgG aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= leader peptide
FT Region 18..130
FT /label= variable region
FT /note= "L'V 1"
FT Region 131..243
FT /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
PN W09106305-A
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR N-PSDB: Q11878.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 5; Fig 16; 104pp; English.
CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
CC the amino acid sequence beyond the first stop codon ("x" in the
CC sequence represents a nonsense codon). The clone is incomplete,
CC starting from the G of the ATG initiator codon, but the initial Met
CC is given. Antibody molecules of the invention can include one or two
CC aberrant light chains containing a duplicated variable region, to
CC produce heavier antibodies. These heavier antibodies were found to
CC have higher avidity than antibodies with just a single copy of the
CC L'V region. The antibodies can be used to treat disease, e.g.
CC infection by Streptococcus agalactiae. They are able to pass across

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CC the placenta.
CC See also Q11879 and Q11880.
SQ Sequence 414 AA;

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Query Match 79.0%; Score 590; DB 2; Length 414;
Best Local Similarity 79.2%; Pred. No. 2.27e-32;
Matches 84; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Db 24 ltqspatlsppgeratlsccrassgsy:lawyggkpgqgprplydasnratgiparfs 83
QY 3 LTQSPATLSVSPGERASLSCFASQSVGNLAWYQKPKQAPPLLIYGGNTPATGIPDPFS 52

Db 84 gsgsgtdftltisslepedfavyvqcdrndwppgatfgggtkveik 129
QY 63 GSGSGTEFTLTISLSQSEDFAVYFCQHYSTWP--LTFGGGTKVEFK 106

Search completed: Tue Feb 24 07:24:52 1998
Job time : 38 secs.

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AC	R12128	standard; Protein: 349 AA.
AC	R12128	
DE	01-AUG-1991	(first entry)
DE	1B1 IgG aberrant light chain with duplicated variable region.	
DE	immunoglobulin G; light chain; variable region; duplication.	
KS	passive immunity; group B streptococci.	
OS	Homo sapiens	
EH	Key	Location/Qualifiers
FT	Peptide	1..17
FT	/label= leader peptide	
FT	Region	18..130
FT	/label= variable region	
FT	/note= "L'V 1"	
FT	Region	131..243
FT	/label= variable region	
FT	/note= "L'V 2"	
FT	Region	244..345
FT	/label= constant region	
PN	FN	WO9106305-A.
PD	16-MAY-1991.	
PD	06-NOV-1990: U06426.	
PP	07-NOV-1989: US-432700.	
PP	(BRIM) BRISTOL-MYERS SQUIB.	
PI	Shutford WM, Harris LJ, Raif HV;	
PI	WPI: 91-163947/22.	
DR	N-P5DB: Q11878.	
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -	
PT	formed by duplicating esp. variable region of light chain of IgG	
PT	class	
PS	Example 5: Fig 16; 104pp; English.	
CC	This sequence is deduced from the cDNA clone 4B9-Vk15 and includes	
CC	the amino acid sequence beyond the first stop codon. The clone is	
CC	incomplete, starting from the G of the ATG initiator codon, but the	
CC	initial Met is given. Antibody molecules of the invention can	
CC	include one or two aberrant light chains containing a duplicated	
CC	variable region, to produce heavier antibodies. These heavier	
CC	antibodies were found to have higher avidity than antibodies with	
CC	just a single copy of the L'V region. The antibodies can be used to	
CC	treat disease, e.g. infection by Streptococcus agalactiae. They are	
CC	able to pass across the placenta.	
CC	See also Q11879 and Q11890.	
CC	Sequence 349 AA;	
CC	Sequence 349 AA;	

```

Query Match      79.0%:   Score 589:   DB 2: Length 345:
Best Local Similarity 79.2%:   Pred. No. 2,27e-32:
Matches      84: Conservative 10: Mismatches 10: Indels 2: Gaps
      24  ltsqspatlsrgeratiscragssvslawvqqqpgqgqaprllydaenratqicparfs 84
      QY      3  LTQSPATLVSVPGERASLSCASQSVNNLAWYLTNPGQAPPELLLYGSGNIPATIGTPGRFS 62
      Db      84  gsgsgdfcltisslepedfavyvcyqrdnwpbgatffggatkveik 129
      QY      63  GSGSGTEFTLTITSSLSQSEDFAVYFCQHYSTWP--LIFGSGIKVEFK 106

RESULT 14
ID R12129 standard: Protein: 401 AA.

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AC	DT	Location/Qualifiers
R12129;	01-AUG-1991	(first entry)
DE	Qp f	light chain variable region clone.
KE	Immunoglobulin G	light chain; variable region; duplication.
KW	passive immunity; group B streptococci.	
OS	homo sapiens.	
FS	key	
FH	key	
FT	Peptide	
FT	/label=	L'V region
FT	/note=	"last 3 amino acids of leader and variable region"
FT	region"	
PN	W09106305-A.	
PD	16-MAY-1991.	
PF	06-NOV-1990:	U06426.

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FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR1
FT Region 97..108
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996; U08743.
PF 11-JUL-1995; US-276852.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection
PS Example; Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein: gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, b6. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The Mab
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 108 AA;

Query Match 79.2%; Score 591; DB 19; Length 108;
Best Local Similarity 74.5%; Pred. No. 1.64e-32;
Matches 79; Conservative 19; Mismatches 7; Indels 1; Gaps 1;

Dd 1 elctqpgtislsgperatiscragqssissnylawyqgkpgqaprllyggsnratgipdr 60
QY 2 ELTQSPATISVSPSPASLSQSPASQSVGN-IAWYQKPGQAPRLLYGGSNTRATGPD 60
Dd 61 fsgsgsgtdftlslsrlpepfavvyccgqgtspytfqggtgldik 106
QY 61 FSGSGSGTEFTLTLSLSLQSEDFAVYFCQHYSTWPLTFGSGTKVEFK 106

RESULT 11
ID W01266 standard; protein; 107 AA.
AC W01266;
DE 28-JAN-1997 (first entry)
DE VL region of HIV neutralising Mab, clone B30.
KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..107
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 used in
PT passive immunotherapy and detection of HIV infection.
PS Example; Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clone, b6. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The Mab
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

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QY 2 ELTQSPATLSVSGERASUSCRASQSVNN-LAWYTKPSQAPRLIYGSNTRFATSIPTP 60
 Db 61 fsgsgstgtltisrlepddfavyscqgqygtspwtfgggtkveik 106
 QY 61 FSGSGGTETLTIISSQSEDFAVYFCQHYSTWPLTFGGGKVEPK 106

RESULT 7
 ID R54307 standard; protein: 108 AA.
 AC R54307;
 DI 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain: variable region: b24.
 KW Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope:
 neutralisation: monoclonal antibody; kappa light chain;
 KW variable region: framework; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; 008743.
 PR 18-JUL-1994; US-276852.
 PA (SCPI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 passive immunotherapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JKL
 CC gene clone, b24. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp150. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 79.58; Score 593; DB 10; Length 108;
 Best Local Similarity 80.2%; Pred. No. 1,18e-32;
 Matches 95; Conservative 11; Mismatches 9; Indels 1; Gaps 1;
 Db 1 eltgspgtlslpgeratlsrscasqsvsnlylawyqkqgqaprllygvsnratgipdr 60
 QY 2 ELTQSPATLSVSGERASUSCRASQSV-GNNLAWYTKPSQAPRLIYGSNTRFATSIPTP 60
 Db 61 fsgsgstgtltisrlepddfavyscqgqygtspwtfgggtkveik 106
 QY 61 FSGSGGTETLTIISSQSEDFAVYFCQHYSTWPLTFGGGKVEPK 106
 RESULT 8
 ID W01265 standard; protein: 108 AA.
 AC W01265;
 DI 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b24.
 KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
 KW anti-HIV antibody; precursor gp160; immunocompetence; human;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2

KW MAB, HIV, human immunodeficiency virus, glycoprotein, gp120, clone:
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; 008743.
 PR 18-JUL-1994; US-276852.
 PA (SCPI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 passive immunotherapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JKL
 CC gene clone, b24. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp150. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 79.58; Score 593; DB 10; Length 108;
 Best Local Similarity 80.2%; Pred. No. 1,18e-32;
 Matches 95; Conservative 11; Mismatches 9; Indels 1; Gaps 1;
 Db 1 eltgspgtlslpgeratlsrscasqsvsnlylawyqkqgqaprllygvsnratgipdr 60
 QY 2 ELTQSPATLSVSGERASUSCRASQSV-GNNLAWYTKPSQAPRLIYGSNTRFATSIPTP 60
 Db 61 fsgsgstgtltisrlepddfavyscqgqygtspwtfgggtkveik 106
 QY 61 FSGSGGTETLTIISSQSEDFAVYFCQHYSTWPLTFGGGKVEPK 106

RESULT 9
 ID W01278 standard; protein: 108 AA.
 AC W01278;
 DI 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone b6.
 KW Heavy chain; light chain; variable region; VH: monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone:
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2

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FT Misc_difference 116
FT /note= "pro encoded by GTT (sic)"
PN W09312232-A.
PD 24-JUN-1993.
PF 10-DEC-1992; U19228
PR 10-DEC-1991; US-804652.
PA (DAND ) DANA FARBER CANCER INST INC
PA (NEWSE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
DR WPI: 93-214174/26
DR N-PSDB: Q42706.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
PS Disclosure: Page 74-75; 109pp; English.
CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
CC other F105 VK sequences given elsewhere in the specification) was
CC compared with germline gene Humv325 (Q42706), showing 97.7%
CC similarity. By nucleotide sequence analysis, F105 appears to
CC be derived from a member of the VK III subgroup gene family.
SQ Sequence 129 AA;

      Query Match      79.9%; Score 596; DB 7; Length 129;
      Best Local Similarity 77.1%; Pred. No. 7.25e-33;
      Matches 81; Conservative 18; Mismatches 5; Indels 1; Gaps 1;

Db 24 lqtsgptlslsppgeratlsctasqssvslawyyqgkpgqaprllygassratgipdrf 83
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 sgsgsgtdftltisrlepedfavyycqygsgspvtfgggtkleik 128
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 SGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106

      Query Match      79.9%; Score 596; DB 7; Length 129;
      Best Local Similarity 77.1%; Pred. No. 7.25e-33;
      Matches 81; Conservative 18; Mismatches 5; Indels 1; Gaps 1;

ID R54311 standard; protein: 107 AA.
AC R54311.
AT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT /label= FR1
FT /label= CDR1
FT /label= CDR1
FT /label= FR2
FT /label= FR2
FT /label= CDR2
FT /label= CDR2
FT /label= FR3
FT /label= FR3
FT /label= CDR3
FT /label= CDR3
FT /label= FR4
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-275852.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DP, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example; Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the F12
CC gene clone, B20. A MAB containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ug of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

      Query Match      79.5%; Score 593; DB 19; Length 107;
      Best Local Similarity 77.4%; Pred. No. 1.18e-32;
      Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 eltgspgtlslsppgeratlsctasqssvslawyyqgkpgqaprllygassratgipdr 60
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 fsgsgsgtdftltisrlepedfavyycqygsgspvtfgggtkleik 106
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106

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CC dicistronic vector to produce a library of fragments. E coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence #54311 is from a gp120-
CC specific clone.
SQ Sequence 107 AA;

      Query Match      79.5%; Score 593; DB 10; Length 107;
      Best Local Similarity 77.4%; Pred. No. 1.18e-32;
      Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 eltgspgtlslsppgeratlsctasqssvslawyyqgkpgqaprllygassratgipdr 60
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 2 ELTGSPATLSVSPGERATLSCTASQSSVSN-LAWYQKPGQAPRLIYGGNTRATGTPDR 60
Db 61 fsgsgsgtdftltisrlepedfavyycqygsgspvtfgggtkleik 106
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 FSGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106

      RESULT 6
      ID W01269 standard; Protein; 107 AA.
      AC W01269.
      DT 28-JAN-1997 (first entry)
      DE VL region of HIV neutralising MAB, clone B20.
      KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
      KW MAB; HIV, human immunodeficiency virus; glycoprotein gp120; clone;
      KW virus infectivity assay; precursor gp160; immunocompetence; human;
      KW anti-HIV antibody; detection; HIV infection.
      OS Homo sapiens.
      FH Key Location/Qualifiers
      FT Region 1..21
      FT /label= FR1
      FT /label= FR1
      FT /label= CDR1
      FT /label= CDR1
      FT /label= FR2
      FT /label= FR2
      FT /label= CDR2
      FT /label= CDR2
      FT /label= FR3
      FT /label= FR3
      FT /label= CDR3
      FT /label= CDR3
      FT /label= FR4
      FT /label= FR4
      PN W09602273-A1.
      PD 01-FEB-1996.
      PF 11-JUL-1995; U08743.
      PR 18-JUL-1994; US-275852.
      PA (SCRI ) SCRIPPS RES INST.
      PI Barbas CF, Burton DP, Lerner RA;
      DR WPI: 96-179601/18.
      PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
      PT passive immuno-therapy and detection of HIV infection.
      PS Example; Fig 11; 366pp; English.
      CC The sequences given in W01261-92 represent the light chain variable
      CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
      CC immunoreactive with HIV glycoprotein gp120 and are capable of
      CC neutralising HIV. This sequence represents the sequence of the F12
      CC gene clone, B20. A MAB containing this VL sequence has the capacity
      CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
      CC by 50 % at a concentration of less than 700 ug of antibody/ml, and
      CC binds mature gp120 preferentially over the precursor gp160. The MAB
      CC may be used for determining immunocompetence of a human anti-HIV
      CC antibody and in the detection of HIV infection.
      SQ Sequence 107 AA;

      Query Match      79.5%; Score 593; DB 19; Length 107;
      Best Local Similarity 77.4%; Pred. No. 1.18e-32;
      Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 eltgspgtlslsppgeratlsctasqssvslawyyqgkpgqaprllygassratgipdr 60

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RESULT 2
ID R50218 standard; Protein: 109 AA.
AC F50218;
DT 31-OCT-1994 (first entry)
DE HSV glycoprotein F binding MAB clone rsv23L VH/VL domain.
KW Complementarity determination region; CDR3: human; bronchiolitis;
KW monoclonal antibody; epitope: glycoprotein F; influenza virus;
KW respiratory syncytial virus; RSV; disease: rhinovirus; coronavirus;
KW lung; pneumonia.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FP1
FT Region 24..34
FT /label= CDR1
FT Region 35..49
FT /label= FR2
FT Region 50..56
FT /label= CDR2
FT Region 57..88
FT /label= FR3
FT Region 89..97
FT /label= CDR3
FT Region 98..109
FT /label= FR4
PN W09406448-A.
PD 31-MAR-1994.
PF 15-SEP-1994; U09786.
PR 16-SEP-1992; US-943515.
PA (SCRI) SCRIPPS RES INST.
PA (USHS) US DPT HEALTH & HUMAN SERVICES.
PI Barbas CF, Burton DR, Chanock PM, Crowe JE, Murphy BR.
DP WPI: 94-118147/14.
PT Human neutralising monoclonal antibodies to respiratory syncytial
PT virus - for treatment prophylaxis and diagnosis of RSV and other
PT diseases of the respiratory tract
PS Disclosure: Fig 4; 104pp; English
CC The sequences given in R50215-19 represent the heavy and light chain
CC variable domains of various clones of a human monoclonal antibody
CC which binds to an epitope on glycoprotein F of respiratory syncytial
CC virus (RSV). These antibodies may be used as a reagent for the
CC diagnosis of RSV disease and other viral mucosal diseases, eg.
CC influenza virus, rhinovirus and coronavirus. They are particularly
CC useful in ameliorating RSV when delivered directly to the lungs, and
CC may also be used for treating pneumonia and bronchiolitis.
SQ Sequence 109 AA;

Query Match 81.5%; Score 608; DB 9; Length 109;
Best Local Similarity 75.5%; Pred No 1 03e-33;
Matches 80; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

Db 2 aeltgspvltlsvspgervalsckasqinadnlawygkpgqaprllygassratgipdr 61
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1 AELTUSPAILSVSPGEPASLSQFASQSVGNLAWYQKPGAPPLIYGNTPTATGTPDR 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 62 fsgsgsgtftltlrlepdafvvygcqygsgpytfggqtkleik 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 FSGSGSGTEFTLTISLSLOSEDFAVYFCOHYSTWPLTFGGGKVEFK 106
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 3
ID R38593 standard; peptide: 107 AA.
AC R38593;
DT 28-OCT-1993 (first entry)
DE Human lambda light chain subgroup 3 (hL3).
KW Antibody: variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 96
FT /note= "residue conserved in less than 50% of the
FT /known sequences of hL3."
PN W09311734-A.

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PD 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-R08464.
PA (XOMA) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GM.
DP WPI: 93-213827/26.
PT Antibodies prep. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Claim 2; Page 93-94; 160pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (hL1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -
CC R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
CC hH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA;

Query Match 80.2%; Score 508; DB 7; Length 107;
Best Local Similarity 76.9%; Pred. No. 5.24e-33;
Matches 80; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Db 4 ltgspgtlslspgeratlscrasqsvsylvawygkpgqaprllygassratgipdrfs 64
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 3 LTQSPATLSVSPGEPASLSQFASQSVGNLAWYQKPGAPPLIYGNTPTATGTPDRFS 62
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 64 gsgsgtftltlrlepdgfvvygcqygsgspxtfggqtdveik 107
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RESULT 4
ID R38672 standard; Protein: 129 AA.
AC R38672;
DT 01-NOV-1993 (first entry)
DE Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;
KW CDR4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Protein 21..129
FT /label= mat_protein
FT Region 1..116
FT /label= vk325
FT Region 117..129
FT /label= Jk2
FT Region 44..55
FT /label= CDR1
FT Region 71..77
FT /label= CDR2
FT Region 110..117
FT /label= CDR3
FT Misc_difference 1
FT /note= "Met encoded by ATC (sic)"
FT Misc_difference 35
FT /note= "Pro encoded by GCA (sic)"
FT Misc_difference 99
FT /note= "Leu encoded by GTG (sic)"
FT Misc_difference 113
FT /note= "Gly encoded by GAT (sic)"
FT Misc_difference 114
FT /note= "Ser encoded by AAC (sic)"

```

[W][O][R][D][S]

(TM)

Release 2 ID John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution Rights by IntelliGenetics, Inc.
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07 24 14 1998, Maspar time 6.61 Seconds
Tabular output not generated.
222,822 Million cell updates/sec
Title: >US-08-844-215-11
Description: (1-106) from US08844215 pep
Perfect Score: 746
Sequence: 1 AELTQSPATLSVSPGPRASL
Scoring table: PAM 150
Gap 11
CQHYSTWPLTFCGGTKVEFK 106

Searched: 111726 seqs, 13880129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 29.550; Variance 174.430; scale 0.169
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	635	85.1	234	9	R52951 Human anti-IgE MAb 11
2	608	81.5	109	9	R50218 HSV glycoprotein F bi
3	598	80.2	107	7	R38593 Human lambda light ch
4	596	79.9	129	7	vk325-JK2
5	593	79.5	107	10	P54311 Anti-HIV gp120 immuno
6	593	79.5	107	10	W01269 VL region of HIV neut
7	593	79.5	108	10	P54307 Anti-HIV gp120 immuno
8	593	79.5	108	19	W01265 VL region of HIV neut
9	591	79.2	108	19	W01278 VL region of HIV neut
10	591	79.2	108	9	R54316 Anti-HIV gp120 immuno
11	590	79.1	107	19	W01266 VL region of HIV neut
12	590	79.1	107	10	P54308 Anti-HIV gp120 immuno
13	589	79.0	349	2	P12128 IBI IgS aberrant high
14	589	79.0	401	2	P12129 Off 1 of IgG light ch
15	589	79.0	414	2	P13111 IBI IgS aberrant high
16	589	79.0	414	2	P13018 IBI IgS aberrant high
17	586	78.6	109	9	R50217 HSV glycoprotein F bi
18	581	77.9	111	10	R54277 Anti-HIV gp41 immunoq
19	581	77.9	111	19	W01322 VL of Fab, GL 41 1, b
20	580	77.7	109	19	W01320 VL of Fab, DL 41 19,

21	590	77.7	109	10	P54275 Anti-HIV gp41 immunoq
22	579	77.6	215	19	W07616 Ulcerative colitis-as
23	578	77.5	107	22	W08949 Kappa light chain var
24	576	77.2	127	22	W08946 Kappa light chain var
25	572	76.7	104	9	R54317 Anti-HIV gp120 immuno
26	572	76.7	104	19	W01279 VL region of HIV neut
27	572	76.7	107	7	P37612 HIV-1 Ab 1 chain V re
28	572	76.7	112	10	R54279 Anti-HIV gp41 immunoq
29	572	76.7	112	19	W01324 VL of Fab, SS 41 8, b
30	570	76.4	107	5	R57729 Humanised VL region o
31	570	76.4	107	22	W08948 Kappa light chain var
32	565	75.7	109	10	R56286 Light chain of Ab 31
33	564	75.6	124	22	W45399 Immunoglobulin F101-2
34	563	75.5	108	19	W01267 VL region of HIV neut
35	562	75.3	112	2	P81245 Anti-pseudomonas aeru
36	562	75.3	128	1	P91001 Anti-F. aeruginosa st
37	561	75.2	127	9	R50191 Light chain variable
38	560	75.1	129	7	P38673 F105VK-F105VK
39	560	75.1	129	7	R41286 F105 rearranged varia
40	557	74.7	214	19	W07615 Ulcerative colitis-as
41	555	74.4	127	9	R50187 Light chain variable
42	555	74.4	127	9	R50192 Light chain variable
43	554	74.3	134	20	W11155 Anti-lung tumour anti
44	551	73.9	108	19	W01289 VL region of HIV neut
45	551	73.9	108	23	W10895 CEA-specific antibody

ALIGNMENTS

RESULT 1
ID R52951 standard; Protein; 234 AA.
AC R52951.
DT 27-OCT-1994 (first entry)
DE Human anti-IgE MAB light chain.
KW Human IgE; CH4 region; triggers mediator release;
KW Mast cells; Monoclonal antibody; allergy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 21..128
FT /label= light chain variable region
FN EF-592230-A.
PD 13-APR-1994.
PF 07-OCT-1993; 308006.
PR 07-OCT-1992; JP-293800.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI Yoshida T;
DR WPI: 94-120330/15.
DR N-PSDB: Q71872.
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine
PT release from mast cells by allergen stimulation, useful for
PT preventing allergies
PS Claim 3; Page 12; 21pp; English.
CC R52951 shows the light chain of a human type anti-IgE peptide
CC monoclonal antibody which inhibits the signal transmission for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
SQ Sequence 234 AA:

Query Match 85.1%, Score 635, DB 9, Length 234.
Best Local Similarity 81.7%; Pred. No. 1,26e-35;
Matches 85; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

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CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA; 11956 MW; 63169 CN;

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Matches 81; Conservative 17; Mismatches 7; Indels 2; Gaps 2;

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QY 1 AELTSPAILLSVSGERASLSQASVSNN-LAWYQKPGQAPRLIYGGNTRATGTPD 59
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Db 62 RFGSGSGADFTLAISRLEPEDFAVYCCQYAG-SHTFCQGTKEIK 107
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QY 60 RFGSGSGTEFTLIISLSQSEDFAVYFCQRYSTWPLIFGGTKVEFK 106
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 Job time : 14 secs.

CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/474,040
 CC FILING DATE: 07-JUN-1995
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 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
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RESULT 14
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 DT 01-JAN-1900
 XX
 DE Sequence 86, Application US/08487200.
 CC
 CC Patent No. 5693762
 CC
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO, Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELINGH, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew
 CC STREET: 179 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
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 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/487,200
 CC FILING DATE: 7-JUN-1995
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 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002610
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
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 CC MOLECULE TYPE: peptide
 CC SEQUENCE 108 AA: 11590 MW: 64079 CN;
 Query Match 78.3%; Score 584; DB 7; Length 108;
 Best Local Similarity 76.2%; Pred. No. 1.43e-35;
 Matches 80; Conservative 17; Mismatches 7; Indels 1; Gaps 1;
 Db 4 LTQSPGTLSPGERATLSCHASQSVSSYLSGWYQQKPGQAPRLIYGSASRATGIDRF 63
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 DT 01-JAN-1900
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 DE Sequence 149, Application PCT/US9508743.
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 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
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CC SOFTWARE: Patent In Release #1.0, Version #1.25
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CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
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CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
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CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
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CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
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CC STRANDEDNESS: single
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Best Local Similarity 76.2% Pred No 1.43e-15:
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Db 64 SGSSGTDFTLITSLRLEPFAVYQYQYVSSLSPIFGGQTKVEIK 108
Qy 52 SGSSGTEFTLITSSLSQSEDFAVYFCQHYSTWELIFGGGQTKVEFK 106
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XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/07634278.
XX Sequence 86, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue

CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
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CC COMPUTER: IBM PC compatible
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CC APPLICATION NUMBER: US 07/590,274
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CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:
SQ
Query Match 78.3% Score 584: DB 6: Length 108:
Best Local Similarity 76.2% Pred. No. 1.43e-35:
Matches 80: Conservative 17: Mismatches 7: Indels 1: Gaps 1:
Db 4 LTSPGTLSPGERATLSCRASQSVSSGYLQWYQKPGQCAPPELLIYGASSPATGIPDRF 64
Qy 3 LTQSPATLSVSPGRASLSRASQSVGN-LAWYQKPGQAPPELLIYGNTGTRATGTPDRF 61
Db 64 SGSSGTDFTLITSLRLEPFAVYQYQYVSSLSPIFGGQTKVEIK 108
Qy 62 SGSSGTEFTLITSSLSQSEDFAVYFCQHYSTWELIFGGGQTKVEFK 106
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XX DT 01-JAN-1900
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CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew

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CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
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CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
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CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PPIOF APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
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CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE: 107 AA; 11654 MW; 62438 CN;

Query Match 79.1%; Score 590; DB 7; Length 107;
Best Local Similarity 79.3%; Pred. No. 4 97e-36;
Matches 83; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

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QY 2 ELTQSPATISVSPGERASUSCRASVSNNVLAWYQDPGQAPRLIYGASNRATGIPDR 60

Db 61 FSGSGSGTFTLTISLSQSDFAVYFCQHYSTWPLTFGGGTVKVEK 106
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RESULT 10
ID PCT-US93-08786-23 STANDARD: PPT: 109 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 23, Application PC/TUS9308786
XX DE Sequence 23, Application PC/TUS9308786
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis F.
CC APPLICANT: Barbas, III, Carlos F.
CC APPLICANT: Chanock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
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CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1980 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08786
CC FILING DATE: 16-SEP-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wetherell, Jr., Ph.D., John R.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: PD-2791
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 6L; 11L; 21L; and 22L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
CC SEQUENCE: 109 AA; 12099 MW; 62556 CN;

Query Match 78.6%; Score 586; DB 11; Length 109;
Best Local Similarity 73.8%; Pred. No. 1.00e-35;
Matches 79; Conservative 18; Mismatches 9; Indels 1; Gaps 1;

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QY 1 ABLTQSPATISVSPGERASUSCRASVSNNVLAWYQDPGQAPRLIYGASNRATGIPDR 53

Db 62 FPGSGSGTFTLTISLSQSDFAVYFCQHYSTWPLTFGGGTVKVEK 108
QY 60 FPGSGSGTFTLTISLSQSDFAVYFCQHYSTWPLTFGGGTVKVEK 106

RESULT 11
ID US-08-477-728-86 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/08477728.
XX DE Sequence 86, Application US/08477728.
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Gary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
```

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CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178 302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN:

Query Match 79.2%; Score 591; DB 7; Length 108;
Best Local Similarity 74.5%; Pred. No. 4.17e-36;
Matches 79; Conservative 19; Mismatches 7; Indels 1; Gaps 1;

Db 1 ELTQSPGTLSPGERATLSCPASQSVSNLYAWYQKPKQCAPPLLIYGASNPATGIPDP 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 2 ELTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPKQCAPPLLIYGSTNTRATGIPDP 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 61 FSGSGSGTDTLTLISLPEDFAVYVCOQYGTSPYTFGGTGKLEIK 106
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Qy 61 FSGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

RESULT 8
ID PCT-US95-08743-87 STANDARD: PRT; 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 87, Application PC/TUS9508743.
XX
CC Sequence 87, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN:

Query Match 79.1%; Score 590; DB 13; Length 107;
Best Local Similarity 78.3%; Pred. No. 4.97e-36;
Matches 83; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

Db 1 ELTQSPGTLSPGERATLSCPASQSVSNLYAWYQKPKQCAPPLLIYGASNPATGIPDP 60
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Qy 2 ELTQSPATLSVSPGERASLSCPASQSVGN-LAWYQKPKQCAPPLLIYGSTNTRATGIPDP 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 61 FSGSGSGTATLTLSLQPEDVAIYYCOQYHSSPYTFGGTGKLEIK 106
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Qy 61 FSGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
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RESULT 9
ID US-08-276-852-87 STANDARD: PRT; 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 87, Application US/08276852.
XX
CC Sequence 87, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
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XX Sequence 86, Application PC/TUS9508743.
DE Sequence 86, Application PC/TUS9508743.
XX GENERAL INFORMATION:
CC APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11769 MW: 65957 CN;
SQ
Query Match 79.5%; Score 593; DB 13; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.93e-36;
Matches 85; Conservative 11; Mismatches 9; Indels 1; Gaps 1;
Db 1 ELTQSPGTLSPGEPATLSGRASQSVISNYLAWYQQRPGQAPPLLIYGVSNPATIGPDR 60
QY 2 ELTQSPATLSVSGEPASLSGRASQSV-GNNLAWYQQRPGQAPPLLIYGVSNPATIGPDR 60
Db 61 FSGSGSGTDFTLTISRLEPEDFVYSCQOYGTSPWTFGGTKVEIK 106
QY 61 FSGSGSGTEFTLTISLQSEDFVYFCQHYSTWPLTFGGTKVEEK 106
RESULT 5
ID US-08-276-852-86 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 86, Application US/08276852.
XX CC Sequence 86, Application US/08276852.
XX CC Patent No. 5652138
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis R
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Lerner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
XX CC STREET: Mail Drop TPC8
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC OPERATING SYSTEM: IBM PC compatible
XX CC SOFTWARE: Patent in Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/276,852
XX CC FILING DATE: 18-JUL-1994

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11769 MW: 65957 CN;
SQ
Query Match 79.5%; Score 593; DB 7; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.93e-36;
Matches 85; Conservative 11; Mismatches 9; Indels 1; Gaps 1;
Db 1 ELTQSPGTLSPGEPATLSGRASQSVISNYLAWYQQRPGQAPPLLIYGVSNPATIGPDR 60
QY 2 ELTQSPATLSVSGEPASLSGRASQSV-GNNLAWYQQRPGQAPPLLIYGVSNPATIGPDR 60
Db 61 FSGSGSGTDFTLTISRLEPEDFVYSCQOYGTSPWTFGGTKVEIK 106
QY 61 FSGSGSGTEFTLTISLQSEDFVYFCQHYSTWPLTFGGTKVEEK 106
RESULT 6
ID US-08-276-852-99 STANDARD: PRT: 108 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 99, Application US/08276852.
XX CC Sequence 99, Application US/08276852.
XX CC Patent No. 5652138
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis R
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Lerner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
XX CC STREET: Mail Drop TPC8
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC OPERATING SYSTEM: IBM PC compatible
XX CC SOFTWARE: Patent in Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/276,852
XX CC FILING DATE: 18-JUL-1994

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 23L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
CC SEQUENCE 109 AA: 11958 MW: 64524 CN:

Query Match 81.5% Score 608; DB 11; Length 109;
Best Local Similarity 75.5% Pred No 2 0ae-37;
Matches 80; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

Db 2 AELTQSPVTLSPGEPVALSCRASQSNINNLAWYQKPGQAPPLLIYGASSPATGIDPR 61
QY 1 AELTQSPATLSVSGEPASLSCRASQSVGNNAWYQKPGQAPPLIYGGNTRATGTDP 60
Db 62 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 107
QY 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 106

RESULT 2
ID US-08-276-R52-90 STANDARD: PPT: 107 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 90, Application US/08276852.
XX CC Patent No. 5652138
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis P
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Lerner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10666 Nc 5652138th Torrey Pines Road, Suite 220.
XX CC STREET: Mail Drop 1068
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent In Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC CLASSIFICATION: 514
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/178,302
XX CC FILING DATE: 30-SEP-1993
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/954,148
XX CC FILING DATE: 30-SEP-1992
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Fitting, Thomas
XX CC REGISTRATION NUMBER: 34,163
XX CC REFERENCE/DOCKET NUMBER: SCF1452P
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 619-554-2937
XX CC TELEFAX: 619-554-6312
XX CC INFORMATION FOR SEQ ID NO: 90:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CLONE: rsv 23L
CC NAME/KEY: Peptide
CC LOCATION: 1..109
CC SEQUENCE 107 AA: 11705 MW: 62938 CN:

Query Match 79.5% Score 593; DB 7; Length 107;
Best Local Similarity 77.4% Pred No 2.93e-36;
Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 ELTQSPCTLSLSPGERATLSGRASQSLNNYLAWYQKPGQAPPLLIYGSSSTPGTGIDPR 60
QY 2 ELTQSPATLSVSGEPASLSCRASQSVGNNAWYQKPGQAPPLIYGGNTRATGTDP 60
Db 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 106
QY 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 106

RESULT 3
ID PCT-US95-08743-90 STANDARD: PPT: 107 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 90, Application PC/TUS9508743.
XX CC Sequence 90, Application PC/TUS9508743
XX CC GENERAL INFORMATION:
XX CC APPLICANT:
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US95/08743
XX CC FILING DATE: 11-JUL-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 09/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC INFORMATION FOR SEQ ID NO: 90:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA: 11705 MW: 62938 CN:

Query Match 79.5% Score 593; DB 13; Length 107;
Best Local Similarity 77.4% Pred No 2.93e-36;
Matches 82; Conservative 16; Mismatches 7; Indels 1; Gaps 1;

Db 1 ELTQSPCTLSLSPGERATLSGRASQSLNNYLAWYQKPGQAPPLLIYGSSSTPGTGIDPR 60
QY 2 ELTQSPATLSVSGEPASLSCRASQSVGNNAWYQKPGQAPPLIYGGNTRATGTDP 60
Db 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 106
QY 61 FSGSGSGTDTLTITRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 106

RESULT 4
ID PCT-US95-08743-86 STANDARD: PPT: 108 AA
XX AC xxxxxx
XX DT 01-JAN-1900
```

[W][O][R][D] (TM)

Release 2 1D John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:50:48 1998: MasPar time 2.95 Seconds
Tabular output not generated.
183.108 Million cell updates/sec

Title: >US-08-844-215-11
Description: (1-106) from US08844215.pep
Perfect Score: 746
Sequence: 1 AELTQSPATLSVSPGPRSL COHYSTWPLTGGTKVEFK 106

Scoring table: GAP 150
GAP 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1-back1 2:51 3:53 4:53 5:54 6:55 7:56 8:56 9:56 10:56
10-PCR92 11-PCR93 12-PCR94 13-PCR95 14-PCR96
Statistics: Mean 27.204: Variance 140.039: scale 0.183
Pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No	Score	Query Match	Length	ID	Description	Pred No	
1	608	81.5	109	11	Sequence 24, Applicati	2,09e-37	
2	593	79.5	107	7	Sequence 90, Applicati	2,93e-36	
3	593	79.5	107	13	Sequence 90, Applicati	2,93e-36	
4	593	79.5	108	13	Sequence 86, Applicati	2,93e-36	
5	593	79.5	108	7	Sequence 86, Applicati	2,93e-36	
6	591	79.2	108	7	Sequence 99, Applicati	4,17e-36	
7	591	79.2	108	13	Sequence 99, Applicati	4,17e-36	
8	590	79.1	107	13	Sequence 87, Applicati	4,97e-36	
9	590	79.1	107	7	Sequence 87, Applicati	4,97e-36	
10	586	78.6	109	11	Sequence 23, Applicati	1,00e-35	
11	584	78.3	108	6	Sequence 86, Applicati	1,43e-35	
12	584	78.3	108	7	Sequence 86, Applicati	1,43e-35	
13	584	78.3	108	7	Sequence 86, Applicati	1,43e-35	
14	584	78.3	108	7	Sequence 86, Applicati	1,43e-35	
15	581	77.9	111	13	Sequence 149, Applicati	2,42e-35	
16	581	77.9	111	7	Sequence 149, Applicati	2,42e-35	
17	580	77.7	109	7	Sequence 147, Applicati	2,88e-35	
18	580	77.7	109	13	Sequence 147, Applicati	2,88e-35	
19	572	76.7	104	7	Sequence 100, Applicati	1,18e-34	
20	572	76.7	104	13	Sequence 100, Applicati	1,18e-34	
21	572	76.7	112	7	Sequence 151, Applicati	1,18e-34	
22	572	76.7	112	13	Sequence 151, Applicati	1,18e-34	



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Db 3 qmcspslsvsgdrvtitcdsqnvnaylnwygdkpqlapklllygnastreaqvsprf 62
QY 2 ELTQSPATLSVSPGERASLSQASQSVGNLAWYQKQPGAPPLLYGNTPATGTGPORF 61

Db 63 sgsqsgtdftlsslpqediayycqynnpptfggqtkvevk 107
QY 62 SSGSGTEFTLTSSLSQSEDFAVYFCQHYSTWPLTFGGGKVEEK 106

RESULT 13
ID KV3C_HUMAN STANDARD: PPT: 100 AA.
AC P01621.
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (NG9) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VEPTERRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; PRIMATES
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 84093600.
PA RENTLEY D.L.
RC NATURE 307:77-80(1984).
CC -1- THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
PIR; A01894; K3HUNG.
DR HSP; P01607; IMGP.
KW IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA.
FT SIGNAL 1 4
FT CHAIN <1 1 IG KAPPA CHAIN V-III REGION (NG9).
FT DISULFID 27 93 BY SIMILARITY
FT NON_TER 100 100
SQ SEQUENCE 100 AA: 10729 MW. 99475222 CPO32.

Query Match 71.2%; Score 531; DB 5; Length 100;
Best Local Similarity 78.9%; Pred No 2 04e-97;
Matches 71; Conservative 15; Mismatches 3; Indels 1; Gaps 1;

Db 8 ltsqpslslsperatlscrasqsvssylwygdkpqpgrlllygststratgipdrf 67
QY 3 LTQSPATLSVSPGERASLSQASQSVGNLAWYQKQPGAPPLLYGNTPATGTGPORF 61

Db 68 sgsqsgtdftlslrlepafayycqayg 97
QY 62 SSGSGTEFTLTSSLSQSEDFAVYFCQHY 91

RESULT 14
ID KVIY_HUMAN STANDARD: PPT: 108 AA
AC P80362;
DT 01-NOV-1995 (REL 32, CREATED)
DT 01-NOV-1995 (REL 32, LAST SEQUENCE UPDATE)
DE 01-NOV-1995 (REL 32, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (WAT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VEPTERRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; PRIMATES
[1]
RN SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1 9 ANGSTROMS).
RX MEDLINE; 95085080.
PA HIANG D.-R., CHANG C.-H., AINSWORTH C., BPUENGER A T., EULITZ M.,
PA SOLOMON A., STEVENS F J, SCHIFFER M;
RL BIOCHEMISTRY 33:14848-14857(1994).
RN [2]
PP SEQUENCE OF 1-35
FX MEDLINE; 81267384.
PA STEVENS F J, WESTHOLM F A, PANAGIOTOPoulos N., SCHIFFER M.,
PA POPP R.A., SOLOMON A.;
FL J MOL BIOL 147:185-193(1991)
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.

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FT DOMAIN 1 23 FRAMEWORK 1
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 IN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11737 MW. 41A2388C CPO32;

Query Match 70.5%; Score 526; DB 5; Length 108;
Best Local Similarity 62.9%; Pred No 3 14e-96;
Matches 66; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

Db 3 qmcspslsvsgdrvtitcdsqnvnaylnwygdkpqlapklllygnastreaqvsprf 62
QY 2 ELTQSPATLSVSPGERASLSQASQSVGNLAWYQKQPGAPPLLYGNTPATGTGPORF 61

Db 63 sgsqsgtdftlsslpqediayycqydtlpltfgggkvdik 107
QY 62 SSGSGTEFTLTSSLSQSEDFAVYFCQHYSTWPLTFGGGKVEEK 106

RESULT 15
ID KV3J_HUMAN STANDARD: PPT: 116 AA.
AC P04434;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VEPTERRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N A
RX MEDLINE; 85087932.
PA RECH M., ZACHAU H G;
FI NUCLEIC ACIDS RES 12:9229-9236(1984)
DR EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR PIR; A01901; K3HUVH.
DR HSP; P01607; IMGP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA: 12757 MW. 27FA1BCE CPO32;

Query Match 69.0%; Score 515; DB 5; Length 116;
Best Local Similarity 78.4%; Pred No 1 27e-93;
Matches 69; Conservative 15; Mismatches 3; Indels 1; Gaps 1;

Db 24 mtdspstlsdpervtlscrasqsvssyltwyqdkpqpgrlllygststratgipdrf 83
QY 3 LTQSPATLSVSPGERASLSQASQSVGNLAWYQKQPGAPPLLYGNTPATGTGPORF 61

Db 84 sgsqsgtdftlsslpqediayycqy 111
QY 62 SSGSGTEFTLTSSLSQSEDFAVYFCQHY 89

Search Completed: Tue Feb 24 07:23:04 1998
Job time : 8 secs.

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RP SEQUENCE.
RA MILSTEIN C.
RL FEBS LETT. 2:301-304(1969);
CC -1- THIS IS A BENCE-JONES PROTEIN

RESULT	9	STANDARD:	PRT:	105 AA.
ID	KV33_HUMAN			
AC	P04206;			
DT	20-MAR-1987	(REL. 04. CREATED)		
DT	20-MAR-1987	(REL. 04. LAST SEQUENCE UPDATE)		
DT	20-MAR-1987	(REL. 04. LAST ANNOTATION UPDATE)		
DE	IG KAPPA CHAIN V-III REGION (GOL) (RHETIMOID FACTOR).			
OS	HOMO SAPIENS (HUMAN).			
CC	FUKAJOOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			

P. X. MEDLINE: 86230578.
NEWKIRK M., CHEN P. P., CARSON D. A., FORSETT D., CAPPA T. D.,
I. MOL. IMMUN. 23:239-244 (1986).
P. PIP: A01893; K3HUGO.

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RESULT 2
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01624:
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RA KLAPPER D G., CAPRA J D.:
RL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01897; K3HUPM.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: A0C42C88 CRC32:

Query Match 82.0%; Score 612; DB 5; Length 109;
Best Local Similarity 79.0%; Pred. No. 9 44e-117;
Matches 83; Conservative 14; Mismatches 7; Indels 1; Gaps 1;

Db 4 mtqspgtlslspgeratlscrasqsvsnslawyqkpgqaprllygastatgiparf 63
QY 3 LTQSPATLSVSPGERASLSCRASQSVGN-LAWYQKPGQAPRLLYGNTATGTPDRF 61

Db 64 sgsqsgtftltisslgsedfavyqgqygnnwptfqqgtrveik 108
QY 62 SSGSGSTFTLTISSLOSEDFAVYQGHYSTWPLTFGGGKVEFK 106

RESULT 3
ID KV3D_HUMAN STANDARD: PRT: 129 AA.
AC P18135:
DT 01-NOV-1990 (REL 16, CREATED)
DT 01-NOV-1990 (REL 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECIPITOP V-III REGION (HAH)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N A
RX MEDLINE: 88171307
RA KIPPS T J., TOMRAVE E., CHEN P P., CAPSON D A.:
RL J. EXP. MED. 167:840-852(1988)
CC -!- DISEASE. THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA
DR PIR: P10022; K3HUHA.
DR HSSP: P01507; 1AAG
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAH).
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 2C44B85E CRC32:

Query Match 80.8%; Score 603; DB 5; Length 129;
Best Local Similarity 79.0%; Pred. No. 1 36e-114;
Matches 83; Conservative 16; Mismatches 5; Indels 1; Gaps 1;

Db 4 mtqspgtlslspgeratlscrasqsvsnslawyqkpgqaprllygastatgiparf 63
QY 3 LTQSPATLSVSPGERASLSCRASQSVGN-LAWYQKPGQAPRLLYGNTATGTPDRF 61

Db 64 sgsqsgtftltisslgsedfavyqgqygnnwptfqqgtrveik 108
QY 62 SSGSGSTFTLTISSLOSEDFAVYQGHYSTWPLTFGGGKVEFK 106

RESULT 4
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01620:
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
FA ANDREWS D W., CAPRA J D.:
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUSI.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 00B5DD5D CRC32:

Query Match 80.7%; Score 602; DB 5; Length 109;
Best Local Similarity 77.1%; Pred. No. 2 36e-114;
Matches 81; Conservative 18; Mismatches 5; Indels 1; Gaps 1;

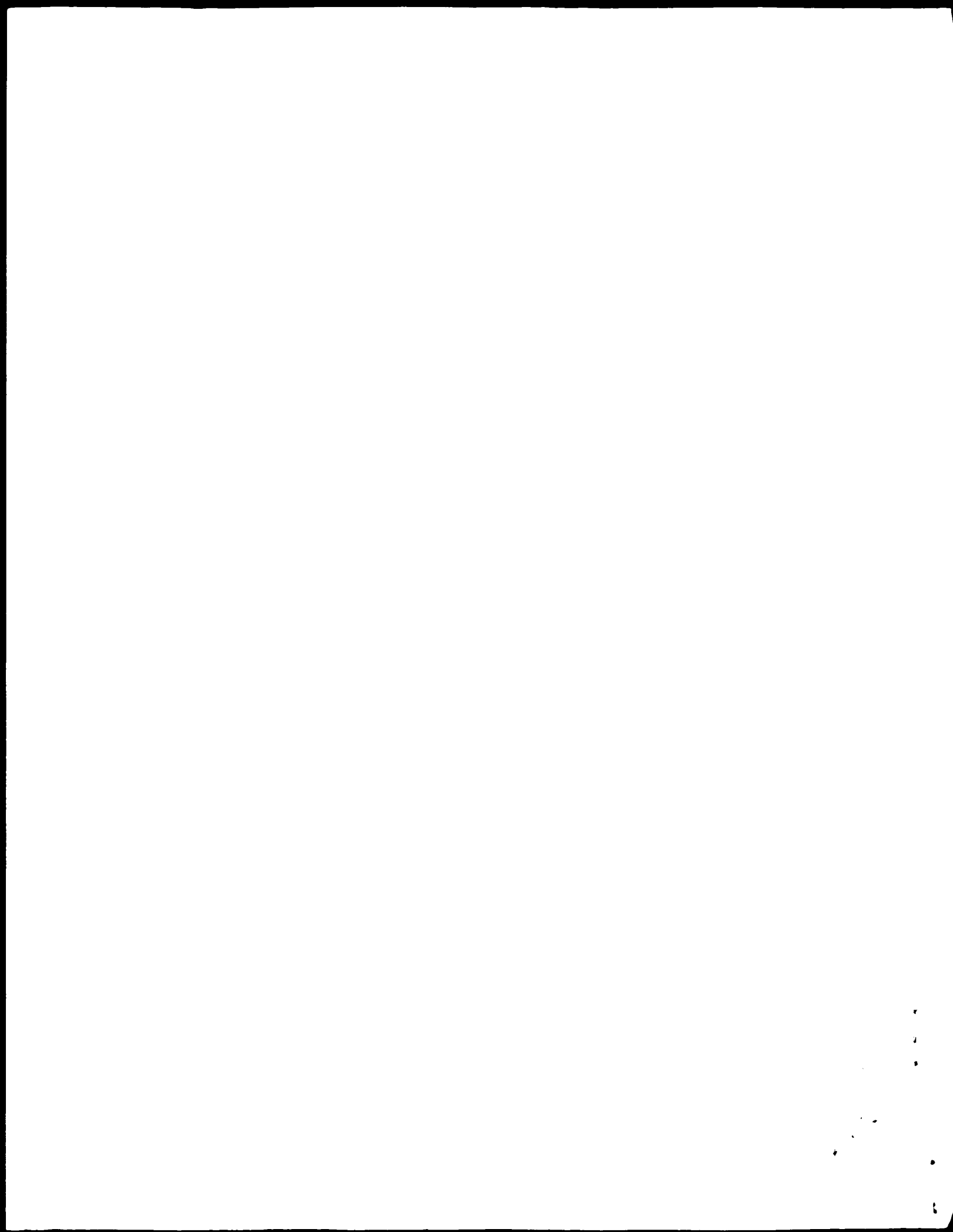
Db 4 ltqspgtlslspgeratlscrasqsvsnslawyqkpgqaprllygastatgiparf 63
QY 3 LTQSPATLSVSPGERASLSCRASQSVGN-LAWYQKPGQAPRLLYGNTATGTPDRF 61

Db 64 sgsqsgtftltisrlpddfavyqgqygnnwptfqqgskveik 108
QY 62 SSGSGSTFTLTISSLOSEDFAVYQGHYSTWPLTFGGGKVEFK 106

RESULT 5
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01622:
DT 21-JUL-1986 (REL 01, CREATED)
DT 21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (T1).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 72188439.
FA SUTEP L., BARNIKOL H U., WATANABE S., HILSCHMANN N.:
PL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 353:189-208(1972).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUTI.
DR HSSP: P01607; 2IMM.
KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: D03795B1 CRC32:

Query Match 79.6%; Score 594; DB 5; Length 109;
Best Local Similarity 78.1%; Pred. No. 1 94e-112;

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ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:89215279
#accession A30608
#status preliminary
#molecule_type protein
#residues 1-109 #label CON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6031

Query Match 81.6% Score 609; DB 7; Length 109;
Best Local Similarity 78.1% Pred. No. 1.38e-59;
Matches 82; Conservative 18; Mismatches 4; Indels 1; Gaps 1;

Db 4 Itqspatlsppgeratlsrscasgsvsylawyqkpgqaprlliygassratgipnrf 63
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Qy 3 LTQSPATLSVSPGERASLSCASQSGVNN-LAWYQKPGQAPRLLIYGGNTRATGTPDRF 61
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Db 64 sgsgsgtdftltisrlepfdavyycqyqyasspytfggqtkveik 108
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Qy 62 SGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
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RESULT 15
ENTRY B26555 #type complete
TITLE Ig kappa chain V-III region (Ger) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 16-Aug-1996
ACCESSIONS B26555
REFERENCE A92630
#authors Muddaugh, C.R.; Litman, G.W.
#journal J. Biol. Chem. (1987) 262:3671-3673
#title Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
#cross-references MUID:87137666
#accession B26555
#molecule_type protein
#residues 1-116 #label MID
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 116 #molecular-weight 12424 #checksum 5108

Query Match 81.2% Score 606; DB 7; Length 116;
Best Local Similarity 79.0% Pred. No. 3.29e-59;
Matches 83; Conservative 14; Mismatches 7; Indels 1; Gaps 1;

Db 4 mtqvpatlsvspgagatlsrscasgsissnlawyqkpgqaprlliyaastratgiparifs 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 3 LTQSPATLSVSPGERASLSCASQSGVNN-LAWYQKPGQAPRLLIYGGNTRATGTPDRFS 62
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Db 64 sgsgsgtdftltisrlepfdavyycqyqyasspytfggqtkveik 108
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Qy 63 SGSGSGTEFTLTISLSQSEDFAVYFCQHYSTWPLTFGGGKVEFK 106
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Search completed: Tue Feb 24 07:23:57 1998
Job time : 36 secs.

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REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Verbeke, S.
TITLE	Direct Submission
JOURNAL	Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE	(2 bases 1 to 507)
AUTHORS	Gallibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferts, P., Bancheireau, J., and Lebecque, S.
TITLE	Anti-CD40 plus interleukin-4-activated human naive B cell lines express unmutated immunoglobulin genes with intrachain heavy chain isotype variability
JOURNAL	Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE	95220422
FEATURES	Location/Qualifiers
SOURCE	1..507 /organism="Homo sapiens" /clone="202-E4" /tissue_type="Blood" /cell_type="B-Lymphocyte"
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Matches	280; Conservative 0; Mismatches 41; Indels 12; Gaps 4;
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OY	1 CTCGAGCAGTCTG35GTGAGSTGAGAAACCTTG35TCCTGGTAAG3TCTCGCANAG 60
Db	127 gctctcgaagcaccttcacgaactatgcatcaagcttggtctgcagacaagcccctggacca 186
OY	61 GCCTCTG3AAGCACATTTGAS3GCATATGATCACTG35TSDCAA3DCCCTG3GAATA 120
Db	187 aggccttaaggatggatggagggatcatccctacccttttgtc-----ac-a-gc---aac 234
OY	121 GGACTTAGTGGATGAG3GAGAGACCATTCCTATTCTTTGGTTCGCCGAACCTACGCTCAAAAC 180
Db	235 tacacacgaagatccagggcagagatcacagattacccggagcaaatccacagacagacc 294
OY	181 TACGCTGCAAAATTCGGSGACAGAGTCTGATATATGGCGAGAAATCCAGACGACGTCG 240
Db	295 taagtggaggtgagcgagcttgagttctggagacagagccgtgttatctctgagtagt 354
OY	241 TTCAATGAGCTGACCAACCTGAGATCTGACGACACGCGCTACTACTGTGCGAGAAC 300
Db	355 ggatggaggaatttatgtagtgtagctacctac 387
OY	301 CCTCCAAATATTTGCACTGTCTGTATATATGTTAC 433
RESULT	6
LOCUS	Hs202E2 507 bp RNA PRI 03-AUG-1995
DEFINITION	H sapiens mRNA for immunoglobulin variable region (clone 202-E2).
ACCESSION	D47256
NID	q619467
KEYWORDS	immunoglobulin; variable region.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote, mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Verbeke, S.
TITLE	Direct Submission
JOURNAL	Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE	(2 bases 1 to 507)
AUTHORS	Gallibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferts, P., Bancheireau, J., and Lebecque, S.

[illegible]

Db 451 gtggtgttctagtagtaccagctgctactactactacggtatgagcgtctgagggccaa 510
 OY 301 CCGCCAGAGATATGAGTGTGTAGATGCTACCGGGGATTTCCAGCAGATGGGGCCAG 360
 Db 511 gggaccagcgtaccgtctctcga 534
 OY 361 GGCACCTCTGTCACCGTCTCTCA 384

RESULT 3
 LOCUS HS203M5 493 bp RNA PRI 03-AUG-1995
 DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 203-M5).
 ACCESSION Z47272
 NID 9619463
 KEYWORDS immunoglobulin; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS Lebecque, S.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Peupliers, B.P. 11 CEDEX, Dardilly, Rhone, 69572, FRANCE
 REFERENCE 2 (bases 1 to 483)
 Galibert, L., van Dooren, J., Durand, I., Roussel, F., Jefferts, R., Bancheureau, J., and Lebecque, S.
 TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines express unmutated immunoglobulin genes with intrachain heavy chain isotype variability
 JOURNAL Eur J Immunol. 25 (3), 733-737 (1995)
 MEDLINE 9520422
 FEATURES
 source location/Qualifiers
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 /organism="Homo sapiens"
 /clone="203-M5"
 /tissue="blood"
 /cell-type="B-lymphocyte"

BASE COUNT 95 a 128 c 156 g 104 t

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 OY 1 CTCGACGAGTCTG355CTGAG3TGA3AACTG35TCTG3ATG3ATG3TCTG3AAG 60
 Db 127 gcttcgagagcactcaagcagctatgctacagctgagctgagcagccttgacaa 186
 OY 61 GCTCTGAGAGGACCTTAA3TGCATTTATACCTG35T35CA3A3G3CCTG3AACA 120
 Db 187 gggcttgatgagatggagggatcaccctctcttggc-----ac-a-gc---aaac 234
 OY 121 GGACTTGAATG3ATG3GAGAGAGCATCCCTATCTTTG3TTCG3AAACTCGCTCAAC 180
 Db 225 taagcagagaagctccagagcagatcacgattacggcagacaatccagcagacagcc 294
 OY 181 TACGCTCAAGAAATTCG3GAGACAGAGTCTGATTTATCCG3GACGATCCAGACACGCTG 240
 Db 295 tacatgagagctgagcagcttagatctgagagacagcagccttactctgagagag 354
 OY 241 TTCAATTGAGCTGAGCAACCTGAGATCTGACGACAGCGGCGCTGCTACTG3GAGAGAC 300
 Db 355 gggagagta-agtgcgaatcttggagtggttctcagtgactggtgacccctgggggca 413
 OY 301 CCTCAAGATATTCAGTGTGCTGAGATGATCCCG3GATTC-TTCCAGCATG3GGGCCA 359
 Db 414 gggagacctgctaccgtctcctca 438
 OY 361 GGCACCTCTGTCACCGTCTCTCA 384

OY 360 GGCACCTCTGTCACCGTCTCTCA 384

RESULT 4
 LOCUS HS202E5 507 bp RNA PRI 03-AUG-1995
 DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 202-E5).
 ACCESSION Z47258
 NID 9619469
 KEYWORDS immunoglobulin; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS Lebecque, S.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Peupliers, B.P. 11 CEDEX, Dardilly, Rhone, 69572, FRANCE
 REFERENCE 2 (bases 1 to 507)
 Galibert, L., van Dooren, J., Durand, I., Roussel, F., Jefferts, R., Bancheureau, J., and Lebecque, S.
 TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines express unmutated immunoglobulin genes with intrachain heavy chain isotype variability
 JOURNAL Eur J Immunol. 25 (3), 733-737 (1995)
 MEDLINE 9520422
 FEATURES
 source location/Qualifiers
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 /organism="Homo sapiens"
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BASE COUNT 106 a 139 c 158 g 104 t

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 Matches 280; Conservative 0; Mismatches 41; Indels 12; Gaps 4;

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 Db 127 gcttcgagagcactcaagcagctatgctacagctgagctgagcagccttgacaa 186
 OY 61 GCTCTGAGAGGACCTTAA3TGCATTTATACCTG35T35CA3A3G3CCTG3AACA 120
 Db 187 gggcttgatgagatggagggatcaccctctcttggc-----ac-a-gc---aaac 234
 OY 121 GGACTTGAATG3ATG3GAGAGAGCATCCCTATCTTTG3TTCG3AAACTCGCTCAAC 180
 Db 225 taagcagagaagctccagagcagatcacgattacggcagacaatccagcagacagcc 294
 OY 181 TACGCTCAAGAAATTCG3GAGACAGAGTCTGATTTATCCG3GACGATCCAGACACGCTG 240
 Db 295 tacatgagagctgagcagcttagatctgagagacagcagccttactctgagagag 354
 OY 241 TTCAATTGAGCTGAGCAACCTGAGATCTGACGACAGCGGCGCTGCTACTG3GAGAGAC 300
 Db 355 gggagagagtgatgagtggtggtgagtgctac 387
 OY 301 CCTCAAGATATTCAGTGTGCTGAGATGATCCCG3GATTC-TTCCAGCATG3GGGCCA 359
 Db 414 gggagacctgctaccgtctcctca 438
 OY 361 GGCACCTCTGTCACCGTCTCTCA 384

RESULT 5
 LOCUS HS202E4 507 bp RNA PRI 03-AUG-1995
 DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 202-E4).
 ACCESSION Z47257
 NID 9619468
 KEYWORDS immunoglobulin; variable region.
 SOURCE human.
 ORGANISM Homo sapiens

(WT.)

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generated

GAGCTCGTCAGACCCCGACT

Gap 6

[illegible]

Existing first 45

eml-new7

genbank101

114:UNA

genbank - new7

emb151_101

mean 9.985; variance 4.551; scale 2.194

er than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution

Result No.	Score	% Match	Query Length	DB	ID	Description	Pred. No.
SUMMARIES							
1	175	44.6	528	99	HUMIGHDYN	Human Ig rearranged H	4,436-127
2	170	45.3	534	99	HUMIGHDON	Human Ig rearranged H	1,416-122
3	167	43.5	483	87	HS20355	H.sapiens mRNA for im	7,020-120
4	167	43.5	507	87	HS20325	H.sapiens mRNA for im	7,020-120
5	167	43.5	507	87	HS20324	H.sapiens mRNA for im	7,020-120
6	167	43.5	507	87	HS20322	H.sapiens mRNA for im	7,020-120
7	167	43.5	510	87	HS20362	H.sapiens mRNA for im	7,020-120
8	167	43.5	510	87	HS20359	H.sapiens mRNA for im	7,020-120
9	167	43.5	510	87	HS20356	H.sapiens mRNA for im	7,020-120
10	167	43.5	510	87	HS20356	H.sapiens mRNA for im	7,020-120
11	167	43.5	522	87	HS20359	H.sapiens mRNA for im	7,020-120
12	167	43.5	525	87	HS20364	H.sapiens mRNA for im	7,020-120
13	167	43.5	525	87	HS20361	H.sapiens mRNA for im	7,020-120
14	166	43.2	421	99	HUMIGHVAN	Human (fetal) Ig rear	5,556-119
15	166	43.2	534	99	HUMIGHDKN	Human Ig rearranged H	5,556-119
16	166	43.2	872	99	HUMIGHDAVA	Human (1051) g	5,556-119
17	165	43.0	387	102	0005032	Human immunoglobulin	4,406-118
18	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
19	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
20	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
21	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
22	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
23	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
24	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
25	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
26	165	43.0	392	91	HS20361	H.sapiens gene for im	4,406-118
27	165	43.0	510	87	HS20361	H.sapiens mRNA for im	4,406-118
28	165	43.0	513	99	HUMIGHDKN	Human Ig rearranged H	4,406-118
29	165	43.0	522	87	HS20356	H.sapiens mRNA for im	4,406-118
30	165	43.0	525	87	HS20356	H.sapiens mRNA for im	4,406-118
31	165	43.0	525	99	HUMIGHDKN	Human Ig rearranged H	4,406-118
32	165	43.0	525	87	HS20363	H.sapiens mRNA for im	4,406-118
33	165	43.0	525	99	HUMIGHDKN	Human Ig rearranged H	4,406-118
34	164	42.7	480	96	HUMIGHG18	H.sapiens gene for im	3,486-117
35	164	42.7	480	96	HUMIGHG18	H.sapiens gene for im	3,486-117
36	164	42.7	474	87	HS20364	H.sapiens mRNA for im	3,486-117
37	164	42.7	475	98	HUMIGHG18	Human (clone MAB57) I	3,486-117
38	164	42.7	501	87	HS20368	H.sapiens mRNA for im	3,486-117
39	164	42.7	501	99	HUMIGHDKN	Human Ig rearranged H	3,486-117
40	164	42.7	501	87	HS20361	H.sapiens mRNA for im	3,486-117
41	164	42.7	501	87	HS20361	H.sapiens mRNA for im	3,486-117
42	164	42.7	510	99	HUMIGHG18	Human Ig rearranged H	3,486-117
43	164	42.7	510	87	HS20361	H.sapiens mRNA for im	3,486-117
44	164	42.7	510	87	HS20361	H.sapiens mRNA for im	3,486-117
45	164	42.7	510	87	HS20361	H.sapiens mRNA for im	3,486-117
ALIGNMENTS							
RESULT LOCUS	1	HUMIGHDYN	528 bp	DNA	09-MAY-1996		
DEFINITION		Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L42, subgroup VH-1.					
ACCESSION		M55104					
NID		9185344					
KEYWORDS		V-region; immunoglobulin heavy chain subgroup VH-1; rearranged DNA.					
SOURCE		Homo sapiens tonsil DNA.					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryote: mitochondrial eukaryotes; Metazoa: Chordata; Vertebrata: Eutheria: Primates: Catarrhini: Hominiidae: Homo.					
AUTHORS		Rapes, T.J. and Duffy, S.F.					
TITLE		Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes					
JOURNAL		J Clin Invest	87 (5)				
MEDLINE		91250563					



Query Match 7.08; Score 27; DB 37; Length 326;
Best Local Similarity 80.58; Pred. No. 9.46e-13;
Matches 33; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 77 ttcgantattgagccaggaatccctggtcaccgtntctc 117
||| | ||||| ||| ||||| |||||
QY 343 TTCAGGAAAGTGGGCGCAAGGACCTCTGTCAGGCTCTCCTC 383

Search completed: Tue Feb 24 09:45:55 1998
Job time : 150 secs.

OS Homo sapiens (human)
 OC Eukaryota: mitochondrial eukaryotes; Metazoa: Chordata:
 OC Vertebrata: Eutheria: Primates: Catarrhini: Homidae: Homo.
 RN [1]
 RP 1-292
 RA NCI-CGAP:
 RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 RT Tumor Gene Index";
 RL Unpublished.
 CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
 CC Robert.Strausberg@nih.gov This clone is available royalty-free
 CC through LHM; contact the IMAGE Consortium (info@image.lln.gov)
 CC for further information. Trace considered overall poor quality
 CC Possible reversed clone; similarity on wrong strand Seq primer:
 CC -28m13 rev2 ET from Amersham High quality sequence stop: 1.
 FH Key Location/Qualifiers
 FT source
 FT 1..292
 FT /organism="Homo sapiens"
 FT /note="Vector: p773D-Pac (Pharmacia) with a modified
 FT polylinker. Site_1: Not I, Site_2: Eco RI, 1st strand cDNA
 FT was prepared from human tonsillar cells enriched for
 FT germinal center B cells by flow sorting (CD20+, IgD-),
 FT provided by Dr. Louis M. Staudt (NCI). Dr. David Allman
 FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 FT primed with a Not I - Oligo(dT) primer
 FT [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCAATTTTCTTTTCTT-
 FT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I
 FT and Eco RI sites of the modified p773 vector. Library was
 FT through one round of normalization, and was constructed by
 FT Bento Soares and M. Fatima Bonaldo."
 FT /clone="685101"
 FT /clone_lib="NCI-CGAP_GCB1"
 FT /issue_type="germinal center B cell"
 FT /lab_host="DH10B"
 FT <1..>292
 FT mRNA
 SQ Sequence 292 BP; 88 A; 76 C; 63 G; 65 T; 0 other;

Query Match 5.28; Score 20; DB 78; Length 292;
 Best Local Similarity 85.78; Pred. No. 2,18e-03;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 112 agaccctccaccctaatgcaatgctgt 139
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 QY 297 AGACCTCTCCACATATTGCAATGCTGT 324

Search completed: Tue Feb 24 09:48:51 1998
 Job time : 153 secs.


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DEFINITION 2x83h07.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 810397
5' similar to gb:U21964 IG HEAVY CHAIN V-II REGION (HUMAN)..
ACCESSION AA464794
NID 92189678
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 511)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubnue, T., Gelsel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 414
Location/Qualifiers
1..511
/organism="Homo sapiens"
/note="Organ: ovary; Vector: p773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCGGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/clone="810397"
/clone_lib="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>511
/db_xref="GDB:6040750"
BASE COUNT 106 a 169 c 124 g 112 t
ORIGIN
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Best Local Similarity 87.9%; Pred. No. 7.68e-10;
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
Db 388 tggggccaagggacacgtcaccgtctccta 420
||||| ||| ||| ||| ||| ||| ||| |||
QY 352 TGGGGCCAGCGCACCTGTCACCTCTCTCA 384

RESULT 9
ID HSA07475 standard; RNA; EST: 435 BP.
AC AA507475;
N1 92243914
DT 05-JUL-1997 (Rel. 52, Created)
DT 16-JUL-1997 (Rel. 52, Last updated, Version 2)
DE nb76c05.s1 NCI-CGAP_Brl.1 Homo sapiens cDNA clone 664424 similar to
DE gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
DE gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OC Homo.

DEFINITION 2x83h07.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 810397
5' similar to gb:U21964 IG HEAVY CHAIN V-II REGION (HUMAN)..
ACCESSION AA464794
NID 92189678
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubnue, T., Gelsel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

PN [1]
PA 1-435
PA NCI-CGAP;
PT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
RT Tumor Gene Index";
RU Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskaluk,
CC M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library
CC Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg
CC Lennon, Ph.D. DNA Sequencing by: Washington University Genome
CC Sequencing Center clone distribution: NCI-CGAP clone distribution
CC Information can be found through the I M A G E Consortium/LNL at:
CC www.bio.llnl.gov/biopr/image/image.html Insert Length: 558 Std
CC Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality
CC sequence stop: 131.
FH key
FH Location/Qualifiers
FT source
FT 1..435
FT /organism="Homo sapiens"
FT /note="Vector: p773D-Pac (Pharmacia) with a modified
FT polylinker; 1st strand cDNA was prepared from pooled bulk
FT breast tumor tissue, and was then primed with a Not I -
FT oligo(dT) primer. Double-stranded cDNA was ligated to Eco
FT RI adaptors (Pharmacia), digested with Not I and cloned
FT into the Not I and Eco RI sites of the modified p773
FT vector. Library is not normalized. (The normalized version
FT of this library is NCI-CGAP_Brl.1) Library was constructed
FT by Bento Soares and M. Fatima Bonaldo."
FT /clone="964424"
FT /clone_lib="NCI-CGAP_Brl.1"
FT /sex="female, pooled"
FT /tissue_type="breast"
FT /lab_host="DH10B"
FT <1..>435
FT mRNA
SQ Sequence 435 BP; 94 A; 128 C; 112 G; 101 T; 0 other;
Query Match 5.7%; Score 22; DB 80; Length 435;
Best Local Similarity 64.9%; Pred. No. 7.62e-06;
Matches 48; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Db 266 gctaaaggtaatcagaggtcgcacagagaggtctcaggaacccccagcgtaccaa 325
||||| ||| ||| ||| ||| ||| ||| |||
Cp 81 GCTGAAGGTGCTCTCCAGAGGCTTGTGAGAGACCTTCAGAGGAGGAGGAGCTTCCTAC 22
Db 326 gctccccccagact 339
| ||| ||| ||| ||| ||| ||| |||
Cp 21 CTCAGCCCCGAGACT 8

RESULT 10
LOCUS AA507475 435 bp mRNA EST 15-JUL-1997
DEFINITION nb76c05.s1 NCI-CGAP_Brl.1 Homo sapiens cDNA clone 664424 similar to
DE gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
DE gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
ACCESSION AA507475
NID 92243914
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubnue, T., Gelsel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

```


[illegible]

	adaptors (Pharmacia). digested with Not I and cloned into
	pCR-Script vector.
	The Not I and Eco RI sites of the modified pTZ19 vector
	were provided by Dr. Minnie Ku, Wayne State Univ. Library
	constructed and normalized by Bento Soares and M.Fátima
	Bonafido."
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	/dev_stage="4 weeks"
	/lab_host="DH10B"
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Dc	120 ctctgaagagatctgaggagaagcttggtagaacctggagacatcaaatccctctgttgtttt 1 CTTCAAGACCTCGTGGACTGAAGATGAGAAGCCTGGGTTCCTTGTAAGAACTGCTCTTAAG
Gy	160 gtctcttgcatcttcctcttgagtgcgccatggagctcgattctgactgatctcctgagagaa 61 GTCTCTTGAAGCATCTCCATTCAAGAGGATAAATGATCACCTGAGTAGAACAGGCCTTGACA
Lb	240 gaacctgaattg 251
Oy	121 GGACTTGACTGAG 132
RESULT	5
ID	XM126365E standard; PNA: EST; seq BP.
AC	AAG72093:
N1	Q2200084
DT	21-JUN-1997 (Rel. 52; Created)
DI	21-JUN-1997 (Rel. 52; Last updated, Version 1)
DE	b750245_r1 Soares mouse mammary gland NbMWG Mus musculus CDNA clone
TE	gb:L3692 Mus musculus germ-line immunoglobulin gamma constant region (MOUSE); .
OS	Mus musculus (house mouse)
OC	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
NC	Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
RN	[1]
RA	Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
PA	Dubugue T., Geisler S., Kucaba T., Lucy M., Le M., Martin J.,
RA	Morris M., Schellenberg K., Stepien M., Tan F., Underwood K.,
RA	Moore R., Theising H., Wylie T., Lennon G., Soares R., Wilson R,
FA	Waterson P.;
LA	"The WashU-HHMI Mouse EST Project";
Unpublshed	.
Contact:	Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
Washington University School of Medicine 444 Forest Park Parkway,	
CC	Box 8501, St. Louis, MO 63108 Tel.: 314.286.1900 Fax: 314.286.1810
Email:	mouseest@watson.wustl.edu This clone is available
royalty-free through LNL; contact the IMAGE Consortium	
(infoimage.lnl.gov) for further information. MG1514504 Seq	
primer:-28ml3 rev2 ET from Amerham High quality sequence stop;	
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FH	key
FH	Location/Qualifiers
FT	Source
FT	1..597
FT	/organism="Mus musculus"
FT	/strain="C57BL/6J"
FT	/note="Vector: pTZ19-Pac (Pharmacia) with a modified
FT	polylinker. Site 1: Not I, site 2: Eco RI, 1st strand cDNA
FT	was primed with a Not I - oligo(dT) primer [5'
FT	TGTTGCCATGTTAAAATGGAGAGAGGAGGAGAAATGGTTTTTTTTTTTTTTTTT
IT	I 3']; double-stranded cDNA was ligated to Eco RI adaptors

FitzGerald, J. L. M., FitzHugh, W. M., Fritchman, J. L., Georghagen, N. S. M.,
 Kelder, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, Jr., P. S.,
 Kelley, J. M., Klinek, K. M., Kelley, J. C., Liu, L. L., Marmirois, S. M.,
 Mericq, J. J. M., Moreno-Palauques, P. F., McDonald, L. A., Nguyen, D. T.,
 Pellegrino, S. M., Phillips, G. A., Pyder, S. E., Scott, J. L.,
 Saudak, D. M., Shirley, R., Small, K. V., Springs, T. A., Utteback, T. R.,
 Weidman, J. F., Li, Y., Rednath, D. P., Cao, L., Cepeda, M. A.,
 Coleman, T. A., Collins, E. J., Dinko, D., Fang, P., Farle, A.,
 Fischer, C., Hastings, G. A., He, W.-W., Hu, J.-S., Greene, J. M.,
 Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kusch, C., Ji, H., Li, H.,
 Meisner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
 Yu, G.-L., Ruben, S. M., Dillon, P. J., Fannon, M. R., Rosen, C. A.,
 Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Bassetpairs of cDNA Sequence
 Unpublished (1995)



Sequence 328: 2P, 599 A, 864 C, 1109 G, 710 T; 0 other.

Query Match	20.8%;	Score 80;	DB 13;	length 3282;
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Best Local Similarity 77.8%; Pred. No. 6.45e-42;
Matches 113; Conservation 0; Mismatches 37

Matches 112; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Db 3053 AGGATTGATCCATCCCATCCACTCAAACTCTGTGTCCGGGGCTGTGGCGACCCCATGAAT 3112

CP 150 AGGATGCTCTCTCCCAICCACTCAAGTCCTTGTCACAGGGGCTGTCCGACCCAGGTGAT 91

Db 3113 AACAAAGTACTGAATCTGTATCCAGAAGCCTGACAAGAAGAACTTCACCTGAGGCCCCAGG 3172

CP 90 AACATGGCCCTGAAGGTGCTTCAGAACTTGCAGGAGACTTCACCGAGGACCCAGG 31

Db 3173 GTTCTTCACTTCAAGCCCGGACTG 3196

CP 30 CTTCCTACCTCAGCCCCAGACTG 7

Search completed: Tue Feb 24 15:05:46 1998
Job time : 64 secs.

SOFTWARE: Patent Release #1 0, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEO ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 241..285
FEATURE:
NAME/KEY: CDS
LOCATION: 373..678
SEQUENCE 813 BP: 204 A; 189 C; 223 G; 197 T; 0 other:

Query Match 41.7% Score 160; DB 7; Length 813;
Best Local Similarity 86.7% Pred. No. 1,93e-103;
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1 CTGACACACTCTGGGCTAGAGTGAAGAAAGCTGGGTCCTCGGTAAAGGTCCTCTGCAG 60
454 GCTTCTGGAGGACCTTCAGACGTAIGCTATCAGCTGGGTCGACAGGCGCCCTGGACAA 513
61 GCTTCTGGAGGACCTTCAGACGTAIGCTATCAGCTGGGTCGACAGGCGCCCTGGACAA 120
514 GGGCTTGAATGATGGGAAGATCATCCTATCCTTGT-----A-TA-GC---AAAC 561
121 GGACTTGAATGATGGGAAGATCATCCTATCCTTGTGGTGGGCAACCTACGCTCAAAAAC 180
562 TACCCACAAAGTTCAGGGGACAGATTCAGGATTACCGGAGAAATCCAGACGACAGCC 621
181 TACCCACAAAGTTCAGGGGACAGATTCAGGATTACCGGAGAAATCCAGACGACGTCG 240
622 TACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 681
241 TTGATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1 0, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..441
SEQUENCE 441 BP: 89 A; 125 C; 135 G; 92 T; 0 other:

Query Match 36.7% Score 141; DB 6; Length 441;
Best Local Similarity 84.1% Pred. No. 1,32e-88;
Matches 248; Conservative 0; Mismatches 35; Indels 12; Gaps 4;

Db 72 GCAAGTCTGGGGCTGAGAGTGAAGAAAGCTGGGTCCTCGGTAAAGGTCCTCTGCAG 141
6 GCAAGTCTGGGGCTGAGAGTGAAGAAAGCTGGGTCCTCGGTAAAGGTCCTCTGCAG 65
132 TGAAGGACCTTCAGCAATTTTCATACGCTGGGTCGACAGGCGCCCTGGACAAAGGACT 125
66 TGAAGGACCTTCAGCAATTTTCATACGCTGGGTCGACAGGCGCCCTGGACAAAGGACT 125
192 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 239
126 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 305
240 ATAGAAATTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 299
186 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 245
300 GCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 354
246 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Sequence 2287 BP: 483 A, 752 C, 654 G, 398 T; 0 other.

Query Match 53.6%; Score 206; DB 14; Length 2287;
Best Local Similarity 84.6%; Pred. No. 115e-139;
Matches 325; Conservative 0; Mismatches 47; Indels 12; Gaps 4;

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1 CTGGAGCAGCTCTGGGGCTGAGGTGAGAGAGCCTGGGTCCTGCGTGAAGCTGCTGGAG 60
DB 142 GCTTCTGAGAGCAGCTTTCAGAGCTATGCTATACAGCTGGGTGCGACAGGCCCTGAGCAA 201
61 GCTTCTGAGAGCAGCTTTCAGAGCTATGCTATACAGCTGGGTGCGACAGGCCCTGAGCAA 120
DB 202 GCGCTTGAATGAGTGGAGAGGATCATGCTTATCTTGT-----AC-A-GC---AAAC 249
121 GGACCTGAGTGGATGGAGAGAGCATGCTTATCTTGTGGTCCGCAAACTACGCTCAAAAC 180
DB 250 TACGACAGAGAGCTTCAGAGGAGAGCTACAGATTACCGCGGAGCAATCCAGCAGCAGAGCC 309
181 TACGCTCAAGAAATTCGGGAGCAGAGCTTCAGATTATCGGCGAGCAATCCAGCAGAGCTCG 240
DB 310 TACATGAGAGCTGAGAGCCTGAGATCTGAGAGCAGCGCGCTGATTTACTGTGCGAGAT 369
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DB 370 AATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 429
301 CTCTCAAGATATTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB 430 GGAACCCCTGTCAGCGCTCTCTCA 453
361 GGGACCCCTGTCAGCGCTCTCTCA 384
Y

RESULT 2
ID US-07-814-519A-53 STANDARD: DNA: UNC: 812 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 53, Application US/07834539A.
CC Sequence 53, Application US/07834539A
CC Patent No. 5633425
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 77
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/814,539A
CC FILING DATE: 19920205
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30, 223
CC REFERENCE/DOCKET NUMBER: 1443-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Exon
LOCATION: 241..335
OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
FEATURE:
NAME/KEY: Exon
LOCATION: 372..677
OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
Sequence 812 BP: 204 A, 188 C, 223 G, 197 T; 0 other.

Query Match 41.7%; Score 160; DB 7; Length 812;
Best Local Similarity 86.7%; Pred. No. 1.93e-103;
Matches 260; Conservative 0; Mismatches 28; Indels 12; Gaps 4;

DB 393 CTGGTGGACCTGCGGGCTGAGGTGAGAGAGCCTGGGTCCTGCGTGAAGCTGCTGGAG 452
1 CTGGAGCAGCTCTGGGGCTGAGGTGAGAGAGCCTGGGTCCTGCGTGAAGCTGCTGGAG 60
DB 453 GCTTCTGAGAGCAGCTTTCAGAGCTATGCTATACAGCTGGGTGCGACAGGCCCTGAGCAA 512
61 GCTTCTGAGAGCAGCTTTCAGAGCTATGCTATACAGCTGGGTGCGACAGGCCCTGAGCAA 120
DB 513 GCGCTTGAATGAGTGGAGAGGATCATGCTTATCTTGT-----A-TA-GC---AAAC 560
121 GGACCTGAGTGGATGGAGAGAGCATGCTTATCTTGTGGTCCGCAAACTACGCTCAAAAC 180
DB 561 TACGACAGAGAGCTTCAGAGGAGAGCTACAGATTACCGCGGAGCAATCCAGCAGCAGAGCC 629
181 TACGCTCAAGAAATTCGGGAGCAGAGCTTCAGATTATCGGCGAGCAATCCAGCAGAGCTCG 240
DB 621 TACATGAGAGCTGAGAGCCTGAGATCTGAGAGCAGCGCGCTGATTTACTGTGCGAGAT 660
241 TTTATGAGAGCTGAGAGCCTGAGATCTGAGAGCAGCGCGCTGATTTACTGTGCGAGAGAT 600
Y

RESULT 3
ID PCT-US92-06185-53 STANDARD: DNA: UNC: 812 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 53, Application PC/TUS9206185.
CC Sequence 53, Application PC/TUS9206185
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 75
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/06185
CC FILING DATE: 19910828
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.

 W O R L D S E R I E S (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPearch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 15:04:42 1998: MasPar time 23.35 Seconds

Tabular output not generated. 756.316 Million cell updates/sec

Title: >US-08-844-215-22

Description: (1-384) from US08844215.soc

Perfect Score: 384

N.A. Sequence: 1 CTGCGAGCAGCTGTGGGCTGA.....CCCTCGTACCGCTCTCTCTCA 384

Comp: GAGCTGTGTAGACCTCGGAGT.....GGGAGCAGTGGCAGAGGAGT

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0: Query 0

Searched: 87531 segs, 2296021 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-issued 1-back 2.53 3.52 4.53 5.54 6.55 7.56 8.57 9.58 10.59

10:PC192 11 PCT94 12 PCT94 13 PCT95 14 PCT96

Statistics: Mean 7.710; Variance 4.085; scale 1.888

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	206	53.6	2287	14	PCT-US96-1	Sequence 9, Applicatio
2	160	41.7	812	7	US-07-834	Sequence 53, Applicati
3	160	41.7	812	10	PCT-US92-0	Sequence 53, Applicati
4	160	41.7	813	10	PCT-US92-1	Sequence 61, Applicati
5	160	41.7	813	7	US-08-053	Sequence 61, Applicati
6	141	36.7	441	6	US-08-217	Sequence 3, Applicatio
7	138	35.9	687	13	PCT-US95-1	Sequence 1, Applicatio
8	138	35.9	687	7	US-08-800	Sequence 1, Applicatio
9	138	35.9	687	12	PCT-US94-0	Sequence 1, Applicatio
10	111	29.9	363	11	US-08-264	Sequence 1, Applicatio
11	92	24.0	363	11	PCT-US93-0	Sequence 7, Applicatio
12	84	21.9	451	11	PCT-US93-1	Sequence 11, Applicati
13	80	20.8	3282	13	PCT-US95-0	Sequence 154, Applicat
14	80	20.8	3282	13	PCT-US95-0	Sequence 154, Applicat
15	80	20.8	3282	13	PCT-US95-0	Sequence 169, Applicat
16	80	20.8	3282	13	PCT-US95-0	Sequence 169, Applicat
17	80	20.8	3282	13	PCT-US95-0	Sequence 156, Applicat
18	80	20.8	3282	13	PCT-US95-0	Sequence 156, Applicat
19	80	20.8	3282	13	PCT-US95-0	Sequence 170, Applicat

20	75	19.5	1254	7	US-08-276	Sequence 170, Applicat	5.45e-42
21	75	19.5	351	13	PCT-US95-0	Sequence 10, Applicati	3.40e-38
22	75	19.5	351	6	US-08-236	Sequence 10, Applicati	3.40e-38
23	75	19.5	357	7	US-08-467	Sequence 1, Applicatio	3.40e-38
24	75	19.5	356	13	PCT-US95-0	Sequence 8, Applicatio	3.40e-38
25	75	19.5	356	7	US-08-040	Sequence 7, Applicatio	3.40e-38
26	75	19.5	366	6	US-08-236	Sequence 8, Applicatio	3.40e-38
27	75	19.5	429	6	US-08-236	Sequence 6, Applicatio	3.40e-38
28	75	19.5	429	13	PCT-US95-0	Sequence 6, Applicatio	3.40e-38
29	75	19.5	660	7	US-08-392	Sequence 1, Applicatio	3.40e-38
30	75	19.5	1572	7	US-08-353	Sequence 23, Applicatio	3.40e-38
31	74	19.3	366	7	US-08-040	Sequence 6, Applicatio	1.87e-37
32	73	19.0	363	7	US-08-040	Sequence 2, Applicatio	1.03e-36
33	73	19.0	363	7	US-08-040	Sequence 1, Applicatio	1.03e-36
34	73	19.0	366	7	US-08-040	Sequence 8, Applicatio	1.03e-36
35	71	18.5	342	6	US-08-235	Sequence 5, Applicatio	3.09e-35
36	71	18.5	363	7	US-08-040	Sequence 4, Applicatio	3.09e-35
37	71	18.5	748	6	US-08-235	Sequence 10, Applicatio	3.09e-35
38	71	18.5	2012	6	US-08-235	Sequence 15, Applicatio	3.09e-35
39	70	18.2	420	11	PCT-US93-1	Sequence 3, Applicatio	1.69e-34
40	70	18.2	443	6	US-07-634	Sequence 9, Applicatio	1.69e-34
41	70	18.2	443	7	US-08-474	Sequence 9, Applicatio	1.69e-34
42	70	18.2	443	6	US-08-477	Sequence 9, Applicatio	1.69e-34
43	70	18.2	443	7	US-08-487	Sequence 9, Applicatio	1.69e-34
44	70	18.2	725	11	PCT-US93-1	Sequence 11, Applicatio	1.69e-34
45	70	18.2	803	13	PCT-US95-1	Sequence 7, Applicatio	1.69e-34

ALIGNMENTS

RESULT 1
 ID PCT-US96-10043-8 STANDARD: DNA; UNC: 2287 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 8, Application PC/TUS9610043.
 CC Sequence 9, Application PC/TUS9610043
 CC GENERAL INFORMATION:
 CC APPLICANT: The General Hospital Corporation
 CC TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
 CC TITLE OF INVENTION: AND METHODS
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Fish & Richardson P.C.
 CC STREET: 225 Franklin Street
 CC CITY: Boston
 CC STATE: MA
 CC COUNTRY: USA
 CC ZIP: 02110-2804
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC Compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Parentin Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US96/10043
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 60/000,213
 CC FILING DATE: 14-JUN-1995
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Lech, Karen F.
 CC REGISTRATION NUMBER:
 CC REFERENCE/DOCKET NUMBER: 00796/294001
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 617/542-8906
 CC TELEFAX: 617/542-8906
 CC TELEX: 200154
 CC INFORMATION FOR SEQ ID NO 8
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 2287 base pairs
 CC TYPE: nucleic acid

PD 14-MAR-1996.
 PF 01-SEP-1995: 011235.
 PR 02-SEP-1994: US-300386.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-171625/17.
 PT Oligonucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PS Example 1: Page 83: 125pp: English.
 CC 115262 and 115203 are the heavy and light chain variable domains of
 CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a pComb3
 CC based expression vector. The heavy and light chain variable domains
 CC are used in an example to demonstrate the prodn. of antibodies for
 CC an antibody library using mutagenic primers. Mutagenic primers of the
 CC invention have sequences at their 3' and 5' ends both capable of
 CC binding different framework regions linked by a sequence 6 to 50
 CC nucleotides long. Different immunoglobulins produced using the
 CC primers may be used to produce antibody libraries having diverse and
 CC novel immunospecificities and affinities. By using mutagenic ONS an
 CC extremely large population of different randomised binding sites can
 CC be created and use of the universal light chain increases the number
 CC of combinations which yield functional heterodimeric antibodies.
 SQ Sequence 687 BP: 155 A, 211 C, 135 G, 126 T;
 Query Match: 35.9%, Score 138, DB 22, Length 687.
 Best Local Similarity: 83.2%; Fred No. 1.06e-77;
 Matches 248; Conservative 0; Mismatches 38; Indels 12; Gaps 9;
 Db 1 ctgaagcagctcgtgagctgaagaaagcctgtgctcctcgtgagagctcctcagag 60
 Uy 1 CTCGACGAGCTCGAGCTGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 60
 Db 61 gctcttgagagcagctcgaacatatagcataagcctggtgagaaagcccttgagaa 120
 Uy 61 GCTTCTGAGAGCTGAGAGCTGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 Db 121 gggcttgagtgatgagagag-g-g-alc--t-tccct--ttccgtaa--taaga- 168
 Uy 121 GGACTTGAGTGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 Db 169 taagcaacaacattccagagagagatcaccattacccagaggaatccagagagagcc 228
 Uy 181 TACGCTGAG 240
 Db 229 tacatgagagctgagagcagctgaagatctgagagacagagccatataattgtgagag 286
 Uy 241 TTCATTGAGCTGAG 298
 RESULT 13
 ID 092546 standard: DNA: 4691 BP.
 AC 092546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;
 KW Gene III; filamentous phage; minor phage coat protein; gpIII; cp3;
 KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120,
 KW combinatorial Fab library; cassette; fd/cp3; lac2 promoter/operator;
 KW ribosome binding site; RBS; Pelb leader; spacer; tether sequence;
 KW MT4; pMT4-3; antibody; ss; cyclic.
 OS Synthetic.
 PN W09511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994: 011907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 95-170235/22
 PT Synthetic human neutralising monoclonal antibodies to human
 immunodeficiency virus - used for diagnosis and immunotherapy of

PT HIV-induced disease.
 PS Example 1: Page 185-188: 249pp: English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, gpIII (cp3), which is expressed
 CC prior to extrusion in the phage assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lac2 promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC Pelb leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lac2 promoter/operator sequence,
 CC followed by an expression control RBS, a Pelb leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the MT4 Fab display phagemid expression vector, pMT4-3 (see also
 CC 032540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 SQ Sequence 4691 BP: 1170 A, 1171 C, 1232 G, 1118 T;
 Query Match: 35.9%, Score 138, DB 16, Length 4691.
 Best Local Similarity: 83.2%; Fred No. 1.06e-77;
 Matches 248; Conservative 0; Mismatches 38; Indels 12; Gaps 9;
 Db 3424 ctgagagagctcgtgagctgagagagagcctgtgctcctcgtgagagctcctcagag 3483
 Uy 1 CTCGACGAGCTCGAGCTGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 60
 Db 3484 gctcttgagagcagctcgaacatatagcataagcctggtgagaaagcccttgagaa 3543
 Uy 61 GCTTCTGAGAGCTGAGAGCTGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 Db 3544 gggcttgagtgatgagagag-g-g-alc--t-tccct--ttccgtaa--taaga- 3591
 Uy 121 GGACTTGAGTGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 Db 3592 taagcaacaacattccagagagagatcaccattacccagaggaatccagagagagcc 3651
 Uy 181 TACGCTGAG 240
 Db 3652 tacatgagagctgagagcagctgaagatctgagagacagagccatataattgtgagag 3709
 Uy 241 TTCATTGAGCTGAG 298
 RESULT 14
 ID 092547 standard: DNA: 6166 BP.
 AC 092547;
 DT 11-MAR-1996 (first entry)
 DE Expression vector, pPho-IT.
 KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b5; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
 KW alkaline phosphatase; phoA; ss; cyclic.
 OS Synthetic.
 PN W09511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994: 011907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;

FT	misc_RNA		290..385
FT	/*tag= q		
FT	/label= FR3		
FT	misc_RNA		386..439
FT	/*tag= h		
FT	/label= CDP3		
FT	misc_RNA		440..472
FT	/*tag= i		
FT	/label= FR4		
FT	misc_RNA		473..763
FT	/*tag= j		
FT	/label= CH1		
FT	misc_RNA		764..811
FT	/*tag= k		
FT	/label= HINGE		
FT	misc_RNA		812..1141
FT	/*tag= l		
FT	/label= CH2		
FT	misc_RNA		1142..1462
FT	/*tag= m		
FT	/label= CH3		
FT	TATA_Signal		1566..1571
FT	/*tag= n		
FN	EP-523949-A.		
PD	20-JAN-1993.		
PF	14-JUL-1992.		306420.
PR	15-JUL-1991.		GB-015284.
PR	01-AUG-1991.		GB-016584.
PR	23-MAR-1992.		GB-006284.
PA	(WELL) WELLCOME FOUND LTD.		
P1	Crowe JS, Lewis AP;		
DR	WPJ: 93-019951/03.		
PT	P-PSDB: R31024.		
PT	Prod. of recombinant primate antibodies - useful for treating		
PI	infections caused by hepatitis A, B and C, herpes,		
PI	cycomegalovirus, AIDS, ARC, also treat multiple sclerosis,		
PI	arthritis etc.		
PS	Disclousre; Fig 2: 35pp; English.		
CC	The sequences given in Q3509-100 encode the heavy and light chains		
CC	of Antibody D respectively. Antibody D is a monoclonal antibody which		
CC	was derived from peripheral blood lymphocytes from a hepatitis A virus		
CC	(HAV) sero positive patient. Antibody D is closely related in nature		
CC	to murine antibody B5B3. Total RNA was isolated from antibody D		
CC	expressing cells and polyadenylated RNA was extracted. These polyA		
CC	RNA's were used to prepare a cDNA library which was screened for human		
CC	kappa light (L) chains and two positive clones were detected.		
CC	Further heavy (H) chain clones were also isolated.		
SQ	Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;		

Query Match 38.8%; Score 149; DB 6; Length 1617;
Best Local Similarity 77.6%; Pred.No.1.58e+85;
Matches 224; Conservative 0; Mismatches 73; Indels 12; Gaps 4;

D6	106 gcaatcgtgagggcggaaglaaaagaacgttggtctcgttgcgttcctgcgaagcatc 165
D6	5 GCATCTGGAGGCGTGAAGGTCAAGACCTGGACTTCCTTGTAAGGTCTCTCAAGGCTTC 65
D6	166 ttgaaggcaccttcagacaactatgctatcgaagtgggtgcgacaaagcccccggagcaaggct 225
D6	56 TGAGGAGAACCTTTAGAGGAGGTATGATATACCTGGAGTGGAGCAAGGAACT 125
D6	226 tgaattgatagagggagatcatccctcttttgtt-----ac-ac-----aaccttatc 273
D6	126 TGAATGATGGAGAAAGATCATCTCATTCTTTGGTCTGCCAATATAGCTCAAAATATAGC 185
D6	274 acaaaaacctccaaaggaagagtlcaagatataaccgaggacaatatccacaagacagccccat 333
D6	186 TCAGAAATTCGCGGAGATAGAGTCTGCATATATCGGAGATTCAGCAAGACGCTCTTCAI 245
D6	334 ggagcttgactcagctcttgagctcttgaggaacaggggtgtatctatctgtgtgagagatcgcta 393
D6	246 TGAGCTTAGAGAACCTGAGATCTGAAGAAGACCGCGGATCTATCTATCTATGAGAGGAACTCTCC 305

US-08-844-215-22.rng

[illegible][illegible]

COMMENT

Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:380026
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 391.
 Location/Qualifiers

FEATURES

source

1..420
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATCTGAAGTGGAGCGCGCGGTGTTTGTGTTTGTGTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through
 three rounds of normalization, and was constructed by
 Bento Soares and M. Fatima Bonaldo."
 /clone="619202"
 /clone_1lb="Soares mouse 3NBMS"
 /sex="male"
 /tissue_type="Spleen"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 <1..>420

MRNA
 BASE COUNT 107 a 119 c 99 g 95 t
 ORIGIN

Query Match 8.4%, Score 31, DB 1, Length 420,
 Best Local Similarity 84.4%, Pred. No. 5,19e-21;
 Matches 38, Conservative 0, Mismatches 7, Indels 0, Gaps 0,

Db 99 taacttgactactgggccaagcacactctcacagtctctctca 143
 |||||||||||||||||||
 QY 325 TACTTGACTACTGGGCTCAGSAACTGTGATCAGCTCTCTCTCA 369

Search completed: Tue Feb 24 10:06:13 1998
 Job time : 146 secs.

Contact: KeriLavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018659423
Email: arkerlav@tigr.org
For close availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hqi/hqi.html>)
Seq primer: M3 Reverse.

Query Match	9.28;	Score 34;	DB 26;	Length 273;
Best Local Similarity	63.28;	Prod No 2.95e+26;		
Matches	79, Conservative	0, Mismatches	46, Indels	0, Gaps

RESULT	12
LOCUS	AA326955 280 bp mRNA
DEFINITION	EST
	EST334657 Colom I Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions.

REFERENCE	ATTN:PS	TITLE	COMMENT	FEATURES	BASE COUNT	ORIGIN
1 (bases 1 to 280)						
Adams, M.D., Perlman, A.P., Fleischman, R.D., Fulton, R.A., White, C.J., Lee, N.H., Kitzner, F.F., Weinstock, K.G., Gocayne, J.D., Smit, A.M., Sutton, G., Blake, J.A., Brandon, P.C., Man, Wai, C., Clayton, P.A., Gillet, T.P., Cotton, M.D., Earl, Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fleischman, J.L., Geoghegan, N.S., Gish, W.B., Green, R.L., Hanna, M.C., Hewlett, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, Y.-T., Marmorek, S.M., Merrick, T.M., Moreno, Palanques, P.P., McDonald, L.A., Nguyen, D.T., Pellier, S.M., Phillips, C.A., Prober, E., Scott, J.L., Sauder, D.M., Shultz, R., Small, K.V., Sprague, T.A., Suter, J.C., Telford, I.P., Waldman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinko, D., Peng, D.-F., Perle, A., Fischer, C., Hastings, G.A., He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hung, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, F., Wing, J., Xu, C., Yu, G.L., Rubin, S.M., Dillion, P.J., Fannon, M.P., Kosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Other ESTs: IH0167575						
Contact: Perlman, AR						
Bioinformatics						
The Institute for Genomic Research						
9712 Medical Center Drive, Rockville, MD 20850 USA						
Tel: 3018699056						
Fax: 3018699423						
Email: arkerla@vcitg.org						
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)						
Seq primer: M3 Reverse						
Location/Qualifiers						
1..280						
/organism="Homo sapiens"						
/note="Organ: colon; Vector: pBluescript SK-; Site: 1;"						
ECORI: Site: 2; XhoI						
/clone_lib="Colon 1"						
/dev_stage="adult"						
<1..>280						
53 a	66 c	83 g	72 t	6 others		
Query Match	8 9%	Score 33:	DB 37:	Length 280:		
Best Local Similarity 62.9%:	Refd No. 1746724:					
Matches 78:	Conservative 0:	Mismatches 46:	Indels 0:	Gaps 0:		
Db	128	ctcgtggaagtcctggggagagcgtgtccagccctggagagtcctcgaacatctccatgaca	187			
	1	CTCCAGCAGAGCTCTGG33CTGAGCTGA3AA33CTG33CTCTG3TGA3G3TCTCTT3TCA3	50			
Db	188	ggccctgattcctcttcgtaataatgctatcctacacgtagcgcgcgcagatccagcaag	247			
	61	GTTTTGGACACCTTCACAGACATATTCAGTGTGTTGGTAAAG33GCTTGTGACAA	120			
Db	248	ggagc 251				
	121	GGGC 124				
RESULT 13						
LOCUS	AA327241	326 bp	mrna	EST	20-APR-1997	
DEFINITION	EST30532 Colon 1 Homo sapiens cDNA 5' end similar to immunoglobulin					
ACCESSION	AA327241					
NID	91979485					
KEYWORDS	EST.					
SOURCE	human.					

ORGANISM

Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.

REFERENCE

1 (bases 1 to 291)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, P.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Keller, J.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)

JOURNAL

Medline

96026280

TITLE

COMMENT

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the tigr Human Gene
index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/note="Organ: small intestine; Vector: pBluescript SK-";
Site_1: ECORI; Site_2: XhoI
/clone_lib="Small intestine I"
/dev_stage="adult"
1..>291
BASE COUNT 67 a 73 c 89 g 61 t 1 others
ORIGIN

Query Match

Best Local Similarity 72.9%; Score 97; DB 58; Length 291;
Pred. No. 2,156-157;
Matches 153; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 81 ctgtgacacattctggagctggaagagcctggtctctctgtgaagintcgtcaag 140
QY 1 CTCGAGCAGTGTGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 60
Db 141 gctatgatacaccctacacattatacattacacacacacacacacacacacac 200
QY 61 GTTTTGGAGACCTTACGACGATACACGATACACGATACACGATACACGATAC 120
Db 201 ggaattgagatgagatgagatgagatgagatgagatgagatgagatgagatg 260
QY 121 GGGCTGAGTGTGGAGTAAATATCATCTCTATATATACACCAACCAACCAAC 180
Db 261 ttctggagagagatgacacacacacacacacacacacacacacacacacac 290
QY 181 TTTCAAGGAGACCTCTGCAATACCGCGCGAC 210

RESULT 4 AA377128 265 bp mRNA EST 21-APR-1997
LOCUS
DEFINITION EST89660 Small intestine 1 Homo sapiens cDNA 5' end similar to

ACCESSION

AA377128
2029456
KEYWORDS
EST.

SOURCE

ORGANISM

human.

REFERENCE

1 (bases 1 to 265)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, P.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brannon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Keller, J.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)

JOURNAL

Medline

96026280

TITLE

COMMENT

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the tigr Human Gene
index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..265
/organism="Homo sapiens"
/note="Organ: small intestine; Vector: pBluescript SK-";
Site_1: ECORI; Site_2: XhoI
/clone_lib="Small intestine I"
/dev_stage="adult"
1..>265
BASE COUNT 57 a 69 c 79 g 58 t 2 others
ORIGIN

Query Match

Best Local Similarity 80.0%; Score 89; DB 58; Length 265;
Pred. No. 1,256-135;
Matches 116; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 104 ctgtgacacattctggagctggaagagcctggtctctctgtgaagintcgtcaag 163
QY 1 CTCGAGCAGTGTGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 60
Db 164 antctgttaccacattacacacacacacacacacacacacacacacacacacac 223
QY 61 GTTTTGGAGACCTTACGACGATACACGATACACGATACACGATACACGATAC 120
Db 224 gggctgagatgagatgagatgagatgagatgagatgagatgagatgagatg 248
QY 121 GGGCTGAGTGTGGAGTAAATATCATCTCTATATATACACCAACCAACCAAC 145

RESULT 5 AA402547 266 bp mRNA EST 16-MAY-1997
LOCUS

Df	264	cgcctaaaggtgaatcccgaggagctgacggagagcgttcacgagaccgcccaagctctaac	323			
Cp	92	CTTGTGAAGCCTCCCTCCACAGAGGCGCTTCGAGAAGACTTTCACTGGAAAGAACATTAAGATTTC	33			
Df	324	aagcctccccagaattccaacagttagactc	355			
Cp	32	ACCTCAGAGGCCTCATCTTGACGACCTGGCACCTG	1			
RESULT	6	AS07475	435 bp	mRNA	EST	15-JUL-1997
LOCUS		nh6c05.s1 NCI-CGAP.Br1 Homo sapiens cDNA clone 964424 similar to				
DEFINITION		gb:X14584 IC HEAVY CHAIN PRECURSOR V-II REGION (HUMAN)..				
ACCESSION		AS07475				
NID		92243914				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;				
		Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae;				
		Homo.				
REFERENCE		NCI-CGAP.				
AUTHORS		1 (bases 1 to 435)				
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
JOURNAL		Tumor Gene Index				
COMMENT		Unpublished (1997)				
		Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskaluk, M D , Ph.D , Michael P. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bhrp/image/image.html				
FEATURES		Insert length: 558 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amershan High quality sequence stop: 131. Location/Qualifiers 1..435 /organism="Homo sapiens" /note="Vector: p713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p713 vector. Library is not normalized. (The normalized version of this library is NCI.CGAP.Br2.) Library was constructed by Bento Soares and M. Fatima Bonaldo." /clone_lib="NCI-CGAP.Br1.1" /sex="female, pooled" /tissue_type="breast" /lab_host="DH10B" <1..->435				
BASE COUNT		94 a 128 c 112 g 101 t				
ORIGIN						
Query Match		7.9%: Score 30; DB 40; Length 435; Best Local Similarity 66.3%; Pred. No. 2.73e-17;				
Matches		61: Conservative 0; Mismatches 31; Indels 0; Gaps 0;				
Df	264	ctgcctaaaggtgaatcccgaggagctgacggagagcgttcacgagaccgcccaagctctaac	323			
Cp	92	CTTGTGAAGCCTCCCTCCACAGAGGCGCTTCGAGAAGACTTTCACTGGAAAGAACATTAAGATTTC	33			
Df	324	aagcctccccagaattccaacagttagactc	355			

[illegible]

mRNA <1 >403
 BASE COUNT 64 a 136 c 110 g 93 t
 ORIGIN
 Query Match 5 64 Score 21; PR 44; Length 483;
 Best Local Similarity 74.4%; Pred. No. 1.46e-04;
 Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 154 gttcgcagacgagatggtcgcacagctgcgcgaactcagc 196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 359 GTTCCGTGCGCCGCGGCTGGAAACGAGCGCCAGCAACTTCAC 317

RESULT 13
 ID HS1138859 standard; RNA; EST; 288 BP.
 AC AA078241;
 NI 91837717
 DT 13-FEB-1997 (Rel. 50, Created)
 DT 13-FEB-1997 (Rel. 50, Last updated, Version 1)
 DE 7H16206 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone
 DE 7H16206.
 KW EST.
 OS Homo sapiens (human)
 OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo
 RN [1]
 RP 1-288
 RA Touchman J.W., Bouffard G.S., Weintraub L.A., Idol J.F., Wang L.,
 RA Robbins C.M., Nisbaum J.C., Lovett M., Green E.D.;
 FT "2.0% Expressed-Sequence Tags Derived from Human Chromosome
 FT 7-Enriched cDNA Libraries";
 RL Genome Res. 7:0-0(0).
 CC Contact: Eric D. Green Genome Technology Branch National Human
 CC Genome Research Institute/NIH 49 Convent Dr., MSC4431, Building 49,
 CC Room 2A08, Bethesda, MD 20892 Tel: 3014020201 Fax: 3014024735
 CC Email: egreen@nhgri.nih.gov Plate: 16 row: G column: 06 Seq primer:
 CC -21M13 (AB1).
 FH Key
 FH Location/Qualifiers
 FT 1..288
 FT source
 FT /organism="Homo sapiens"
 FT /note="Vector: PAM10; cDNA was generated from cytoplasmic
 FT RNA using a mixture of random DNA hexamers and oligo(dT).
 FT From this pool of cDNA, human chromosome 7-enriched cDNA
 FT was isolated by direct cDNA selection using chromosome 7
 FT genomic DNA (cosmids). The resulting direct-selected cDNA
 FT was cloned into a plasmid vector using a non-directional
 FT uracil DNA glycosylase (UDG)-mediated cloning strategy."
 FT /clone="7H16206"
 FT /clone_lib="Chromosome 7 HeLa cDNA Library"
 FT /sex="female"
 FT /cell_line="HeLa cell line; ATCC"
 FT /lab_host="E. coli strain DH5 alpha"
 FT <1 >288
 FT mRNA
 FT Sequence 288 BP; 75 A 87 C 72 G 53 T 1 other.

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 Best Local Similarity 80.5%; Pred. No. 2.42e-03;
 Matches 33; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Db 216 caaacactcagacacatagctgctgctgagctgctgctgctgca 256
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 302 CAAACATTGCATGCTGGAG-ITCTGGGCTGGTGGTGGCA 341

RESULT 14
 LOCUS HUMSWS3933 302 bp cDNA STS
 DEFINITION human chromosome 7 STS SWSS3933.
 ACCESSION G31805
 NID g1916530
 KEYWORDS STS sequence, primer, sequence tagged site.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.
 1 (bases 1 to 302)
 Bouffard G.S., Lovett M., Idol J.F., Braden V.V., Cunningham A.E.,
 Weintraub L.A., Mohr-Tidwell P.M., Peluso D.C., Fulton P.S.,
 Leckie M.P. and Green E.D.
 A collection of 18.4 human chromosome 7-specific STS
 Genome Res. 7 (1): 59-64 (1997)
 97189344
 2 (bases 1 to 302)
 Green E.D.
 Human chromosome 7 STS
 Unpublished (1997)
 Contact: Eric D. Green
 Genome Technology Branch
 National Human Genome Research Institute/NIH
 49 Convent Dr., MSC4431, Bldg 49, Rm 2A08, Bethesda, MD 20892
 Tel: 3014020201
 Fax: 3014024735
 Email: egreen@nhgri.nih.gov
 Primer A: CTACACCTTCATCTTC
 Primer B: CTAAGTTCATGTTATCACC
 STS size: 134
 PCR Profile:
 Presoak: 0 degrees C for 0.00 minute(s)
 Denaturation: 92 degrees C for 0.17 minute(s)
 Annealing: 55 degrees C for 1.00 minute(s)
 Polymerization: 72 degrees C for 1.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: PerkinElmer 9600
 Protocol:
 Template: 30-100 ng
 each 1 uM
 DNTPs: each 200 uM
 Tag Polymerase: 0.05 units/ul
 Total Vol: 10 ul
 Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3
 The sequence for this STS was derived from a single sequencing
 read. For additional information about the NHGRI chromosome 7
 mapping project, see <http://www.nhgri.nih.gov/DIR/STG/STG7/>. Also
 see Genomics 11:548-64 (1991) (url:90128337).
 FEATURES
 source
 1..302
 /organism="Homo sapiens"
 /map="77"
 STS
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 BASE COUNT 95 a 70 c 70 g 67 t
 ORIGIN

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 Best Local Similarity 75.0%; Pred. No. 2.42e-03;
 Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 128 gctggccacagaaactcgaagaagccagccgaagg 167
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 197 GCAAGATACATTAACGCGGAGAGGATACAGCGGCAAGG 236

RESULT 15
 LOCUS HUMSWS3933 302 bp cDNA STS
 DEFINITION human chromosome 7 STS SWSS3933.
 ACCESSION G31805

Search completed: Tue Feb 24 13:44:30 1998
Job time : 374 secs.

NTD
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 302)
AUTHORS Bouffard, G. G., Iyer, L. M., Idol, J. P., Braden, V., Cunningham, A. F.,
Weintraub, L. A., Mohr-Tidwell, R. M., Peluso, D. C., Fulton, R. S.,
Leckie, M. P., and Green, E. D.
TITLE A collection of 1814 human chromosome 7-specific STSs
JOURNAL Genome Res. 7 (1), 59-64 (1997)
MEDLINE 97189344
REFERENCE 2 (bases 1 to 302)
AUTHORS Green, E. D.
TITLE Human chromosome 7 STSs
JOURNAL Unpublished (1997)
COMMENT
Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: edgreen@nhgri.nih.gov
Primer A: CTACACACCTTCATCTTC
Primer B: CTAAGTTCATTGTATCACC
STS size: 134
PCR Profile:
Presoak: 0 degrees C for 0.00 minute(s)
Denaturation: 92 degrees C for 0.17 minute(s)
Annealing: 55 degrees C for 1.00 minute(s)
Polymerization: 72 degrees C for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600
Protocol:
Template: 30-100 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

The sequence for this STS was derived from a single sequencing read. For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID-92128937].

FEATURES
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/organism="Homo sapiens"
/map="7"
STS 109..242
primer_bind 109..126
primer_bind complement(21..242)
BASE COUNT 95 a 70 c 67 t
ORIGIN
Query Match 5.3%; Score 20; DB 12; Length 302;
Best Local Similarity 75.0%; Prev No 2.42e-03;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 128 gctggccacgaagaaactcggaagaaagccacgacgcaaaag 167
197 GLAGAGTCACAAATACCGCGGACGCAATCCACGCGCACAGG 236

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 2287 BP; 483 A; 752 C; 654 G; 398 T; 0 other;

Query Match 69.6%, Score 263; DB 14; Length 2287;
Best Local Similarity 86.6%; Pred. No. 8,68e-184;
Matches 329; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

Db 74 AGGTGACAGCTGCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCT 133
|||||
Oy 2 AGGTGACAGCTGCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCT 61
Db 134 CCTGCAAGGCTTCTGAGAGCAGCTTCAAGCAGTATGCTATGAGTGGGCGAGAGCC 193
|||||
Oy 62 CCTGCAAGGCTTCTGAGAGCAGCTTCAAGCAGTATGCTATGAGTGGGCGAGAGCC 121
Db 194 CTGGCAAGGCTTCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCTAG 253
|||||
Oy 122 CTGGCAAGGCTTCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCTAG 181
Db 254 CACAGAACTTCCAGGAGAGATCAGATTCAGCGGAGCAATCCAGAGACAGAGCTTAC 313
|||||
Oy 182 CACAGAACTTCCAGGAGAGATCAGATTCAGCGGAGCAATCCAGAGACAGAGCTTAC 241
Db 314 TGGAGCTGAGCAGCCTGAGATCTGAGAGCAGCGGCTGTATTAATGCTGGAGAGATATG 373
|||||
Oy 242 TGGAGCTGAGCAGCCTGAGATCTGAGAGCAGCGGCTGTATTAATGCTGGAGATCCCTATC 301
Db 374 GAGGCTATTGAGTGTGATGCTGATCTGAGTGGGCTGGTGGAGCCCTGGGCGAGAGAA 433
|||||
Oy 302 CAAAGATTCAGTGTGAGAGTGTG---GGGCTGTGTGAGCCCTGGGCGAGAGAA 358
Db 434 CCTGTGTACCGTCTCTTCA 453
|||||
Oy 359 CTGTGTACCGTCTCTTCA 378

RESULT 2
ID US-07-834-539A-53 STANDARD; DNA: UNC; 812 BP.
DT 01-JAN-1900
AC xxxxxx
DE Sequence 53, Application US/07834539A.
CC Sequence 53, Application US/07834539A
CC Patent No. 5633425
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 77
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/834,539A
CC FILING DATE: 19920205
CC CLASSIFICATION: 600
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600

CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 812 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 241..335
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 372..677
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
SQ Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

Query Match 59.0%, Score 223; DB 7; Length 812;
Best Local Similarity 88.3%; Pred. No. 3.72e-152;
Matches 257; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 385 AGGTGACAGCTGCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCT 444
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Oy 2 AGGTGACAGCTGCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCT 61
Db 445 CCTGCAAGGCTTCTGAGAGCAGCTTCAAGCAGTATGCTATGAGTGGGCGAGAGCC 504
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Oy 62 CCTGCAAGGCTTCTGAGAGCAGCTTCAAGCAGTATGCTATGAGTGGGCGAGAGCC 121
Db 505 CTGGCAAGGCTTCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCTAG 564
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Oy 122 CTGGCAAGGCTTCTGAGTGGGCTGAGTGAAGAGCCTGGGCTCTGGTGAAGTCTAG 181
Db 565 CACAGAACTTCCAGGAGAGATCAGATTCAGCGGAGCAATCCAGAGACAGAGCTTAC 624
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Oy 182 CACAGAACTTCCAGGAGAGATCAGATTCAGCGGAGCAATCCAGAGACAGAGCTTAC 241
Db 625 TGGAGCTGAGCAGCCTGAGATCTGAGAGCAGCGGCTGTATTAATGCTGGAG 575
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Oy 242 TGGAGCTGAGCAGCCTGAGATCTGAGAGCAGCGGCTGTATTAATGCTGGAG 292

RESULT 3
ID PCT-US92-06185-53 STANDARD; DNA: UNC; 812 BP.
DT 01-JAN-1900
AC xxxxxx
DE Sequence 53, Application PC/TUS9206185.
CC Sequence 53, Application PC/TUS9206185
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 75
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/06185
CC FILING DATE: 19910828
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.

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CC REGISTRATION NUMBER: 47654
CC REFERENCE/DOCKET NUMBER: 14643-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 812 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 241..335
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 373..677
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
CC Sequence 812 bp: 204 A; 188 C; 223 G; 197 T; 0 other;

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CC NUMBER OF SEQUENCES: 70
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute
 CC STREET: 10666 North Torrey Pines Road, TPC8
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/11235
 CC FILING DATE: 01-SEP-1995
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/300,386
 CC FILING DATE: 02-SEP-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/826,623
 CC FILING DATE: 27-JAN-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1 (PC)
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 687 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC Sequence 687 BP: 155 A; 211 C; 195 G; 126 T; 0 other;
 Query Match 51.98; Score 196; DB 13; Length 687;
 Best Local Similarity 85.58; Pred. No. 6,60e-131;
 Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

D8 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 67
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 D17 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 76
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 D68 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 127
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 D77 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 136
 |||||
 D128 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 187
 |||||
 D137 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 196
 |||||
 D188 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 247
 |||||
 D197 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 256
 |||||
 D248 TGACATCTGAGAGAGCGCCCAATATATATGTCGGA 283
 |||||
 D257 TGACATCTGAGAGAGCGCCCAATATATGTCGGA 292
 |||||

RESULT 8
 ID US-08-300-386A-1 STANDARD: DNA: UNC: 687 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application US/08300386A.
 CC Sequence 1, Application US/08300386A
 CC Patent No. 5667988
 CC GENERAL INFORMATION:
 CC APPLICANT: Barbas, Carlos F, III
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
 CC NUMBER OF SEQUENCES: 70
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute
 CC STREET: 10666 North Torrey Pines Road, TPC8
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/300,386A
 CC FILING DATE: 02-SEP-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/826,623
 CC FILING DATE: 27-JAN-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 687 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC Sequence 687 BP: 155 A; 211 C; 195 G; 126 T; 0 other;
 Query Match 51.98; Score 196; DB 7; Length 687;
 Best Local Similarity 85.58; Pred. No. 6,60e-131;
 Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

D8 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 67
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 D17 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 76
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 D68 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 127
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 D77 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 136
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 D128 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 187
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 D137 AGTGTGGGCTGAGTGAAGAGCTGGTCTGCTGAGAGTCTCTCAGAGCTTCTG 196
 |||||
 D188 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 247
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 D197 GAGGACCTTCACAAATATGTCATGCTGGTGGCAGAGGCGCTTGACAAAGGCTTG 256
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 D248 TGACATCTGAGAGAGCGCCCAATATATATGTCGGA 283
 |||||
 D257 TGACATCTGAGAGAGCGCCCAATATATGTCGGA 292
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QY 77 GAGGAGCTTCAGAACTTCAATTGCGGTGCGACAGGCCCTCGACAGCTCTTG 136
 DB 128 AGTGGATGGAGGAGGATCTTCCTTCCTTAATACAGAAAGTACGACACACTTCGAG 187
 QY 137 AGTGGATGGAGGAGGATCTTCCTTCCTTAATACAGAAAGTACGACACAGAGTTTACG 196
 DB 188 GCAGAGCTCACCTTACCGGCGAGCAATCCAGGGGACGCTACATGAGCTGACGACC 247
 QY 197 GCAGAGCTCACCTTACCGGCGAGCAATCCAGGGGACGCTACATGAGTTGAGCAGTC 256
 DB 248 TGAGATCTGAGGACAGGGCCATATATTGTTGCGA 283
 QY 257 TGAGATCTGAGGACAGGGCCATATATTGTTGCGA 292
 RESULT 9
 ID PCT-US94-01258-1 STANDARD; DNA; UNC; 687 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application PC/TUS9401258.
 CC Sequence 1, Application PC/TUS9401258
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC TITLE OF INVENTION: USING UNIVERSEAL OF RANDOMIZED IMMUNOLOGICAL LIGHT
 CC CHAINS
 CC NUMBER OF SEQUENCES: 61
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/01258
 CC FILING DATE: 02-FEB-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 687 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHEICAL: NO
 CC ANTI-SENSE: NO
 SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T; 0 other:
 Query Match 51.9%; Score 196; DB 12; Length 687;
 Best Local Similarity 85.5%; Pred. No. 6,60e-131;
 Matches 236, Conservative 0; Mismatches 40; Indels 0; Gaps 0.

QY 257 TCGAGCTGAGAGACAGCGCCCTTATTACTGTCCGA 292
 RESULT 10
 ID US-08-264-093-1 STANDARD; DNA; UNC; 363 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application US/08264093.
 CC Sequence 1, Application US/08264093
 CC Patent No. 5639863
 CC GENERAL INFORMATION:
 CC APPLICANT: Michael D. Dan
 CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
 CC TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Ridout & Maybee
 CC STREET: 2300 Richmond-Adeleide Centre
 CC STREET: 101 Richmond Street West
 CC CITY: Toronto
 CC STATE: Ontario
 CC COUNTRY: Canada
 CC ZIP: M5H 2J7
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: MS-DOS 6.00
 CC SOFTWARE: ASCII Editor
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/264,093
 CC FILING DATE:
 CC CLASSIFICATION: 536
 CC PRIOR APPLICATION DATA: No. 5639863 applicable
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Lake, James R.
 CC REGISTRATION NUMBER: 31081
 CC REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (416) 868-1482
 CC TELEFAX: (416) 362-0823
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 363 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single stranded
 CC TOPOLOGY: linear
 SQ Sequence 363 BP; 84 A; 97 C; 108 G; 74 T; 0 other:
 Query Match 45.5%; Score 172; DB 7; Length 363;
 Best Local Similarity 79.7%; Pred. No. 4.11e-112;
 Matches 231, Conservative 0; Mismatches 59; Indels 0; Gaps 0.

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CC nucleotides long. Different immunoglobulins produced using the
CC primers may be used to produce antibody libraries having diverse and
CC novel immunospecificities and affinities. By using mutagenic ONS an
CC extremely large population of different randomised binding sites can
CC be created and use of the universal light chain increases the number
CC of combinations which yield functional heterodimeric antibodies.
SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T;

Query Match 51.9%; Score 196; DB 22; Length 687;
Best Local Similarity 85.5%; Pred. No. 1.72e-117;
Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

DB 8 agctggagcgtgaagtaagaagcctggtctcgtggaagctctcgtgaagcctcgtg
OY 17 AGCTGGGCTCTGAGGTGAGAGAGCCTGGGTTCTTGGTGAAGGTCTCTGAGGCTCTG 76
DB 68 gaggcaaccttaacaatgatccacgtggtgacagagccctggaagagcttg 127
OY 77 GAGGAGCCTTCAAGAGCTACAAATTCATTGGGTGGCAGAGCCCTGAGCAAGTCTTG 136
DB 128 agtggatggagagatcttccttcctgtaataacagcaagtaacacacacccag 187
OY 137 AGTGGATGGAGGAGCTATCCCTATGTTGGACAGCAAACTACGACAGAGTTTACG 196
DB 188 gcaagatcacattaccgcgcagcaatccacagcagcctacatgagctgagcagcc 247
OY 197 GCAGAGTACAAATTCACCGGACCAATCCACGCCACAGCTACATGAGTTGAGCAGTC 256
DB 248 tgaagatctgaagacacgagccatataattatgtgcga 283
OY 257 TGAGATCTGAGAGACAGCGCCCTTATTACTGTGCCA 292

RESULT 15
ID 092546 standard; DNA: 4691 BP.
AC 092546;

DT 11-MAR-1996 (first entry)
DE pComb3 expression vector.
KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;
KW Gene III; filamentous phage; minor phage coat protein; cpII; cp3;
KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120;
KW combinatorial Fab library; cassette; Fd/cp3; lacZ promoter/operator;
KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;
KW MT4; pMT4-3; antibody; ss; cyclic.
OS Synthetic.
PN MO9511317-A1.
PD 27-APR-1995.
PF 19-OCT-1994; U11907.
PR 19-OCT-1993; US-139409.
PR 26-APR-1994; US-233619.
PR 19-SEP-1994; US-308841.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 95-170235/22.
PT Synthetic human neutralising monoclonal antibodies to human
PT Immunodeficiency virus - used for diagnosis and Immuno:therapy of
PT HIV-induced disease
PS Example 1; Page 185-188; 249pp; English.
CC This sequence represents the pComb3 phagemid expression vector. This
CC vector has been designed to allow for anchoring of expressed proteins on
CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
CC the 406 residue minor phage coat protein, cpII (cp3), which is expressed
CC prior to extrusion in the phage assembly process on a bacterial membrane
CC and accumulates on the inner membrane facing into the periplasm of E.
CC coli. This plasmid was used within the scope of the invention to express
CC various mutagenised human Fab's which comprise heavy and light variable
CC regions which bind to HIV gp120. pComb3 allows for both surface display
CC and soluble forms of the Fabs. The vector was designed for the cloning
CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
CC two cassettes to express one fusion protein, Fd/cp3, and one soluble
CC protein, the light chain. The finished vector comprises, operatively
CC linked, 5' to 3', a first cassette consisting of lacZ promoter/operator
CC sequences, a NotI restriction site, a ribosome binding site (RBS), a

CC PelB leader, a spacer region, a cloning region bordered by 5' XhoI and
CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
CC bacteriophage cpI followed by a stop codon, a NotI restriction site
CC between the two cassettes, and a second lacZ promoter/operator sequence,
CC followed by an expression control RBS, a PelB leader, a spacer region, a
CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
CC followed by expression control stop sequences and a second NotI
CC restriction site. The pComb3 expression vector forms the basic construct
CC of the MT4 Fab display phagemid expression vector, pMT4-3 (see also
CC 092540), used in the invention for the production of synthetic human Fab
CC antibodies against gp120 of HIV.
SQ Sequence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T;

Query Match 51.9%; Score 196; DB 16; Length 4691;
Best Local Similarity 85.5%; Pred. No. 1.72e-117;
Matches 236; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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DB 3491 gaggcaaccttaacaatgatccacgtggtgacagagccctggaagagcttg 3550
OY 77 GAGGAGCCTTCAAGAGCTACAAATTCATTGGGTGGCAGAGCCCTGAGCAAGTCTTG 136
DB 3551 agtggatggagagatcttccttcctgtaataacagcaagtaacacacacccag 3610
OY 137 AGTGGATGGAGGAGCTATCCCTATGTTGGACAGCAAACTACGACAGAGTTTACG 196
DB 3611 gcaagatcacattaccgcgcagcaatccacagcagcctacatgagctgagcagcc 3670
OY 197 GCAGAGTACAAATTCACCGGACCAATCCACGCCACAGCTACATGAGTTGAGCAGTC 256
DB 3671 tgaagatctgaagacacgagccatataattatgtgcga 3706
OY 257 TGAGATCTGAGAGACAGCGCCCTTATTACTGTGCCA 292

Search completed: Tue Feb 24 13:18:47 1998
Job time : 105 secs.

(TM)

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FEATURES
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              /note="G00-118-731"
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              /product="Ig heavy chain"
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              /translation="MDPTMRPLFVMAATGOSVOLNOSGAEVKKKSSVYSCKAS
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              SLRSEDTAVYCARGGMGVSGSGCYWEPDPOGTLTVSS"
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              /note="G00-118-731"
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              /product="Ig heavy chain"
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              /note="G00-118-731"
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              /note="G00-118-731"
              /codon_start=1
              /product="Ig heavy chain"
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  exon        143..528
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  Query Match      67.2% Score 254; DB 99; Length 528:
  Best Local Similarity 85.7% Pred. No. 4,95e-200:
  Matches 323; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
  Db 155 aggtcagctggtgacgtctggagctggaagctggaagctggtcctcggtgaagctc 214
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  QY 2 AGGTGACAGCTCTGAGAGCTGTGGGTCTGAGTGAAGAAAGCTGGGTCTCGTGAAGCTCT 61
  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
  Db 215 cctgcaagctcttgaaagcactcaagcactatgcatagctgggttgagcaagccc 274
  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
  QY 62 CCTGCAAGGCTCTGAGAGCTGTGGGTCTGAGTGAAGAAAGCTGGGTCTCGTGAAGCTCT 121
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  Db 275 ctgcaagagcttgatgagctggaagcactcactcctatcttgatgagcaagcactag 334
  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
  QY 122 CTGCAAGAGCTCTGAGTGAAGTGAAGCATTCAATTTCAATTTGGGTGCGAGAGGCC 181
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  Db 335 cagcaagcttcagagcagagctcaagctatccagcagcgaatccagcagcagcctaca 394
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  QY 182 CACAGAGATTGAGGAGAGCTCACAAATTACCGGAGAGATCCAGCGCACAGGCTTACA 241
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  Db 395 tggagctgagcagccttgagctgagcagcagcagcagcagcagcagcagcagcagc 454
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  QY 242 TGGAGTTGAGCAGCTGTGAGATCTGAGACAGCGCGTTTATTACTGTGCATGCCCATC 301
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  Db 455 tgggatatgtgagtggtgagctgcta---ctggttcgacccctgggccaaggaacc 511
  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
  QY 302 CAAAACATTGCGAGTGTGAGATTGCTGGGCTGTGACCCCTCGGGGCGAGGAACTC 361
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  QY 362 TGGTACCGCTGTCTTCA 378
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LOCUS      HS202E5      507 bp      RNA      PRI      03-AUG-1995
DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 202-E5).
ACCESSION  Z47258
NID        9619469
KEYWORDS   immunoglobulin; variable region.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Eukaryota; Eukaryota; Eukaryota; Eukaryota;
            Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 507)
            Lebecque, S.
            Direct Submission
            Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
            Scleriting Plough, Laboratory for Immunological Research, 27, Chemin
            des Peupliers, B.P. 11 CEDEX, Bardilly, France, 69572, FRANCE
            2 (bases 1 to 507)
            Bancheau, J., van Dooren, J., Durand, L., Pousset, F., Taffris, P.,
            Galibert, L., van Dooren, J., Durand, L., Pousset, F., Taffris, P.,
            Bancheau, J., van Dooren, J., Durand, L., Pousset, F., Taffris, P.,
            Anti-CD40 plus interleukin-4-activated human naive B cell lines
            express unmutated immunoglobulin genes with intrachain heavy chain
            isotype variability
            Eur. J. Immunol. 25 (3), 733-737 (1995)
            9520422
FEATURES
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  Best Local Similarity 83.0% Pred. No. 2.02e-195:
  Matches 313; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
  Db 59 aggtcagctggtgacgtctggagctggaagctggaagctggtcctcggtgaagctc 118
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  QY 2 AGGTGACAGCTCTGAGAGCTGTGGGTCTGAGTGAAGAAAGCTGGGTCTCGTGAAGCTCT 61
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  QY 62 CCTGCAAGGCTCTGAGAGCTGTGGGTCTGAGTGAAGAAAGCTGGGTCTCGTGAAGCTCT 121
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  Db 179 ctgcaagagcttgatgagctggaagcactcactcctatcttgatgagcaagcactag 238
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  QY 122 CTGCAAGAGCTCTGAGTGAAGTGAAGCATTCAATTTCAATTTGGGTGCGAGAGGCC 181
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  Db 239 cagcaagcttcagagcagagctcaagctatccagcagcgaatccagcagcagcctaca 298
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  QY 182 CACAGAGATTGAGGAGAGCTCACAAATTACCGGAGAGATCCAGCGCACAGGCTTACA 241
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  Db 299 tggagctgagcagccttgagctgagcagcagcagcagcagcagcagcagcagcagc 358
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  QY 242 TGGAGTTGAGCAGCTGTGAGATCTGAGACAGCGCGTTTATTACTGTGCATGCCCATC 301
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  QY 302 CAAAACATTGCGAGTGTGAGATTGCTGGGCTGTGACCCCTCGGGGCGAGGAACTC 361
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  QY 362 TGGTACCGCTGTCTTCA 378
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  LOCUS      HS202E4      507 bp      RNA      PRI      03-AUG-1995
  DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 202-E4)
  ACCESSION  Z47257
  NID        9619468
  KEYWORDS   immunoglobulin; variable region.
  SOURCE     human.
  ORGANISM   Homo sapiens

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Oy	2 AGGTGAGCGCTGCTCGAGTCGTGGGCTTGAGGTGAAGAACCCTGGGCTTCGTGAAGTCT 61												
Dn	156 ccctgcaagcctcttgaggacacctcaaaagtaactgtacaactgggtgcgaagccc 215												
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Dn	216 ctggacaagcctctgtgtgatggaggcatcacctccattcttgtttacagcaaatag 275												
Oy	122 CTGGACAAGGCTCTTGAGTGGATGGAGGATCATATCTTATTTGGAAACGCAAACTACG 181												
Dn	276 cacagagctccagggacgaactcacattaccgcggaagcaatcacagacagacactaca 335												
Oy	182 CACAGAAAGTTTCAGGCGCAGAGTCACAAATTACGCGGAGAAATCGACGGCCACAGGTACA 241												
Dn	336 ttgagacctgagcagccccaatcttgatgacaagcgccggtattctctgtgcgagagaatac 395												
Oy	242 TCGAGTTGACCACTCTGAGATCTGAAGACAGGCCGCTTATTACTGTGCCATCCCCCTCA 301												
Dn	396 tcgatatctcggaacttatatttcttcacggttgcttgactcctggcgccagagaa 455												
Oy	302 CAATAAGCTT-GCAGTCTGTGGAAGT--TCTTGGGCTTGTTTGACACCTCGGCGCACAGGAA 358												
Dn	456 occctgtacacgtctcccca 475												
Oy	359 CTCGTGTCACCGTGTCTTCA 378												
RESULT	LOCUS	DEFINITION	ACCESSION	NID	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	FEATURES	source
8	HS22JM3	480 bp RNA	P1	03-MYC-1995		Homo sapiens	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	1 (bases 1 to 480)	Lebecque,S. Direct Submission Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Schering-Plough, Laboratory for Immunological Research, 27, des Peupliers, B.P.11 CEDEX, Dardilly, France, 69572, FRANCE 2 (bases 1 to 480) Calbert,L., van Dooren,J., Durand,I., Roussel,F., Jefferis,K., Banchereau,J. and Lebecque,S. Anti-CD40 plus interleukin-4-activated human naive B cell lines express unmutated immunoglobulin genes with intralocational heavy chain isotype variability Eur.J. Immunol. 25 (3), 733-737 (1995)	9520422	Location/Qualifiers 1..480 /organism="Homo sapiens"		

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Qy	2	AGGTCACTGCTGCTGAGTCTGGGTGTGAGGTGAACAAACCTGGGCTTGGGTGAAGGCTCT	61	
Db	119	ccctgaagaagctcttgaagagcacttcaacagctatgcatcaagctgggttgcagaagccc	178	
Qy	62	CCTGAGAGGCCCTCTGACCGCACGCTTCAAAAGCTAAATTTTAATTTGGGTGGAGAGGCC	121	
Db	179	ctggaacaagggtctgaagtgaatgggaaggatcatccctctcttggtagcaagaactacg	238	
Qy	122	CTGGACAAGGCTTTAGTGTGATGGAGAGCATCATCTATGTTGGAAACAGCAAACTACG	181	
Db	239	cacagaagttcccaaggcagagatcacgattlaccgcgagacgaalccaagacacagactaca	298	
Qy	182	CACAGAACTTTAGGGCAGAGTCACAAATTAACGGGAGAAATCCAGCGCCACAGGCTTCA	241	
Db	299	tggagctgaagcagccctgaagatctgaagaaacagccggttatacactgtgcaagtgaagat	358	
Qy	242	TGGAGTTGAGCGCTGTGATCTCTGAAGACACGGCGGCTTTATTACTGTGCGATGGCCATTC	301	
Db	359	gggagaagttgtagtgtgtgtgtgctgcactcaagagatatagaacgtctctggggccaaygacca	418	
Qy	302	CAAAAATTGCGTGTGTGAAGTTGCTTGGGGCTGTGTTGACCCCTCGGGGCCAAGGAACTC	361	
Db	419	cggtacacgtctcccca	435	
Qy	362	TGGTCAACCGTGTCTTCA	378	

RESULT	10			PRI	03-AUG-1995
LOCUS	HS203M5	483 bp	RNA		
DEFINITION	H.sapiens mRNA for immunoglobulin variable region (clone 203-M5).				
ACCESSION	Z47272				
MID	9619483				
KEYWORDS	immunoglobulin; variable region.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;				
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 483)				
JOURNAL	Lebecque, S.				
	Direct Submission				
	Submitted (14-Dec-1994) Serge Lebecque, Molecular Biology,				
	Schering-plough, Laboratory for Immunological Research, 27, Chemin				
	des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69592, FRANCE				
	2 (bases 1 to 483)				
	Gailbert,L., van Dooren,J., Durand,I., Rousset,F., Jefferis,R.,				
	Banchereau,J. and Lebecque,S.				
	Anti-CD4 plus interleukin-4-activated human naive B cell lines				
	express unmutated immunoglobulin genes with intracellular heavy chain				
	isotype variability				
	Eur. J. Immunol. 25 (3), 733-737 (1995)				
	95220422				
TITLE	Location/Qualifiers				
JOURNAL MEDLINE FEATURES	1..483				
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	/tissue.type="blood"				
	/cell-type="B-lymphocyte"				
BASE COUNT	95 a 128 c 156 g 104 t				
ORIGIN					

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	Best Local Similarity	98.9%	Ped.	6.82e-190;	
	Matches	319; Conservative	0; Mismatches	58; Indels	3; Gaps
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Qy	2	AGGTCACACTGCTCGAGTCTGGGTGTGAAGTAACAACCCTGGGCTCTCGGTGAAGGCTC	61		

Db	119	ccctcgaagctctcttgaaagcactctcaacaactatgtatcaacctggatggaacagacc	178
Qy	62	ccctcgaagcgcctctgtagagcagaccttcaaaagcttgcatttcaatttggctgcacagcc	122
Db	179	cttgacaagaagccttgagtgatgggaaggatcatccctatcctttgttgacagcaactacg	235
Qy	122	cttgacacaaagctcttgatgttgatgagagggacatcatctcttattgttggcaaaagtaaacctaacg	181
Db	239	cacagaagctccacgagccagagtcacagatctaccggcgacaatcccaagacacagacttaca	298
Qy	182	cacagaagcttccagggcagacagtcacaaattaccggcgacacatccacagggccacagacttaca	241
Db	299	tggagcctgaaacagccctgaagatcttgaaagacagagccctgatattcgttggaagagggggg	358
Qy	242	tggagcttgaaacagctctgaaatcttgaaagacagagccgcttttttactgttggaag-gccctat	300
Db	359	ctaaagctcgaatttttgaaatgagtttcaatgagtaagttcgaaacccctgagccagagaa	418
Qy	301	ccaaacacattgcagctgttgaaagttgc-tggag-ctggcttgagaccccttgagccacagaa	358
Db	419	ccctgagctacagctctccca	438
Qy	359	ctctgtgtcacctgtcttca	378

LOCUS	HS203E7	510 bp	RNA	PRI	03-AUG-1995
DEFINITION	H sapiens mRNA for immunoglobulin variable region (clone 203-E').				
ACCESSION	247266				
NTD	9619477				
KEYWORDS	immunoglobulin; variable region.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Carnivora; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 510)				
TITLE	Lebecque,S.				
JOURNAL	Direct Submission				
	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Peupliers, B.P.11 CEDEX, Darailly, Rhone, 69572, FRANCE				
REFERENCE	2 (bases 1 to 510)				
AUTHORS	Galibert,L., van Dooren,J., Durand,I., Rousset,F., Jefferis,R., Banchearea,J. and Lebecque,S.				
TITLE	Anti-CD40 plus interleukin-4-activated human naive B cell lines express unmutated immunoglobulin genes with intrachain heavy chain isotype variability				
JOURNAL	Eur.J. Immunol. 25 (3), 733-737 (1995)				
MEDLINE	95220422				
FEATURES	Location/Qualifiers				
source	1..510				

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Best Local Similarity	83.9%	Pred. No. 6,82e-190;			
Matches	319; Conservative	0; Mismatches 58; Indels 3; Gaps 3;			
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OY	2 aggtgcacactctctgcagctctggctctgagcgaagaagccttgagctcttcggtaaagctct	61			
Db	119 cctgcaaggtctctcgtgaagcacccttcacagcctatgctacaagctgggtgcgaagccct	178			
OY	62 cctgcagagcctctctggaagcaggtttcagaagctaaacatttcaatttgagtgccacgaagcc	121			
Db	119 ctggaacaaggtcttgatgtgatgtggaaggaatccctactcttggtataagcaaacactaag	238			
OY	122 ctggcacaaggtcttgatgaggaatgggaagcctatcattccctatggtggaaacgcaaacactaag	181			

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Db	299	tggagctgcagcaacccccaagatctcgagacacagcgccgtatlaactgtgcagaagagggg	358
Oy	242	TGGAGTTAGACAAATCTTGAGATCTGAAAGACAGGCGCTTTATTCGTGTGGAT-GGCCATAT	300
Db	359	ctaaagtcgaatttttgcgaatggtttcatbgtatcctgttcgaacccctcggggccagggaa	418
Oy	301	CCAAACATTCGACGTGTTGGAAGTTGC-TGGCG-CTGTGTTGACCCCTCGGGCCAGGGAA	358
Db	419	ccctgcgtcacgcgtctctca	438
Oy	359	CTCTGCTCACCGCTGCTTCA	378

RESULT	LOCUS	LOCUS	LOCUS	LOCUS
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DEFINITION	H.sapiens mRNA for immunoglobulin variable region (clone 203-E5).			
ACCESSION	Z47267			
NID	9619478			
KEYWORDS	immunoglobulin: variable region.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;			
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 510)			
JOURNAL	Lebecque S.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,			
TITLE	Scherling-Pouoh, Laboratory for Immunological Research, 27, Chemin			
JOURNAL	des Peupliers, B P 11 CEDEX, Dardilly, Phone, 69572, FRANCE			
REFERENCE	2 (bases 1 to 510)			
AUTHORS	Galibert,L., van Dooren,J., Durand,I., Roussel,F., Jeffers,R.,			
TITLE	Banchereau,J. and Lebecque,S.			
JOURNAL	Anti-CD40 plus interleukin-4-activated human naive B cell lines			
FEATURES	express unmutated immunoglobulin genes with intracellular heavy chain			
LOCUS	isotype variability			
DEFINITION	Eur. J. Immunol. 25 (3), 733-737 (1995)			
ACCESSION	95220422			
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ACCESSION	105 a 142 c 155 g 108 t			

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			Indels	3
			Gaps	3
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QY	2	AGGTGCAAGCTGTCTGAGTCTGTGGTCTGAGTGAAAGACCTGGGCTCTTGGTGAAAGTCT	61	
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QY	62	CCCTGCAAGGCTCTTGAGGACAGCTTCAAGAACTTTCAAATTGGGTGCAACAGGCGCC	121	
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QY	182	CACACAGAGTTTTCAGGCGACAGATCAATTAATTCGCGGAGCAATTCGACGCGCACAGGCTACA	241	
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[illegible]

RESULT	13			
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DEFINITION	H.sapiens mRNA for immunoglobulin variable region (clone 203-E2).			
ACCESSION	Z47264			
NID	9619475			
KEYWORDS	immunoglobulin; variable region.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Ekmayotac; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 510)			
TITLE	Lebecque,S			
JOURNAL	Direct Submission			
REFERENCE	Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology, Schering-Plough, Laboratory for Immunological Research, 27, Chemin des Penilliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE			
AUTHORS	2 (bases 1 to 510)			
	Galbier,L., van Dooren,J., Durand,I., Fosselet,P., Joffeiris,R., Bancherreau,J. and Lebecque,S.			
TITLE	Anti-CD40 plus interleukin-4 activated human naive B cell lines express unmutated immunoglobulin genes with intrachain heavy chain isotype variability			
JOURNAL	Eur J Immunol 25 (3), 733-737 (1995)			
MEDLINE	95220422			
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SOURCE	1..510			

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Qy	62	CCCTGCAGAGCTCTTGGAGAGCAGCTTCAAGAGCTTCAAGAGCTCAATTTCAGTATGGTGGCAGCAGGCC	121		
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Qy	122	CTGGACAAAGGCTCTTGAAGTGGAG	181		
Db	239	cacagaagttccagagcagaacttccagattaccggcgagcaaatccacagacacagacttaca	298		
Qy	182	CACAGAAAGTTTCAAGGAG	241		
Db	299	tggagctggacagccttgagatctaaagacacacagcagcagctgctatcgttgaggagaagggagag	358		
Qy	242	TGGAGTTGAGACATCTTGAAGATTTGAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	300		
Db	359	ctaaagctcgaattttggagagtgattcagctgagctacagatccagcccttggagagccagagaa	418		
Qy	301	CTAAAGATTAATTTGCAAGTCTTGAAGAGTCTCTGGAGCTTGGATTCAGAGAGAGAGAGAGAGAGAGAG	358		
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OY      359  CTCTGGTCAACCGTCTTCA 378
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LOCUS      HS203E6      510 bp      RNA
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ACCESSION  Z47265
NID        9619476
KEYWORDS   immunoglobulin: variable region.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE   Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:
AUTHORS     Vertebrata: Eutheria: Primates: Catarrhini: Homnidae: Homo.
            Lebecque, S.
TITLE       1 (bases 1 to 510)
JOURNAL     Direct Submission
            Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
            Schering-Plough, Laboratory for Immunological Research, 27, Chemin
            des Peupliers, B.P. 11 CEDEX, Dardilly, France, 69572, FRANCE
REFERENCE   2 (bases 1 to 510)
AUTHORS     Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
            Bancheureau, J., and Lebecque, S.
TITLE       Anti-CD40 plus interleukin-4-activated human naive B cell lines
            express unmutated immunoglobulin genes with intrachain heavy chain
            isotype variability
JOURNAL     Eur J Immunol. 25 (3), 733-737 (1995)
MEDLINE     95220422
FEATURES
source      Location/Qualifiers
            1..510
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            /clone="203-E6"
            /tissue-type="blood"
            /cell-type="B-lymphocyte"
BASE COUNT  105 a 142 c 155 g 108 t
ORIGIN
Query Match      64.3%; Score 243; DB 87; Length 510;
Best Local Similarity 83.9%; Pred. No. 6,82e-190;
Matches 319; Conservative 0; Mismatches 58; Indels 3; Gaps 3;

Db      59  aagtcagctggtcagctcgtgagctgagtgaaagacccctggtcctcgatgaagtc 118
      |||||
OY      2  AGGTGACGTCGTGCGAGCTGTGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 61
      |||||
Db      119  cctgcaagctctcgtgagcaccctcagcagctatgctatcagcctggtggtggaagccc 178
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OY      62  CCTGCAGGCGCTCTGAGAGCAGCTTCAGAACTTTCATTGAGTGTGAGAGGCC 121
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Db      179  ctggacaaggttgatgagtgatgagtgatcaccctatctcttggtacagcaactacg 238
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OY      182  CACAGAGATTTCAGGGCAAGTTCACAAATTACCGGACGAATCCACGCGCACAGGCTACA 241
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Db      299  tgaagctgaagcagccctgaatcctgaagcagcagcgtgtattactgtcgaagagggggg 358
      |||||
OY      242  TGGAGTTGAGCAGCTGTGAGATCTGAAGACAGCGCGTTTATTAGTGTGAGT-GCCCTAT 300
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Db      359  ctaagctgaatttttgagtggttcattcattgagtgatggttgcagcccttgagggcagga 418
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OY      301  CCAAAACATTGCAAGTGTGAGAGTGTG-TGGAG-CTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 358
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Db      419  ccctgtcagcgtctcctca 438
      |||||
OY      359  CTCTGGTCAACCGTCTTCA 378

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ACCESSION  Z47271
NID        9619482
KEYWORDS   immunoglobulin: variable region.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE   Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:
AUTHORS     Vertebrata: Eutheria: Primates: Catarrhini: Homnidae: Homo.
            Lebecque, S.
TITLE       1 (bases 1 to 525)
JOURNAL     Direct Submission
            Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
            Schering-Plough, Laboratory for Immunological Research, 27, Chemin
            des Peupliers, B.P. 11 CEDEX, Dardilly, France, 69572, FRANCE
REFERENCE   2 (bases 1 to 525)
AUTHORS     Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
            Bancheureau, J., and Lebecque, S.
TITLE       Anti-CD40 plus interleukin-4-activated human naive B cell lines
            express unmutated immunoglobulin genes with intrachain heavy chain
            isotype variability
JOURNAL     Eur J Immunol. 25 (3), 733-737 (1995)
MEDLINE     95220422
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            /clone="203-G4"
            /tissue-type="blood"
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      |||||
Db      119  cctgcaagctctcgtgagcaccctcagcagctatgctatcagcctggtggtggaagccc 178
      |||||
OY      62  CCTGCAGGCGCTCTGAGAGCAGCTTCAGAACTTTCATTGAGTGTGAGAGGCC 121
      |||||
Db      179  ctggacaaggttgatgagtgatgagtgatcaccctatctcttggtacagcaactacg 238
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      |||||
OY      301  CCAAAACATTGCAAGTGTGAGAGTGTGAG-TGGAG-CTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 358
      |||||
Db      419  ccctgtcagcgtctcctca 438
      |||||
OY      359  CTCTGGTCAACCGTCTTCA 378

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Search completed: Tue Feb 24 13:16:41 1998
Job time : 1057 secs.

CC	M.D., P.D., Michael R. Emmert-Buck, M.D., Ph.D.	cDNA Library Arrayed by: Greg
CC	Preparation: M. Bento Soares, Ph.D.	cDNA Library Arrayed by: Greg
CC	Lennon, Ph.D.	DNA Sequencing by: Washington University Genome
CC	Information Center Clome distribution	NCI-CGAP clone distribution
CC	www.bio.linn.gov/bdip/image/image.html	Insert Length: 558 Std
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CC	Sequence stop: 131	
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FT		/note="Vector: pT73-Pac (Pharmacia) with a modified
FT		polylinker; 1st strand cDNA was prepared from pooled bulk
FT		tumor tissue, and was then primed with a Not I -
FT		oligo(dT) primer. Double-stranded cDNA was ligated to Eco
FT		RI adaptors (Pharmacia), digested with Not I and cloned
FT		into the Not I and Eco RI sites of the modified pT73
FT		vector. Library is not normalized. (The normalized version
FT		of this library is NCI-CGAP-B2.) Library was constructed
FT		by Bento Soares and M. Fatima Ronaldo."
FT		/clone.lib="NCI-CGAP.Br.1.1"
FT		/sex="female, pooled"
FT		/tissue.type="breast"
FT		/lab.host="DH10B"
FT	mrna	<1..>435
SO	Sequence 435 BP, 94 A, 128 C, 112 G, 101 T, 0 other,	
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Best Local Similarity 67.1% Pred. No. 4,71e-38;		
Matches 114; Conservative 0; Mismatches 53; Indels 3; Gaps 2;		
Db	186 ccactctactagctaacctgaaccacctctaaaccttccttgagggaaccgaa	245
Cp	167 GCACCTAAAAAGACTCTCCTCAATCCACTCCATTCCTTCCGTGGCGAACC	108
Db	246 ctatgcctcgcgtgctgctacgtcctaaagtgtaatccagaagctcgacaggaagattccag	305
Cp	107 CTCGACTAGTAGTACTGCCTGTGAAGGAGGCC--AA--CCAGAGAACAGTGTAAGGAGACAGG	51
Db	306 aaccgcccaagctgtctaccaagctcccaccagaagctccaagagttgcacctc	355
Cp	50 GTCCCGCAGAGCTTCACACAGTCTGTGGCCGCCGACCTGACACACTTCACACTC	1
RESULT	4	
LOCUS	AA507475	435 bp mRNA EST 15-JUL-1997
DEFINITION	n76605.s1 NCI-CGAP Br.1 Homo sapiens cDNA clone 964424 similar to	
ACCESSION	AB507475	
NID	92243914	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens;	
	Eukaryota; Eukaryotes; Metazoa; Chordata;	
	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;	
REFERENCE	1 (bases 1 to 435)	
AUTHORS	NCI-CGAP.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).	
JOURNAL	Tumor Gene Index	
COMMENT	Unpublished (1997)	
	Contact: Robert Strausberg, Ph D	
	Tel.: (301) 496-1550	
	Email: Robert.Strausberg@nih.gov	
	Tissue Procurement: Christopher Moskalik, M.D., Ph.D.; Michael R.	
	Emmert-Buck, M.D., Ph.D.	
	cDNA Library Preparation: M. Bento Soares, Ph D	
	cDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be	

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Found through the IMAGE Consortium URL at:  
www.bio.lnln.gov/image/image.html  
  
Insert Length: 558      Std Error: 0.00  
Seq Primer : -46mT fwd ET from Amershams  
High quality sequence stop: 131.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/note="Vector: pTR73d-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from pooled bulk  
breast tumor tissue, and was then primed with a Not I +  
clgag(ori) primer. Double-stranded cDNA was ligated to EcoRI  
adaptors (pharmacis), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pTR73  
vector. Library is not normalized (the normalized  
version of this library is NCI-CCAP_Bt2). Library was  
constructed by Bento Soares and M. Fatima Ronaldo."  
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ORIGIN
MENA
<=====
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Best Local Similarity 67.1%; Prod. No. 4,71e+38;  
Matches 114, Conservative 0; Mismatches 53; Indels 3, Gaps 2;
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Df        186 ccactgaatctgtataccattgaaaccacctgatagaacccccttcctcttgaggcctggagaaacca 245  
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Cp         167 GCACCTAAAAAGACTTTGTCATCATGCATCACTCGAATGGGTTCCTTGCTGGGAGGCCGAACCACA 108  
                ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db         246 ctcatgcctatcgtagctagtcaaatggaagttgaaaaccagagctgcagagagagaggtcttcagg 305  
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Cp         107 CTCACCAACGATGATGCTGTGATTGATGTAAGAATC-A-GCTAAATAAGTAGTATGATGATGAGGATAG 51  
                ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Df         306 aaacccccccaagcttatcaccaaacctccccccaagcatacaaaattgacatc 355  
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Cp          50 GTCCCCGAGGCTTCACCACTGCTGAGCGCGGACATCGAACATCGACATC 1  
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RESULT              5  
ID     HS1202138 standard; RNA; EST; 266 BP.  
AC     AA402547;  
NI     g2056386  
DT     01-MAY-1997 (Rel. 51, Created)  
ET     23-MAY-1997 (Rel. 52, Last updated; Version 2)  
DE     ZNF707 f1 Scores ovary tumour NHBT Homo Sapiens cDNA clone 741161  
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KW     Est.  
OS     Homo sapiens (human)  
OC     Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
CC     Vertebrates; Eutheria; Primates; Carnivora; Homniidae; Homo-  
       [1]  
RA     Hillier L., Allen M., Bowles J., Dubugue T., Geisel G., Jost S.,  
       Moore R., Schellenberg K., Steptoe M., Tan F., Theising B.,  
       White Y., Wyllie T., Waterston R., Wilson R.;  
       "WashU-Merk EST Project 1997";  
       Unpublished.  
CC     Contact: Wilson RK WashU-Merk EST Project Washington University  
       School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,  
       MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email:  
       oregon@wustl.edu This clone is available royalty-free through  
       CC LML; contact the IMAGE Consortium (info@image.llnl.gov) for  
       further information. Seq primer: -28m13 rev2 ET from Amersham.  
RH     Key Location/Qualifiers  
FH     source 1..266
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Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: ATCTGGGAGTACATACCC
Primer B: GGCTGTCTTGACTCTC
STS size: 142

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

DNTPs: each 200 uM

Taq Polymerase: 0.05 units/uL

Total Vol: 10 uL

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs derived from X04217 -- Unigene.

FEATURES
Location/Qualifiers

source 1..264

STS 81..222

primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

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primer_bind 81..100

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primer_bind 81..100

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primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

primer_bind 81..100

CC Fax: 3018699423 Email: mdadams@icr.org

EH Key Location/Qualifiers

FT source 1..335

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FT /note="Human"

FT /clone="HFBEN40"

FT

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FT

Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 53 ctgttgccttgacttctctaagaagatgaag 83
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 Cp 234 CTGCTCCTTGACTGTCTACAGACATGAAG 204

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 AC AA461207;
 NI 92186327

DT 13-JUN-1997 (Rel. 52, Created)
 DT 13-JUN-1997 (Rel. 52, Last updated, Version 1)
 DE ZX70H07.s1 Soares total fetus NB2HF8 9w Homo sapiens cDNA clone
 DE 796861 3' similar to gb:X04217 PORPHOBILINOGEN DEAMINASE (HUMAN);.
 KW EST.

OS Homo sapiens (human)
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]

RP 1-516
 RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
 RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
 RA Moore B., Scheinberg K., Steptoe M., Tan F., Theising B.,
 RA White Y., Wylie T., Waterston P., Wilson R.;
 RT "Washu-Merck EST Project 1997";

RL Unpublished
 CC Contact: Wilson RK Washu-Merck EST Project Washington University
 CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
 CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@wustl.wustl.edu This clone is available royalty-free through
 CC LNL; contact the IMAGE Consortium (info@image.llnl.gov) for
 CC further information. Seq primer: -41m3 fwd. Et from Amersham High
 CC quality sequence stop: 316.

FH Key location/Qualifiers

FT source

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 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer (5'
 TGTTCACATCTGAGTGGAGCGCGCTTAATTTTATTTTT 3').
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library was

FT through one round of normalization, and was constructed by
 Bento Soares and M. Fatima Bonaldo.

/clone="796861"

/clone_lib="Soares total fetus NB2HF8 9w"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

complement(<1 >516)

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 Best Local Similarity 83 94; Prnd. No 3 16e-04;

Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 53 ctgttgccttgacttctctaagaagatgaag 83
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 Cp 234 CTGCTCCTTGACTGTCTACAGACATGAAG 204

Search completed: Tue Feb 24 12:58:36 1998
 Job time : 454 secs.

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SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 346)
JOURNAL	Frohme, M. and Hohenfels, J. Direct Submission Submitted (29-MAR-1996) Marcus Frohme, Moleculargenetic Genome Analysis, German Cancer Research Center, Im Neuenheimer Feld 506, Heidelberg 69120, Germany
FEATURES	Location/Qualifiers
source	1..346
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	L01412"
	/clone="7/24"
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Qy	113 TCGGCCAGCCGCCGAGGAAGGAGCTGGAGTGTGAGAGTGCTTTTAGTGGAGAACA 172
Dd	63 ccaactacaatcttcctctcagaantcgagtcaccatctcagttagaacagctccaagaac 122
Qy	173 CCATCTTCACCAACCCTATCCTCCACGATCGAGCTTCATGCTGTGTAGACCAAGTCCAAAGCAC 212
Dd	123 agctcccccctgagaccttgagactctggaacgccgtggaacaagcgtgtgatttcgcgcq 181
Qy	233 AGGCTGCCTCATGAGGCGTCGACTGTGTGACGCCGCCGACACACGCGCGCTGTATTACTGTGG 291
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LOCUS	Human clone 8/24 mRNA sequence.
DEFINITION	U53086
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NID	ESt.
KEYWORDS	human.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 437)
JOURNAL	Frohme, M. and Hohenfels, J. Direct Submission Submitted (29-MAR-1996) Marcus Frohme, Moleculargenetic Genome Analysis, German Cancer Research Center, Im Neuenheimer Feld 506, Heidelberg 69120, Germany
FEATURES	Location/Qualifiers
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	4b mRNA, GenBank Accession Number S64477"
	/clone="8/24"
	/tissue_type="pancreatic tumor"
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Matches 144:	Conservative 0; Mismatches 38; Indels 2; Gaps 2;
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Qy	113 TCGGCCAGCCGCCGAGGAAGGAG-ACTGGAGTGGATTGGAGAAAGTCTTTTAGTGGAGA-AG 170

D6		63	caccagctacgacccccccccaagaagtgcgtatcaccatatgaaggacacgtcacaaga	122
Cy	171	171		230
Lb	123	ccatttcctccctaagaagtgcgtctctgtgacgcgctcgacacgcgcagtcgntttmnnnn	182	
Cy	211	CCAGAGTTCCTGCTGAGGTGGACTCTTGACCGCGCGGACACAGCATATTAATGTCG	290	
D6		183	nana	186
Cy	291	GACA	294	
RESULT	7			
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DEFINITION	EST11989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, V region (GB:I12364) (HT:3115).			
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KEYWORDS	EST.			
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AUTHORS	1 (bases 1 to 180) Adams,M.D., Keplavage,A.P., Fleischmann,P.N., Paulner,P.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W., Claydon,P.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.I., Geoghegan,N.S.M., Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblow,E., Hinkle Jr,P.S., Kelley,U.M., Klineck,K.M., Kelley,J.C., Liu,L.I., Marmaro,S.M., Merrick,J.W., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,F., Small,K.V., Spriggs,T.A., Trierbach,R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dinke,D., Feng,P., Fertile,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,T., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Welty,T., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Pannon,M and Venter,J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995)			
TITLE				
JOURNAL				
COMMENT	Contact: Venter, JC The Institute For Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@db.tigr.org For clone availability additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org). Location/Qualifiers: 1..180 /organism="Homo sapiens"			
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source				
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Best Local Similarity	80.6%;	Pred. No. 5,12e-127;		
Matches	145,	Conservative	0,	Mismatches 30,
			Indels	5,
			Gaps	3;
D6		1	tncagctgcgagagctcgcgtcagagactgttaaacgttcanagacctgtccctcaact	60
Cy	5	TGCAGTTGCTGCTGAGGTGGACTCTTGACCGCGCGGACACAGCATATTAATGTCG	64	

NID	KEYWORDS	EST.
9661858	human cJone-79452 library=Stratagene lung (#97210)	
SOURCE	vector-BLuescript SK- host-SOLR cells (Kanamycin resistant) primer-M13Pst1 Pst1-e1-EcoRI Pst1-e2-XhoI Normal lung tissue from a 7 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb, Uni-ZAP XR Vector, 5' adaptor sequence: 5'-GATTCGGGACGAG-3', 3' adaptor sequence: 5'-CTCCGAGTTTCTTTTTTTTTTT-3'.	
ORGANISM	Homo sapiens Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 367)	
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,P., Treviskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.	
TITLE	WashU-Merck EST Project	
JOURNAL	Unpublished (1995)	
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 243 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers 1..367 /organism="Homo sapiens" /clone="79452"	
FEATURES		
Source		
BASE COUNT	71 a 112 c 94 g 84 t 6 others	
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Query Match	16.1%; Score 61; DB 3; Length 367;	
Best Local Similarity	89.6%; Prid NO. 1,59e-71;	
Matches	69; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
Db	1 acacgtcagaagagccattctccctcaactagcctcgtgacgcgcgcacacagccgc 60 	
OY	218 ACAAGTCCAAAGACACAGCTCTCCCTGAGCTGAGCTGTGTGACCCCGGAGACAGCGCC 277	
Db	61 tatattactgtgcaga 77 	
OY	278 TGTATTACTGTGCGACA 294	
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LOCUS	T29661 253 bp mRNA EST 06-SEP-1995	
DEFINITION	EST894449 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, VDJ regions (CB:214165) (HT:3116).	
ACCESSION	T29661	
NID	96611759	
KEYWORDS	EST.	
SOURCE	human primer-M13 Reverse library-Human Small intestine. Homo sapiens	
ORGANISM	Homo sapiens Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcosteygali; Chonata; Retropoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 253)	
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W., Clayton,R.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georghiou,N.S.M., Glock,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,D.M., Klier,R.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,	

TITLE
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

**JOURNAL
COMMENT**

Contact: Venter, JC
The Institute for Genomic Research
932 Colpper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org).

FEATURES
Location/Qualifiers
source
1..253
/organism="Homo sapiens"
<1..>253

BASE COUNT
mRNA
52 a 72 c 65 g 60 t 4 others

ORIGIN

Query Match 14.3%; Score 54; DB: 58; Length 253;
Best Local Similarity 70.8%; Pred. No. 2.8/e-56;
Matches 114; Conservative 0; Mismatches 44; Indels 3; Gaps 2;

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QY 217 GACAAAGTCCGAAGAACGACGACTGCCCTGCAGCGTCGTGGAGCAGCGCAAGCG 276
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 gtattactatgctgagaaggcttaagaaggagcaattgagt-agc--aggtagtaactttgatgt 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GTGATTTACTGTCGCGAATCCGCCATTAAAAATGAAATCATGGGAAAGATGTTTGATGCC 336
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 118 tttnatatctggggagacaaggacaaatgcttcacgcgtccttc 158
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 337 TTGTATATCTGGGGCCAGSGGACATCTGTCATCTGTCCTT 377

RESULT 12
LOCUS AA170256 823 bp mRNA EST 16-FEB-1997
DEFINITION MS87810.1 Scores mouse 3kBS Mus musculus cDNA clone 618594.5,
similar to gb:X1584 IG HEAVY CHAIN PRECURSOR V-J17 REGION (HUMAN);
gb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the
C-terminalus (MOUSE).
ACCESSION AA170256
NID A1748794
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE
AUTHORS 1 (bases 1 to 823)
Marrin, M., Hillier, L., Allen, M., Bowles, N., Dietrich, N., Dubuque, T.,
Geisel, S., Knabbe, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, P.
TITLE The MashU-HMI Mouse EST Project
JOURNAL COMMENT Unpublished (1996)

Contact: Marrin M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

 WISEWISE (TM)

Release 2.1D John F. Collins, BioComputing Research Unit,
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by IntelliGenetics, Inc.

Msearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 15:51:53 1998: MasPar time 23.03 Seconds
 754.842 Million Cell Updates/sec

Tabular output not generated.

Title: >US-08-844-215-26
 Description: (1-378) from US08844215.seq
 Perfect Score: 378
 N A Sequence: 1 GAGGTGACAGTGTGAGTGC
 Comp: CTGACGTGTGAGTGTGAGTGC
 CACTGTCTCATGCTGTCTTTC 378
 GTGACGATGACGAGAGAGAG

Scoring table: TABLE default

Nmatch STD: Dbase 0: Query 0

Searched: 87531 seqs, 22956021 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-issued
 1 back: 2 51 3 52 4 53 5 54 6 55 7 56 8 PCT90 9 PCT91
 10 PCT92 11 PCT93 12 PCT94 13 PCT95 14 PCT96

Statistics: Mean 7.812: Variance 4.313: scale 1.811

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description	Pred. No.
1	176	46.6	402	7	US-08-468- Sequence 5, Applicatio	5.88e-111
2	176	46.6	402	7	US-08-259- Sequence 5, Applicatio	5.88e-111
3	176	46.6	420	7	US-08-478- Sequence 107, Applicati	5.88e-111
4	176	46.6	423	7	US-08-379- Sequence 19, Applicati	5.88e-111
5	176	46.6	423	7	US-08-481- Sequence 19, Applicati	5.88e-111
6	89	23.5	798	11	PCT-US93-0 Sequence 71, Applicati	2.14e-46
7	89	23.5	798	11	US-08-133- Sequence 99, Applicati	2.14e-46
8	89	23.5	830	11	PCT-US93-0 Sequence 88, Applicati	2.14e-46
9	89	23.5	830	7	US-08-113- Sequence 115, Applicati	2.14e-46
10	75	19.8	402	11	PCT-US93-0 Sequence 15, Applicati	2.36e-36
11	75	19.8	402	10	US-08-111- Sequence 15, Applicati	2.36e-36
12	75	19.8	402	6	US-08-211- Sequence 15, Applicati	2.36e-36
13	75	19.8	402	7	US-08-211- Sequence 27, Applicati	2.36e-36
14	75	19.8	826	11	PCT-US93-0 Sequence 27, Applicati	2.36e-36
15	75	19.8	826	6	US-08-111- Sequence 27, Applicati	2.36e-36
16	75	19.8	357	13	PCT-US95-1 Sequence 61, Applicati	1.21e-35
17	72	19.0	357	7	US-08-470- Sequence 61, Applicati	1.21e-35
18	72	19.0	357	7	US-08-467- Sequence 61, Applicati	3.18e-34
19	72	19.0	357	7	US-08-467- Sequence 61, Applicati	3.18e-34

20	70	18.5	923	7	US-08-401- Sequence 25, Applicati	8.25e-33
21	70	18.5	1289	7	US-08-401- Sequence 36, Applicati	8.25e-33
22	70	18.5	1952	7	US-08-401- Sequence 16, Applicati	8.25e-33
23	70	18.5	3654	6	US-08-148- Sequence 1, Applicati	8.25e-33
24	69	18.3	369	12	PCT-US93-1 Sequence 37, Applicati	4.18e-32
25	69	18.3	432	5	US-08-026- Sequence 1, Applicati	4.18e-32
26	68	18.0	363	7	US-08-275- Sequence 8, Applicati	2.12e-31
27	68	18.0	363	7	US-08-211- Sequence 19, Applicati	2.12e-31
28	68	18.0	363	11	PCT-US93-0 Sequence 19, Applicati	2.12e-31
29	68	18.0	363	6	US-08-111- Sequence 19, Applicati	2.12e-31
30	68	18.0	363	7	US-08-275- Sequence 15, Applicati	2.12e-31
31	68	18.0	369	6	US-08-122- Sequence 7, Applicati	2.12e-31
32	68	18.0	414	7	US-08-467- Sequence 32, Applicati	2.12e-31
33	68	18.0	414	7	US-08-474- Sequence 32, Applicati	2.12e-31
34	68	18.0	414	6	US-08-477- Sequence 32, Applicati	2.12e-31
35	68	18.0	414	6	US-07-634- Sequence 32, Applicati	2.12e-31
36	67	17.7	294	11	PCT-US93-1 Sequence 47, Applicati	1.07e-30
37	67	17.7	334	7	US-08-467- Sequence 3, Applicati	1.07e-30
38	67	17.7	334	13	PCT-US95-1 Sequence 1, Applicati	1.07e-30
39	67	17.7	334	7	US-08-470- Sequence 1, Applicati	1.07e-30
40	67	17.7	334	7	US-08-470- Sequence 5, Applicati	1.07e-30
41	67	17.7	334	7	US-08-470- Sequence 3, Applicati	1.07e-30
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43	67	17.7	334	7	US-08-467- Sequence 1, Applicati	1.07e-30
44	67	17.7	334	13	PCT-US95-1 Sequence 3, Applicati	1.07e-30
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ALIGNMENTS

RESULT 1
 ID US-08-468-671-5 STANDARD: DNA: UNC: 402 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 5, Application US/08468671.
 CC Sequence 5, Application US/08468671
 CC Patent No. 5648077
 CC GENERAL INFORMATION:
 CC APPLICANT: OSLBERG, LAIS G.
 CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
 CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
 CC N
 CC NUMBER OF SEQUENCES: 16
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, Eighth Floor
 CC CITY: San Francisco
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94111-3834
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.10
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/468,671
 CC FILING DATE: 06-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/259,372
 CC FILING DATE: 14-JUN-1994
 CC APPLICATION NUMBER: US 07/871,426
 CC FILING DATE: 21-APR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/676,036
 CC FILING DATE: 27-MAR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/538,796
 CC FILING DATE: 15-JUN-1990
 CC PRIOR APPLICATION DATA: US 07/192,754
 CC APPLICATION NUMBER:
 CC FILING DATE: 11-MAY-1998

ID	US-08-478-039-107	STANDARD	DNA	UNC	420 BP
AC	xxxxxx				
DT	01-JAN-1900				
DE	Sequence 107, Application US/08478039.				
CC	Sequence 107, Application US/08478039				
CC	Patent No. 5641722				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Newman, Poland A.				
CC	APPLICANT: Hanna, Nabli				
CC	APPLICANT: Raab, Ronald W				
CC	TITLE OF INVENTION: Recombinant Antibodies for Human Therapy				
CC	NUMBER OF SEQUENCES: 114				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS				
CC	STREET: 699 Prince St.				
CC	CITY: Alexandria				
CC	STATE: VA				
CC	COUNTRY: USA				
CC	ZIP: 22113-1404				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/478,039				
CC	FILING DATE: 07-JUN-1995				
CC	CLASSIFICATION: 435				
CC	Prior Application DATA:				
CC	APPLICATION NUMBER: US 08/373,072				
CC	FILING DATE: 25-JAN-1995				
CC	Prior Application DATA:				
CC	APPLICATION NUMBER: US 07/912,292				
CC	FILING DATE: 10-JUL-1992				
CC	Prior Application DATA:				
CC	APPLICATION NUMBER: US 07/856,281				
CC	FILING DATE: 23-MAR-1992				
CC	Prior Application DATA:				
CC	APPLICATION NUMBER: US 07/735,064				
CC	FILING DATE: 25-JUL-1991				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Teskin Esq., Robin L.				
CC	REGISTRATION NUMBER: 35,030				
CC	PREFERENCE/PACKET NUMBER: 012712-160				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: 703-836-6620				
CC	TELEFAX: 703-836-2021				
CC	INFORMATION FOR SEU ID NO: 107:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 420 base pairs				
CC	TYPE: nucleic acid				
CC	STRANDEDNESS: not relevant				
CC	TOPOLOGY: not relevant				
CC	MOLECULE TYPE: peptide				
CC	ORIGINAL SOURCE:				
CC	ORGANISM: Monkey				
CC	POSITION IN GENOME:				
CC	CHROMOSOME/SEGMENT: Anti-CD4 VH				
CC	FEATURE:				
CC	NAME/KEY: CDS				
CC	LOCATION: 4..420				
CC	FEATURE:				
CC	NAME/KEY: mat-peptide				
CC	LOCATION: 61..420				
CC	Sequence 420 BP: 84 A; 121 C; 113 G; 102 T; 0 other:				

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Query Match:          46.5%   Score 176; DB 7; Length 420;
Local Similarity    82.4%; Pctd No 5 8be-11j;
Matches      243; Conservative     0; Mismatches 49; Indels       3; Gaps        1
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Db 62 AGGTGACCTGTGAAGAAATGGAGTTCATTGCATCAATAAATTTTGACAATAATTAATCCATCA 121
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Cc 2 AAGTAGCAGCTGTGCGAGTGTGGGCCCATGACTGTGTGAAGCTTTTGAGGAGAACCCTGTCCCTTCA 61
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Cy 179 ACAAGCCATCTCTCTCAAACATGAGTCTGCATTTTAATAGACAGCTCCAAGACCTCTTCT 238

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Cy 239 CGCTGAAGTGTGAAGTCTGTGAATGGTGGTGGACACAGCGCTGTATTACTGTGGAG 263

RESULT 4
ID US-08-379-072A-19 STANDARD; DNA: UNC; 423 BP.
AC xxxxxx
DE 01-JAN-1900
DT Sequence 19, Application US/08379072A.
CC Sequence 19, Application US/08379072A
CC Patent No. 5658570
CC GENERAL INFORMATION:
CC APPLICANT : NEWMAN, Roland A.
CC APPLICANT : HANNA, Nabil
CC TITLE OF INVENTION : PERMEINANT ANTIBODIES FOR HUMAN THERAPY
CC NUMBER OF SEQUENCES : 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Burns, Dwayne Shecker & Mathis
CC STREET: P.O. Box 1404
CC CITY: Alexandria
CC STATE: Virginia
CC COUNTRY: United States
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MK-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/379,072A
CC FILING DATE: 25-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,292
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/856,281
CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Rea, Teresa Stanek
CC REGISTRATION NUMBER: 30,427
CC REFERENCE/DOCKET NUMBER: 012712-067
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703) 836-6620
CC TELEFAX: (703) 836-2021
CC INFORMATION FOR SEQ ID NO.: 19:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 402 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..402
SQ Sequence 402 bp; 107 A; 113 C; 88 G; 94 T; 0 other;

Query Match 19.8%; Score 75; DB 11; Length 402;
Best Local Similarity 65.2%; Pred. No. 2,36e-36;
Matches 193; Conservative 0; Mismatches 100; Indels 3; Gaps 2;

Db 1 GAGGTCCAGCTGTGAGAGCTGTGAGCTGTGATCAAGTCATCAAGTCAATGCTTCTTC 60
1 GAGGTCCAGCTGTGAGAGCTGTGAGCTGTGATCAAGTCATCAAGTCAATGCTTCTTC 60
QY 1 GAGGTCCAGCTGTGAGAGCTGTGAGCTGTGATCAAGTCATCAAGTCAATGCTTCTTC 60
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61 ACCTGCATAGTCTGTGATTCCTCATCAAGTAGTAGTATTGCTGGCAGCTGATCCGC 117
QY 61 ACCTGCATAGTCTGTGATTCCTCATCAAGTAGTAGTATTGCTGGCAGCTGATCCGC 117
Db 121 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 180
121 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 180
QY 118 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 177
118 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 177
Db 181 TATAGTCATTCATCAAAAGCCGAGACCATCTCCAGACACATCTCTGAACAGATTC 240
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QY 178 TACAAACCATCTCCATCAAGATGAGTCTTCTATGTCGTAGACAGTCCAAAGCCAGGTC 237
178 TACAAACCATCTCCATCAAGATGAGTCTTCTATGTCGTAGACAGTCCAAAGCCAGGTC 237
Db 241 TTATCCAGCTAGTCTGTGACAAATGAGAGACACTGCCATGATTAATGTTCCAG 296
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QY 238 TCCCTGAGGCTGAGCTCTGTGACCGCGCGGACACGCGCTGTATTACTGTGGAG 293
238 TCCCTGAGGCTGAGCTCTGTGACCGCGCGGACACGCGCTGTATTACTGTGGAG 293

RESULT 11
ID PCT-US92-07111-14 STANDARD; DNA; UNC; 402 bp.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 14, Application PC/TUS9207111.
CC Sequence 14, Application PC/TUS9207111
CC GENERAL INFORMATION:
CC APPLICANT: Ohno, Tsuneya
CC TITLE OF INVENTION: HIV Immunotherapeutics
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: Two First National Plaza, 20 South Clark
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/07111
CC FILING DATE: 19920824
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/748,562
CC FILING DATE: 22-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31016
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 984-9740

CC TELEX: 25-3856
CC INFORMATION FOR SEQ. ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 402 base pairs
CC TYPE: Nucleic Acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..402
SQ Sequence 402 bp; 107 A; 113 C; 88 G; 94 T; 0 other;

Query Match 19.8%; Score 75; DB 10; Length 402;
Best Local Similarity 65.2%; Pred. No. 2,36e-36;
Matches 193; Conservative 0; Mismatches 100; Indels 3; Gaps 2;

Db 1 GAGGTCCAGCTGTGAGAGCTGTGAGCTGTGATCAAGTCATCAAGTCAATGCTTCTTC 60
1 GAGGTCCAGCTGTGAGAGCTGTGAGCTGTGATCAAGTCATCAAGTCAATGCTTCTTC 60
QY 1 GAGGTCCAGCTGTGAGAGCTGTGAGCTGTGATCAAGTCATCAAGTCAATGCTTCTTC 60
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61 ACCTGCATAGTCTGTGATTCCTCATCAAGTAGTAGTATTGCTGGCAGCTGATCCGC 117
QY 61 ACCTGCATAGTCTGTGATTCCTCATCAAGTAGTAGTATTGCTGGCAGCTGATCCGC 117
Db 121 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 180
121 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 180
QY 118 CAGCCCCCAGAGAGGGGTAGAGTGTAGTGGGCGCATATGTTATGAGGTTCAATAGAC 177
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RESULT 12
ID US-08-111-080-15 STANDARD; DNA; UNC; 402 bp.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 15, Application 08/111080.
CC Sequence 15, Application 08/111080
CC Patent No. 5558865
CC GENERAL INFORMATION:
CC APPLICANT: Ohno, Tsuneya
CC TITLE OF INVENTION: HIV Immunotherapeutics
CC NUMBER OF SEQUENCES: 38
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Borun
CC STREET: 6300 Sears Tower, 233 S. Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: 08/111,080
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/748,562
CC FILING DATE: 22-AUG-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/07111
CC FILING DATE: 24-AUG-1992
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/039,457
 CC FILING DATE: 22-APR-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Borun, Michael F.
 CC REGISTRATION NUMBER: 25,447
 CC REFERENCE/DOCKET NUMBER: 31629
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (312) 474-6300
 CC TELEFAX: (312) 474-0448
 CC TELEX: 25-3856
 CC INFORMATION FOR SEQ ID NO: 15:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 402 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1..402
 SQ Sequence 402 BP: 107 A; 113 C; 88 G; 94 T; 0 other:

Query Match 19.8%; Score 75; DB 6; Length 402;
 Best Local Similarity 65.2%; Pred. No. 2,36e-36;
 Matches 193: Conservative 0; Mismatches 100; Indels 3; Gaps 2;

Db 1 GAGGTCCAGCTGCAGAGCTCTGACCTGCTGTCACTCAAGCCTACAGCTACTGCTCTC 60
 1 GAGGTCCAGCTGCAGAGCTCTGACCTGCTGTCACTCAAGCCTACAGCTACTGCTCTC 60
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 61 ACCTGCATAGTCTCTGATTCCTCCATCAGACAGTAGTATTGCTGGCAGCTGCAGTCCG 120
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 ID US-08-211-980-15 STANDARD: DNA; UNC; 402 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 15, Application US/08211980.
 CC Sequence 15, Application US/08211980
 CC Patent No. 5665569
 CC GENERAL INFORMATION:
 CC APPLICANT: Onno, Tsuneya
 CC TITLE OF INVENTION: HIV Immunotherapeutics
 CC NUMBER OF SEQUENCES: 38
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 CC STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CC CITY: Chicago
 CC STATE: Illinois
 CC COUNTRY: USA
 CC ZIP: 60606
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/211,980

CC FILING DATE: 424
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/07111
 CC FILING DATE: 24-AUG-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/039,457
 CC FILING DATE: 22-APR-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Borun, Michael F.
 CC REGISTRATION NUMBER: 25,447
 CC REFERENCE/DOCKET NUMBER: 31629
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (312) 474-6300
 CC TELEFAX: (312) 474-0448
 CC TELEX: 25-3856
 CC INFORMATION FOR SEQ ID NO: 15:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 402 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1..402
 SQ Sequence 402 BP: 107 A; 113 C; 88 G; 94 T; 0 other:

Query Match 19.8%; Score 75; DB 7; Length 402;
 Best Local Similarity 65.2%; Pred. No. 2,36e-36;
 Matches 193: Conservative 0; Mismatches 100; Indels 3; Gaps 2;

Db 1 GAGGTCCAGCTGCAGAGCTCTGACCTGCTGTCACTCAAGCCTACAGCTACTGCTCTC 60
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 1 GAGGTCCAGCTGCAGAGCTCTGACCTGCTGTCACTCAAGCCTACAGCTACTGCTCTC 60
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 61 ACCTGCATAGTCTCTGATTCCTCCATCAGACAGTAGTATTGCTGGCAGCTGCAGTCCG 117
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 121 CAGCCCCCAGGAAGGGGTGAAGTGAAGTGGGGCCCATATGTTATGAAGTTCAATAGAC 180
 Qy 118 CAGCCCCCAGGAAGGGGTGAAGTGAAGTGGGGCCCATATGTTATGAAGTTCAATAGAC 177
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 Db 181 TATAGTCATCTCTGATTCCTCCATCAGACAGTAGTATTGCTGGCAGCTGCAGTCCG 240
 181 TATAGTCATCTCTGATTCCTCCATCAGACAGTAGTATTGCTGGCAGCTGCAGTCCG 240
 Qy 178 TACACCCATCTCTGATTCCTCCATCAGACAGTAGTATTGCTGGCAGCTGCAGTCCG 237
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 Db 241 TTATCCAGCTGAGTCTGTGTGACAAATGAGACACTGCCATATTACTGTTCCAG 296
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 ID US-08-211-980-27 STANDARD: DNA; UNC; 826 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 27, Application US/08211980.
 CC Sequence 27, Application US/08211980
 CC Patent No. 5665569
 CC GENERAL INFORMATION:
 CC APPLICANT: Onno, Tsuneya
 CC TITLE OF INVENTION: HIV Immunotherapeutics
 CC NUMBER OF SEQUENCES: 38
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 CC STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CC CITY: Chicago
 CC STATE: Illinois
 CC COUNTRY: USA
 CC ZIP: 60606
 CC COMPUTER READABLE FORM:

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SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.
 REFERENCE 1 (bases 1 to 307)
 AUTHORS Adams M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C.,
 Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geochagen, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, P.,
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Willy,
 Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F.J.,
 Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M., and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 COMMENT

Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

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 Db 194 cccgggaaggactggaatggattggctatatctattacatgggaacacaaactacaa 253
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 Db 254 tccctccctcaagatcgagtcacatctatcagtagacagctcccaacacag 305
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RESULT 4 AA301099 199 bp mRNA EST 18-APR-1997
 LOCUS

DEFINITION EST14127 Testis tumor Homo sapiens cDNA 5' end similar to similar
 to immunoglobulin mu heavy chain, VDJ regions (GB:X54445).
 ACCESSION AA301099
 NID g1953546
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.
 REFERENCE 1 (bases 1 to 199)
 AUTHORS Adams M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C.,
 Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geochagen, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, P.,
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Willy,
 Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F.J.,
 Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M., and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 COMMENT

Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

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 /dev_stage="adult"
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 Db 56 aggtcagttcagagtcggggccagagtcgggaacctcggagacccctaccctna 115
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RESULT 5 AA360196 239 bp mRNA EST 21-APR-1997
LOCUS EST69375 Lymph node I Homo sapiens cDNA 5' end similar to similar
DEFINITION to immunoglobulin mu heavy chain, V region.
ACCESSION AA360196
NID 92012574
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 239)
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
White,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
Bult,C.J., Sutton,G., Blake,J.A., Brandon,R.C., Wang,Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,S.A.,
He,W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.P., Posen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT 96026280

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
FEATURES
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Location/Qualifiers
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/note="Organ: lymph node; Vector: pBluescript SK-; Site_1:
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/clone.lib="Lymph node I"
/dev_stage="adult"
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Matches 147; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

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Db 119 cctgcactgtctcgtggctcgcagtagtggtgacctcttactgagttgagtcacncc 178
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Db 179 agcccnacggaggaagactngatggatcggaattttctatnacagnggatccanccnct 238
QY 119 AGCCCCCAGGCAAGGACTGGAGTGGATTGGAGAGTCTTTTTTAGTGGAGGACCATCT 178

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Db 239 a 239
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RESULT 6 AA098196 364 bp mRNA EST 15-FEB-1997
LOCUS mn86h06.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
DEFINITION 551003 5' similar to gb:214164 IG HEAVY CHAIN V-II REGION (HUMAN);.
ACCESSION AA098196
NID 91643751
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 364)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
MGI:331795
Seq primer: -28ml3 rev1 ET from Amersham.
FEATURES
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Location/Qualifiers
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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QY	122	CCCCAGGGAAGGGACTGGATGG	149

RESULT	8
LOCUS	AA295042 158 bp mRNA EST 14-APR-1997
DEFINITION	EST100181 Pancreas tumor I Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, VDJ regions (GB:X67906).
ACCESSION	AA295042
KEYWORDS	Q1947376 NID
SOURCE	EST.
ORGANISM	human.
REFERENCE	1 (bases 1 to 158)
AUTHORS	Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Feldner,P.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,I.M., Fitzhugh,W.M., Fritchman,J.I., Geochaghen,N.S., Glodzik,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancques,P.F., McDonald,J.L.A., Nguyen,D.T., Pelligrino,S.A., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Rednark,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,G., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE	95026280
COMMENT	Other ESTs: THC169164 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tadb/hgi/hgi.html) Seq primer: M13 Reverse.
FEATURES	Location/Qualifiers
Source	1..158 /organism="Homo sapiens" /note="Organ: pancreas; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI" /clone_lib="Pancreas tumor I" /dev_stage="adult" <1..>158
BASE COUNT	25 a 51 c 42 g 38 t 2 others
ORIGIN	
Query Match	16.1%; Score 61; DP 24; Length 158;
Best Local Similarity	89.5%; Pred. No. 8,85e-73;
Matches	68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db	82 gtcagcgtccaggaatcgggcccgagactggtgaagcttcactgaacctatccatnacc 141
QY	4 GTCCAGTGTCTGATCTGGAGGCTCAGATGGTGAAGGCTTCGAGAGCCCTGTCCTCACC 63
Db	142 tgcactgtctctgtggtg 157

Db	229	gctccaggggaaggcgctggagctgg	252
QY	121	CCCCCAGGGAAGGACTGGAGTGG	144

RESULT	10	AA792989	306 bp	mPNA	RST	16-MAY-1997
LOCUS		zt47f09.r1				
DEFINITION		5', similar to qb:L21964				
		IG HEAVY CHAIN V-II REGION (HUMAN):.				

REFERENCE	VERTEBRATA: Mammalia; Eutheria; Primates; Catarrhini, Hominoidea.
AUTHORS	1 (bases 1 to 366)
	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, R., Schellenberg, K., Steproe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE	WashU-Merck EST Project 1997
	Unpublished (1997)
JOURNAL	

This gene was identified by a BLAST search of the IMAGE Consortium (imga.image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 1.

FEATURES
High quality sequence stop: 1.
Location/Qualifiers
1..306
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker. Site 1 Not I Site 2 Eco RI; strand cDNA was primed with a Not I - oligo(dT) primer TGTTCACATCTGAATGCGAGCGCGCGGTTTTTTTTTTT 3'.) double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fátima Bonaldo."

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/clone="725513"
/clone_lib="Soares ovary tumor N5HOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>306
/db_xref="GDB:5937384"
74 a 76 g 63 t
BASE COUNT
ORIGIN

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Query Match      12.2%; Score 45; DB 100; Length 306;
Best Local Similarity 62.7%; Pred. No. 1.73e-44;
Matches 175; Conservative 0; Mismatches 99; Indels 5; Gaps

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Db	25	gagttggtctcagcgtggtgaaaca-cacaggccctcagctgagctgcaactctct	83
QY	16	GAGTCGGGCCCAGGANTGCTGAAGGCTTTGCGGACATCTGTCTTCATCTTCACATGCTCTCT	75
Db	84	gggttctcactcagcacctagtgagtggtggtggtggtccgtcagccccagagaaag	143
QY	76	GCTGCGCTCTCATAGTAGTAGCTC-ACCTGG-TG-GAGTTTGGTTCAGCTAGCTCTTAGGGAAG	122
Db	144	ggccttgagtgagctgcaactcttactgggtgatgaaagcgtacagccatctct	203

Quero

Best Local	Similarity 98.8%,	Pred. NO. 9.56e-27,	
Matches	66; Conservative	0, Mismatches	30;
		Indels	0.
		Gaps	0.

Best Local	Similarity 98.8%,	Pred. NO. 9.56e-27,	
Matches	66; Conservative	0, Mismatches	30;
		Indels	0.
		Gaps	0.

[illegible][illegible]

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259 ACCGCCGGGACACGGCCGTATTACTGTGGAGA 294

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Accession	Gene	Species	Library	Size (bp)	Library
U05001	3T3	Mouse	3T3	420	3NbMS
U05002	3T3	Mouse	3T3	420	3NbMS
U05003	3T3	Mouse	3T3	420	3NbMS
U05004	3T3	Mouse	3T3	420	3NbMS
U05005	3T3	Mouse	3T3	420	3NbMS
U05006	3T3	Mouse	3T3	420	3NbMS
U05007	3T3	Mouse	3T3	420	3NbMS
U05008	3T3	Mouse	3T3	420	3NbMS
U05009	3T3	Mouse	3T3	420	3NbMS
U05010	3T3	Mouse	3T3	420	3NbMS
U05011	3T3	Mouse	3T3	420	3NbMS
U05012	3T3	Mouse	3T3	420	3NbMS
U05013	3T3	Mouse	3T3	420	3NbMS
U05014	3T3	Mouse	3T3	420	3NbMS
U05015	3T3	Mouse	3T3	420	3NbMS
U05016	3T3	Mouse	3T3	420	3NbMS
U05017	3T3	Mouse	3T3	420	3NbMS
U05018	3T3	Mouse	3T3	420	3NbMS
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U05040	3T3	Mouse	3T3	420	3NbMS
U05041	3T3	Mouse	3T3	420	3NbMS
U05042	3T3	Mouse	3T3	420	3NbMS
U05043	3T3	Mouse	3T3	420	3NbMS
U05044	3T3	Mouse	3T3	420	3NbMS
U05045	3T3	Mouse	3T3	420	3NbMS
U05046	3T3	Mouse	3T3	420	3NbMS
U05047	3T3	Mouse	3T3	420	3NbMS
U05048	3T3	Mouse	3T3	420	3NbMS
U05049	3T3	Mouse	3T3	420	3NbMS
U05050	3T3	Mouse	3T3	420	3NbMS
U05051	3T3	Mouse	3T3	420	3NbMS
U05052	3T3	Mouse	3T3	420	3NbMS
U05053	3T3	Mouse	3T3	420	3NbMS
U05054	3T3	Mouse	3T3	420	3NbMS
U05055	3T3	Mouse	3T3	420	3NbMS
U05056	3T3	Mouse	3T3	420	3NbMS
U05057	3T3	Mouse	3T3	420	3NbMS
U05058	3T3	Mouse	3T3	420	3NbMS
U05059	3T3	Mouse	3T3	420	3NbMS
U05060	3T3	Mouse	3T3	420	3NbMS
U05061	3T3	Mouse	3T3	420	3NbMS
U05062	3T3	Mouse	3T3	420	3NbMS
U05063	3T3	Mouse	3T3	420	3NbMS
U05064	3T3	Mouse	3T3	420	3NbMS
U05065	3T3	Mouse	3T3	420	3NbMS

chain gamma (MOUSE); .
2217560

KEYWORDS

ORGANISM	Mus musculus
Duke University	

vertebrata, Eucnelliid, Koenigella, Sciurus
Mus.

AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles

Schellensberg, K.; Steptoe, M.; Ian, F.; O
Theising, B.; Wylie, T.; Lennon G.; Scar

TITLE The WashU-HHMI Mouse EST Project

COMMENT: Contact: Marra M/Vouse EST project

Washington University School of Medicine

TEL: 314 286 1800
FAX: 314 286 1810

This clone is available royalty-free to

MG1:380026
Seq primer: -28M13 rev2 from Amersham

CHARACTERISTICS	Location/Qualifiers
1. <u>General</u>	
2. <u>Specific</u>	
3. <u>Other</u>	

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/organism="Mus musculus"  
/strain="C57BL/6J"
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polylinker; Site_1: Not I; Si

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3': double-stranded cDNA was

and Eco RI sites of the modif

three rounds of normalization
Pinto Soares and M. Fatima Bon

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/clone_lib="Soares mouse 3NbM"
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/tissue_type="Spleen"
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mRNA
/tad_host= DRIVE
<1.,>420
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IGIN

Query Match 9.3%: Score 45; DH 1; Best Local Similarity 75.4%: pred. No 3.12e-2

[illegible]

WASHU

(TM)

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MPsrch_nn n.a. - n.a database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 13:40:16 1998; MasPar time 127.67 seconds
Tabular output not generated. 746 944 Million cell updates/sec

Title: >US-08-844-215-27
Description: (1-378) from US08844215 seq
Perfect Score: 378
N.A. Sequence: 1 GAGGTGACGTCGTCGAGTC.....CTTGTCACCGTGTCTTCA 378
Comp: CTCACGTCGTCGACGAGTCAG.....GAGACGAGTCGACAGAGT

Scoring table: TARTe default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 33433 seqs, 125143548 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
1 STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19 20:STS20
21:STS21 22:STS22 23:STS23 24:STS24 25:STS25 26:STS26
27:STS27 28:STS28 29:STS29 30:STS30 31:STS31 32:STS32
33:STS33 34:STS34 35:STS35 36:STS36 37:STS37 38:STS38 39:STS39
40:STS40 41:STS41 42:STS42 43:STS43 44:STS44 45:STS45
46:STS46 47:STS47 48:STS48 49:STS49 50:STS50 51:STS51
52:STS52 53:STS53 54:STS54 55:STS55 56:STS56 57:STS57
58:STS58 59:STS59 60:STS60 61:STS61 62:STS62 63:STS63 64:STS64
65:STS65 66:STS66 67:STS67 68:STS68 69:STS69 70:STS70
71:STS71 72:STS72 73:STS73 74:STS74 75:STS75 76:STS76
77:STS77 78:STS78 79:STS79 80:STS80 81:STS81 82:STS82
83:STS83 84:STS84 85:STS85 86:STS86 87:STS87 88:STS88
89:STS89 90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96

Statistics: Mean 9.902; Variance 1.885; scale 5.254
Pred No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES			
Result	Query	Description	Pred. No
No.	Score	Match Length DB	ID
1	78	20.6	256 54
2	45	11.9	210 57

3	38	10.1	238	69	HS1300461	aa63g01.r1	NCI_CGAP_G	2 39e-30
4	38	10.1	238	35	AA505044	aa63g01.r1	NCI_CGAP_G	2 39e-30
5	30	7.9	435	80	HSAA7475	ab76c05.s1	NCI_CGAP_B	2 73e-17
6	30	7.9	435	40	AA507475	ab76c05.s1	NCI_CGAP_B	2 73e-17
7	27	7.1	597	24	AA472093	vb10a05.r1	Soares mcy	9 34e-13
8	27	7.1	597	83	MM1263658	vb10a05.r1	Soares mcy	9 34e-13
9	24	6.3	511	63	HS1258634	z883b07.r1	Soares ova	1 72e-08
10	24	6.3	511	17	AA454794	z883b07.r1	Soares ova	1 72e-08
11	21	5.6	403	73	HS121118	n51b07.s1	NCI_CGAP_P	1 46e-04
12	21	5.6	403	44	AA531145	n51b07.s1	NCI_CGAP_P	1 46e-04
13	20	5.3	288	95	HS1138859	7H16G06	Chromosome 7	2 42e-03
14	20	5.3	302	11	HUMSWS3933	human chromosome 7	ST	2 42e-03
15	20	5.3	302	12	HUMSWS3933	human chromosome 7	ST	2 42e-03
16	20	5.3	374	58	HS123238	z47d12.s1	Soares ova	2 42e-03
17	20	5.3	397	50	HS1177148	z86c04.r1	NCI_CGAP_G	2 42e-03
18	20	5.3	397	19	AA253889	z86c04.r1	NCI_CGAP_G	2 42e-03
19	20	5.3	412	75	HS8381	EST037327	Homo sapiens	2 42e-03
20	20	5.3	454	23	AA4595PR	z327g08.r1	NCI_CGAP_G	2 42e-03
21	20	5.3	454	62	HS1254438	z327g08.r1	NCI_CGAP_G	2 42e-03
22	20	5.3	1023	4	HS1254438	human STS	CHIC 17p11	2 42e-03
23	20	5.3	2775	9	HS1254438	human STS	SHGC 35785	2 42e-03
24	19	5.0	259	30	AA488043	ab12f07.r1	Stratagene	3 55e-02
25	19	5.0	334	20	HS1174298	z825b12.r1	NCI_CGAP_G	3 55e-02
26	19	5.0	324	20	AA537099	z825b12.r1	NCI_CGAP_G	3 55e-02
27	19	5.0	344	16	AA451658	z592b10.r1	Soares mcy	3 55e-02
28	19	5.0	349	81	MM1239198	z422b04.r1	Knowles So	3 55e-02
29	19	5.0	396	91	HS1239198	EST00012	TGRH 16p27	3 55e-02
30	19	5.0	400	9	HS1239198	human STS	SHGC 35785	3 55e-02
31	19	5.0	416	37	AA503753	ne50g02.s1	NCI_CGAP_C	3 55e-02
32	19	5.0	442	90	PMMA35257	z44a02.s1	Knowles So	3 55e-02
33	19	5.0	444	90	MMAA35322	z44a02.s1	Knowles So	3 55e-02
34	19	5.0	445	18	AA465902	z44a02.s1	Knowles So	3 55e-02
35	19	5.0	444	50	HS1173165	z422b04.r1	NCI_CGAP_G	3 55e-02
36	19	5.0	451	76	HSAA30659	z410b03.r1	Stratagene	3 55e-02
37	19	5.0	460	75	HSAA30659	z410b03.r1	NCI_CGAP_G	3 55e-02
38	19	5.0	496	26	AA477595	z44a02.r1	Soares ova	3 55e-02
39	19	5.0	498	84	MM1265515	z44a02.r1	Soares ova	3 55e-02
40	19	5.0	501	23	AA286927	z566a05.r1	NCI_CGAP_G	3 55e-02
41	19	5.0	524	57	HS1236054	z47b07.r1	Soares ova	3 55e-02
42	19	5.0	538	30	AA495574	ab16e08.s1	Stratagene	3 55e-02
43	19	5.0	542	73	HS122042	n13b10.s1	NCI_CGAP_P	3 55e-02
44	19	5.0	568	25	AA475554	z413g05.r1	Soares mcy	3 55e-02
45	19	5.0	577	73	HS123234	ab87c01.s1	NCI_CGAP_B	3 55e-02

ALIGNMENTS

RESULT 1
IC HS1202138 standard. RNA, EST. 266 BP.
AC AA02547,
NI G2056386

DT 01-MAY-1997 (Rel. 51, Created)
RT 22-MAY-1997 (Rel. 52, Last updated, Version 2)
DE z47b07.r1 Soares ova; NCBI NCHOT Homo sapiens cDNA clone 741181
EE 5' similar to g1 M87789 IS GAMMA-1 CHAIN C REGION (HUMAN);

KW EST.
QS Homo sapiens (human)
CC Eukaryotic, mitochondrial eukaryotes; Metazoa, Chordata,
CC Vertebrata, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
RN [1]
PP 1-266

RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kuraba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Stroppe W., Tan F., Theising B.,
RA White Y., Wyllie T., Waterston P., Wilson R.,
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson PK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 268 1400 Fax: 314 268 1410 Email:
CC est@washington.wustl.edu This clone is available royalty-free through
CC the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: 26613 rev2 ET from Amersham.

 WIRE (TM)

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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 12:25:57 1998; WasPar time 55.47 Seconds
 786.410 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-844-215-26
 Description: (1.378) from US08844215.seq
 Perfect Score: 378
 N.A. Sequence: 1 GAGGTGACAGCTGCTGAGTC
 Comp: CTCGACGTCGACGAGCTGAG

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0
 Searched: 159651 seqs, 5769962 bases x 2
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-genes30
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.204; Variance 4.969; scale 1.651
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	225	59.5	372	28	Human lung cancer spe	1.41e-133
2	223	59.0	624	13	Human immunoglobulin	3.42e-132
3	222	58.7	800	13	Human immunoglobulin	1.69e-131
4	208	55.0	348	7	VH415.	8.18e-122
5	204	55.0	348	7	VH411	8.15e-122
6	207	54.8	1212	13	Human immunoglobulin	4.00e-121
7	205	54.5	348	7	VH71-4.	1.96e-120
8	206	54.5	348	7	VH416.	1.96e-120
9	206	54.5	622	13	Human immunoglobulin	1.96e-120
10	205	54.2	351	7	AS26.	9.63e-120
11	204	54.0	650	13	Human immunoglobulin	4.71e-119
12	203	53.7	799	13	Human immunoglobulin	2.31e-118
13	200	52.9	408	32	Immunoglobulin rB6B7	2.72e-116
14	198	52.4	366	5	MAB 1-3-1 variable re	6.51e-115
15	198	52.4	372	2	Anti-human PHD PAG-1	6.51e-115

Anti-human RHD FOM-1 1.56e-113
 F105Vh. 3.72e-112
 F105 rearranged varia 3.72e-112
 Human immunoglobulin 3.72e-112
 Monoclonal antibody 3.72e-112
 Human immunoglobulin 1.82e-111
 Anti-rhesus D monoclo 4.33e-110
 Anti-rhesus D recombi 4.33e-110
 Human immunoglobulin 2.12e-109
 Anti-human PHD FOM-A 1.04e-108
 Human immunoglobulin 5.04e-108
 Sequence of human im 2.46e-107
 CEA-specific antibody 2.46e-107
 LfVJ regions of human 1.20e-106
 CEA-specific antibody 5.87e-106
 MAB GAH variable regi 5.87e-106
 Primatised anti-human 5.87e-106
 Human immunoglobulin 2.84e-105
 Human immunoglobulin 6.73e-104
 Human gamma-4PE heavy 3.76e-101
 Human gamma-4 heavy c 3.76e-101
 Human gamma-4E heavy 3.76e-101
 Anti-human RHD MAD-2 8.97e-100
 Monoclonal antibody z 8.87e-100
 Monoclonal antibody z 8.87e-100
 Sequence of the VH re 8.87e-100
 Monkey anti-CD4 heavy 8.87e-100
 Anti-CD4 VH coding se 8.87e-100
 Anti-human RHD FOG-B 1.15e-95
 Anti-human RHD FOG-1 1.47e-91

ALIGNMENTS

RESULT 1
 ID T45035 standard; cDNA; 372 BP.
 AC T45035;
 DT 23-MAY-1997 (first entry)
 DE Human lung cancer specific antibody heavy chain variable region cDNA.
 KW Heavy chain; light chain; variable region; human; monoclonal antibody;
 OS lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss.
 OS Homo sapiens. Location/Qualifiers
 FH Key
 FT misc_PNA 91..108
 FT /tag= a
 FT /product= CDR1
 FT /note= "Fig 5, Claim 7"
 FT /misc_difference 139..141
 FT /tag= b
 FT /codon= seq:gag, aa:Gln
 FT misc_RNA 151..198
 FT /tag= c
 FT /product= CDR2
 FT /note= "Fig 6, Claim 7"
 FT misc_RNA 295..339
 FT /tag= d
 FT /product= CDR3
 FT /note= "Fig 7, Claim 7"
 PN J08280386-A.
 PD 29-OCT-1996.
 PP 14-APR-1995: 112671.
 PR 14-APR-1995: JP-112671.
 PA (WAMI) MORINAGA & CO LTD
 WP1: 97-014849/02.
 P-PSDR: W06474
 DT Antibody specifically reactive to human lung cancer cells - also
 corresponding cDNA, used to diagnose cancer, or for purification of
 cancer-specific antigen
 CC Claim 1: Fig 1: 9pp; Japanese.
 CC The sequences given in T45035:36 encode the heavy chain and light
 chain variable regions from a human monoclonal antibody which is
 specific for human lung cancer tissue. The monoclonal antibody may
 be used for clinical diagnosis of cancers, for immunological therapy

CC or for purification of a cancer-specific antigen.
SQ Sequence 372 BP; 77 A; 102 C; 117 G; 76 T;

Query Match 59.5%; Score 225; DB 28; Length 372;
Best Local Similarity 88.4%; Pred. No. 1.41e-133;
Matches 259; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 2 aggtgcagctgcagagtcggggcccgagactggtgaagccttcggggaccctgtccctca 61
|||||
Qy 2 AGTGTGACAGTCTCTGAGTCTGGGCGGCGGAGTGGTGAAGCTTCGGGGAGCCCTGTCTCCCTCA 61
|||||
Db 62 ctgcgctgtctctgtggtgcctcatcagcagtagtaactggtgagctgggtccgcacg 121
|||||
Qy 62 CTTGCATCTGTCTCTGCTGGTCTCCATCAGGAGCAGTCTCTGCTGGAGTGGTGGTCCGCCAGC 121
|||||
Db 122 cccagggaaagggtgagtgatgggaaatctcatatgagtgaggagcaccactata 181
|||||
Qy 122 CCCCAGGGAAGGAGTGGAGTGGATTGGAGAGTCTTTTATTAGTGGNAGGACCATCTACA 181
|||||
Db 182 accgtccctcaagagtcgagtcaccatcatcagcgagacagcgtcccaagacagttctccc 241
|||||
Qy 182 ACCATCCCTCAAGATCGAGTCTTTCATGCTGTAGACAAAGTCCAAAGGACCAAGTCTCTCCC 241
|||||
Db 242 tgaaggtgaactctgtcaccgcgcgagacacgcccgtgtattactgtgcgaga 294
|||||
Qy 242 TGAAGTGTAGCTCTGTGACCCGCGGAGACAGCGCCGTGTATTACTGTGGGAGA 294
|||||

RESULT 2
ID Q78966 standard; DNA; 624 BP.
AC Q78966;
DT 03-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #28.
KW cosmid; placenta; human; immunoglobulin; variable; heavy chain;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 151..583
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 197..278
FT /tag= b
FT /tag= c
FT /tag= c
FT /note= "miscellaneous signal, does not conform to
terminator or splice site sequence"
PN WO9426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB: R66320.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
production of human immunoglobulin in mammalian hosts
PS Disclosure; Page 67-68; 130pp; Japanese.
CC A series of genes (078939-79002) encoding human immunoglobulin variable
heavy chains. The genes were isolated and cloned from a series of cosmid
constructs: Y202; Y103; Y21; Y6:Y24; 3-31; M84; M18 and M131, by PCR
amplification using primers Q78917-38. The genes are subdivided into 5
families of Vh genes. The fragments cover a region of 800 kb. The DNA
fragments were isolated from high molecular weight DNA from human
placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
were collected. The fragments were ligated with ClaI-digested cosmid
vector pJB81. The ligation products were in vitro packed and infected
CC - into E.coli 490A. The fragments were then subcloned by colony
hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 624 BP; 141 A; 179 C; 168 G; 136 T;

Query Match 59.08; Score 223; DB 13; Length 624;

Best Local Similarity 88.1%; Pred. No. 3.42e-132;
Matches 258; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 291 aggtgcagctgcagagtcggggcccgagactggtgaagccttcggggaccctgtccctca 350
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Qy 2 AGTGTGACAGTCTCTGAGTCTGGGCGGCGGAGTGGTGAAGCTTCGGGGAGCCCTGTCTCCCTCA 61
|||||
Db 351 ctgcgctgtctctgtggttactccatcagcagtagtaactggtgagctgggtccgcacg 410
|||||
Qy 62 CTTGCATCTGTCTCTGCTGGTCTCCATCAGGAGCAGTCTCTGCTGGAGTGGTGGTCCGCCAGC 121
|||||
Db 411 cccagggaaaggagctgagtgagtgattgggtacatctattatagtgaggagacactactaca 470
|||||
Qy 122 CCCCAGGGAAGGAGTGGAGTGGATTGGAGAGTCTTTTATTAGTGGNAGGACCATCTACA 181
|||||
Db 471 accgtccctcaagagtcgagtcaccatcatcagtcagtagacacgctcccaagacagttctccc 530
|||||
Qy 182 ACCATCCCTCAAGATCGAGTCTTTCATGCTGTAGACAAAGTCCAAAGGACCAAGTCTCTCCC 241
|||||
Db 531 tgaaggtgaactctgtcaccgcgcgagacacgcccgtgtattactgtgcgaga 583
|||||
Qy 242 TGAAGTGTAGCTCTGTGACCCGCGGAGACAGCGCCGTGTATTACTGTGGGAGA 294
|||||

RESULT 3
ID Q78993 standard; DNA; 800 BP
AC Q78993;
DT 04-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #55.
KW cosmid; placenta; human; immunoglobulin; variable; heavy chain;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 230..675
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 276..358
FT /tag= b
FT /tag= c
FT /tag= c
FT /tag= d
FT /note= "miscellaneous signal, does not conform to
terminator or splice site sequence"
PN WO9426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB: R66343.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
production of human immunoglobulin in mammalian hosts
PS Claim 62; Page 102-103; 130pp; Japanese.
CC A series of genes (078939-79002) encoding human immunoglobulin variable
heavy chains. The genes were isolated and cloned from a series of cosmid
constructs: Y202; Y103; Y21; Y6:Y24; 3-31; M84; M18 and M131, by PCR
amplification using primers Q78917-38. The genes are subdivided into 5
families of Vh genes. The fragments cover a region of 800 kb. The DNA
fragments were isolated from high molecular weight DNA from human
placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
were collected. The fragments were ligated with ClaI-digested cosmid
vector pJB81. The ligation products were in vitro packed and infected
CC - into E.coli 490A. The fragments were then subcloned by colony
hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 800 BP; 184 A; 235 C; 219 G; 154 T;

Query Match 58.7%; Score 222; DB 13; Length 800;
Best Local Similarity 87.8%; Pred. No. 1.09e-131;

[illegible]

```

DE 01-NOV-1993 (first entry)
DE V4116.
KW Monoclonal antibody; MAb; envelope, glycoprotein, gp120, HIV, AIDS,
KW CD4, receptor, hybridoma, polymerase chain reaction, PCR, heavy, light,
KW chain; epitope; immune deficiency; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..348
FT /*tag= b
FT misc_RNA 148..162
FT /*tag= c
FT /label= CDR1
FT /label= CDR2
FT misc_RNA 205..252
FT /*tag= d
FT /label= CDR2
PN WO9312232-A.
PD 24-JUN-1993.
PR 10-DEC-1992; U10928.
PR 10-DEC-1992; US-804652.
PA (DAND) DANA FARBER CANCER INST INC.
PA (NEW) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
PI WPI: 93-214174/26.
DR DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
PS Disclosure: Page 56-58; 109pp; English.
CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
CC to several similar germline Vh IV genes. F105 Vh shares greatest
CC sequence similarity with germline Vh 71-4 (Q42697). Non-rearranged
CC Vh IV germlines Vh 4.11 (Q42699), 4.15 (Q42700) and 4.16 (Q42701),
CC that were identified by PCR amplification of genomic DNA from an
CC adult healthy Caucasian donor, are most closely related to Vh 71-4.
SQ Sequence 348 BP, 72 A, 102 C, 96 G, 78 T.

Query Match 54.5%; Score 206; DB 7; Length 348;
Best Local Similarity 87.7%; Pred No. 1,96e-120;
Matches 257; Conservative 0; Mismatches 33; Indels 3; Gaps 2;

Db 59 aggtcagctgcagagtgagtcggccgagcagactggtgaagccttcggacacccctgtccctca 118
QY 2 AGGTGAGCTGCTCGAGTCGGCGCCGAGGACTGGTGAAGCCCTTCGGGAGCCCTGTCCCTCA 61

Db 119 cctgcaactctctagtgagtcacatcagtaagt--t-actactgagctgaatccgagc 175
QY 62 CTGCACTCTCTGTGGCTTCATCAGAGCAGTCACCTGCTGGAGTGGTGGTGGTGGTGGTGG 121

Db 176 ccccaagggaaggagctgagtgagtgattgggtatctattacagtgaggagcaccacactaca 235
QY 122 CCCCAGGGAAGGAGTGGAGTGGATTGGAGAGAGTCTTTTGTAGTGAAGCACCACCTACATA 181

Db 236 accctccctcaagagtcagatcaccatcatcagtagacacatcccaagaaccagttctccc 295
QY 182 ACCATCCCTCAACGATCGAGCTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241

Db 296 tgaagctgagctctgtgacccgtgcggacagccgctgtattactgtgcgaga 348
QY 242 TGAGGCTGAGCTCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGTGTGTGTGTGTGT 294

RESULT 9
ID Q78997 standard; DNA: 622 BP.
AC Q78997.
DE 04-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #59.
KW Primer: PCR amplification of human immunoglobulin, variable, heavy chain,
KW cosmid; placenta; vector: pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..351
FT CDS
FT /*tag= b

/prefix= human immunoglobulin variable heavy chain
FT intron 198..279
FT /*tag= b
FT misc_signal 592..584
FT /*tag= c
FT /note= "miscellaneous signal, does not conform to
FT terminator or splice site sequence"
PN WO9426895-A.
PD 24-NOV-1994.
PR 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NISB) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
PI WPI: 95-006791/01.
DR P-FSDB: P65346
DP DNA fragment comprising human immunoglobulin Vh genes - for the
DP production of human immunoglobulin in mammalian hosts
PS Disclosure: Page 107-108; 130pp; Japanese.
CC Protein sequences (R66300-51) are novel human immunoglobulin heavy chain
CC sequences encoded by 50 novel genes. The genes (Q78044-79002) were
CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
CC Y6Y24; 3-31; M84; M18 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TagI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with clai-digested cosmid vector pJB81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
CC immunoglobulin in mammalian hosts.
SQ Sequence 622 BP; 144 A; 180 C; 160 G; 138 T;

Query Match 54.5%; Score 206; DB 13; Length 622;
Best Local Similarity 87.7%; Pred No. 1,96e-120;
Matches 257; Conservative 0; Mismatches 33; Indels 3; Gaps 2;

Db 292 aggtcagctgcagagtcggccgagcagactggtgaagccttcggacacccctgtccctca 351
QY 2 AGGTGAGCTGCTCGAGTCGGCGCCGAGGACTGGTGAAGCCCTTCGGGAGCCCTGTCCCTCA 61

Db 352 cctgcaactctctgtgagtcacatcagtaagt--t-actactgagctgaatccgagc 408
QY 62 CTGCACTCTCTGTGGCTTCATCAGAGCAGTCACCTGCTGGAGTGGTGGTGGTGGTGGTGG 121

Db 409 ccccaagggaaggagctgagtgagtgattgggtatctattacagtgaggacacacactaca 468
QY 122 CCCCAGGGAAGGAGTGGAGTGGATTGGAGAGAGTCTTTTGTAGTGAAGCACCACCTACATA 181

Db 469 accctccctcaagagtcagatcaccatcatcagtagacacatcccaagaaccagttctccc 528
QY 182 ACCATCCCTCAACGATCGAGCTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241

Db 529 tgaagctgagctctgtgacccgtgcggacagccgctgtattactgtgcgaga 581
QY 242 TGAGGCTGAGCTCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGTGTGTGTGTGTGT 294

RESULT 10
ID Q42702 standard; DNA: 351 BP.
AC Q42702.
DE 01-NOV-1993 (first entry)
DE Ab26.
KW Monoclonal antibody; MAb; envelope, glycoprotein, gp120; HIV; AIDS;
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..351
FT /*tag= b

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FT misc_RNA 148..165
FT /*tag= c
FT /label= CDR1
FT misc_RNA 208..255
FT /*tag= d
FT /label= CDR2
PN W09312232-A.
PD 24-JUN-1993.
PF 10-DEC-1992; U10928.
PR 10-DEC-1991; US-804652.
PA (DAND ) DANA FARBER CANCER INST INC.
PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sotiroski JS.
DR WPI: 93-214174/26.
DR P-PSDB: R38669.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection.
PS Disclosure: Page 62-63; 109pp; English.
CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
CC to two monoclonal antibodies (Ab26 - Q42702) and 268-D - Q42703),
CC which by nucleotide sequence analysis, appear to use a rearranged
CC Vh 71-4 gene (Q42697).
CC Ab26 (Q42702) was derived from CD5+ B cells of a healthy donor and
CC represents a naturally occurring polyclonal antibody which binds to
CC many antigens. Ab26 shares greatest sequence similarity with germline
CC Vh 71-4.
SQ Sequence 351 BP, 72 A, 99 C, 99 G, 81 T;

Query Match 54.2%, Score 205, DB 7; Length 351.
Best Local Similarity 85.2%; Pred. No. 9, 62e-120;
Matches 248, Conservative 0, Mismatches 43, Indels 0, Gaps 0;

Db 59 aggtgcagctgcaggagtcggccagagctgtgaagccttcacagaccctgtccctca 118
QY 2 AGGTGCAGCTGCTGTCGAGTGGGCGCCAGGACTGTGGAAGCTTCGGGGAGCCCTGTCCCTCA 61

Db 119 ctgcaactgtctgtgctccatcagtagtggtgattactggagctggagtcgcgcagc 178
QY 62 CTGCACTGCTCTGTGTCCTCCATCAGGAGCAGTCACTGTCGAGTGGGTCCGCGCAGC 121

Db 179 acccaggaaggcgtggagtgattgggtacatatattacagtgaggagcaccacataca 238
QY 122 CCCAGGAAAGGACTGGAGTGGATTGGAGAGTCTTTTATAGTGAAGCACCATTCTACA 181

Db 239 accctccctcaagactgagtgccatcagtaggcacgtcttaagaccagttctccc 298
QY 182 ACCATCCCTCAACGATCGAGTCTTCATGCTGTGTAGACAAGTCTAAGGACCCAGGTCTCCC 241

Db 299 tgaagctgagctgtgaccgctgcggacacgcccgtgtattactgtgcga 349
QY 242 TGAGGCTGAGCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCGA 292

RESULT 11
ID Q78942 standard; DNA; 650 BP.
AC Q78942;
DT 07-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #4.
KW Primer; PCR, amplify; human; immunoglobulin, variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 91..519
FT /*tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 137..217
FT /*tag= b
FT misc_signal 520..522
FT /*tag= c
FT /note= "miscellaneous signal, does not conform to
FT terminator or splice site sequence"
PN W09426895-A.

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PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NISB ) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-PSDB: R66298.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Disclosure: Page 34-35; 130pp; Japanese.
CC A series of genes (Q78939-7902) encoding human immunoglobulin variable
CC heavy chains. The genes were isolated and cloned from a series of cosmid
CC constructs: Y202; Y103; Y21; Y6.Y24; 3-31; M84; M118 and M131; by PCR
CC amplification using primers Q78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 650 BP, 142 A, 186 C, 199 G, 123 T;

Query Match 54.0%; Score 204; DB 13; Length 650;
Best Local Similarity 87.4%; Pred. No. 4, 71e-119;
Matches 256, Conservative 0, Mismatches 34, Indels 3, Gaps 2;

Db 230 aggtgcagctgcaggagtcggccagagctgtgaagccttcggagagcctgtccctca 240
QY 2 AGGTGCAGCTGCTGTCGAGTGGGCGCCAGGACTGTGGAAGCTTCGGGGAGCCCTGTCCCTCA 61

Db 290 cctgcagctgtctgtggtccctccatcagtagt--t-actactggagctggatccggcagc 346
QY 62 CTGCACTGCTCTGTGTCGTCCTCCATCAGGAGCAGTCACTGTCGAGTGGGTCCGCGCAGC 121

Db 347 ccgcgcggaaggagctgagtggtgattgggggtattaccagtgaggagcaccacataca 406
QY 122 CCCAGGAAAGGACTGGAGTGGATTGGAGAGTCTTTTACTGGAAGCACCATTCTACA 181

Db 407 accctccctcaagagctgagtcacccatgtcagtagacgctcccaagaccagttctccc 466
QY 182 ACCATCCCTCAACGATCGAGTCTTCATGCTGTGTAGACAAGTCTAAGGACCCAGGTCTCCC 241

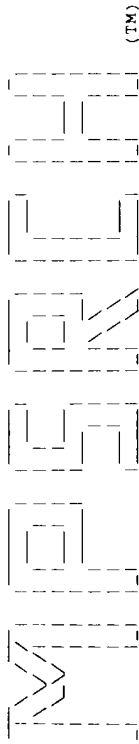
Db 467 tgaagctgagctgtgaccgctgcggacacgcccgtgtattactgtgcga 519
QY 242 TGAGGCTGAGCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCGA 294

RESULT 12
ID Q78977 standard; DNA; 799 BP.
AC Q78977;
DT 04-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #39.
KW Primer; PCR, amplify; human; immunoglobulin, variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 268..703
FT /*tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 314..395
FT /*tag= b
FT misc_signal 704..706
FT /*tag= c
FT /note= "miscellaneous signal, does not conform to
FT terminator or splice site sequence"
PN W09426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NISB ) JAPAN TOBACCO INC.

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PI Honjo T, Matsuda F.
 DR WPI: 95-006791/01.
 DR P-PSDB: R66329.
 PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PS production of human immunoglobulin in mammalian hosts
 PS Disclosure: Page 81-82, 130pp, Japanese.
 CC A series of genes (Q78939-79002) encoding human immunoglobulin variable
 CC heavy chains. The genes were isolated and cloned from a series of cosmid
 CC constructs: Y202, Y103, Y21, Y6, Y24, 3-31, M84, M18 and M131. By PCR
 CC amplification using primers Q78917-38. The genes are subdivided into 5
 CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
 CC fragments were isolated from high molecular weight DNA from human
 CC placenta. The DNA was partially digested with *TaqI* restriction enzyme.
 CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
 CC were collected. The fragments were ligated with *ClaiI*-digested cosmid
 CC vector pJBB1. The ligation products were in vitro packed and infected
 CC into *E.coli* 490A. The fragments were then subcloned by colony
 CC hybridisation. The Vh genes and the DNA fragments encoding them are
 CC useful in producing human immunoglobulin in mammalian hosts.
 SQ Sequence 799 BP: 181 A: 224 C: 227 G: 165 T:
 Query Match 53.7% Score 203; DB 13; Length 799;
 Best Local Similarity 86.8%; Pred. No. 2.31e-118;
 Matches 257; Conservative 0; Mismatches 36; Indels 3; Gaps 2;
 Db 408 agctcagctgcagagtcgagccagcagactgctgaacccctcagagaccctatccctca 467
 QY 2 AGTGTGAGCTGTCTGAGTCTGGGCTCCAGGACTGTGTGAAGCTTCGGGACCTGTGCTCCCA 61
 Db 468 cctgcactgtctctgtggtcctccatcagcagtagtagtactactggtgggtggatccgcc 527
 QY 62 CCGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 118
 Db 528 aaccccaaggaagggctggaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 587
 QY 119 AGCCCCCGGAGGAGGACTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 178
 Db 588 acaaccctccctcagagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 647
 QY 179 ACAACCCATCCCTCAACGATGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 238
 Db 648 cctgaagctgagctctgtaacccgcagcagcagcagcagcagcagcagcagcagcagcag 703
 QY 239 CCTGAGGCTGAGCTGTGTGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 294
 RESULT 13
 ID T79919 standard: DNA: 408 BP.
 AC T79919;
 DT 09-OCT-1997 (first entry)
 DE Immunoglobulin rB6H7 heavy chain variable region coding sequence.
 KW Immunoglobulin: variable region; heavy chain; thyrotropin receptor;
 KW thyroid stimulating activity; light chain; Basedow's disease; antibody;
 KW peripheral blood lymphocyte; ss.
 OS Homo sapiens.
 PN J09140386-A.
 PD 03-JUN-1997.
 PF 22-NOV-1995; 328235.
 PR 22-NOV-1995; JP-328235.
 PA (EIKE) EIKEN KAKAKU KK.
 DR WPI: 97-344899/32.
 DR P-PSDB: W24536
 PT Antibody containing immunoglobulin heavy chain mutation - with
 PT thyroid function stimulating activity
 PS Claim 1: Page 12; 18pp; Japanese.
 CC T79919-T79922 represent the immunoglobulin heavy and light chain variable
 CC regions isolated from peripheral blood lymphocyte strains. These
 CC blood lymphocytes of a Basedow's disease patient. These sequences are
 CC replaced, deleted or inserted into an antibody. To create the antibodies
 CC of the invention. The antibodies of the invention have thyroid function
 CC stimulating activity, and act by combining with thyrotropin receptor. The
 CC antibody can be used in a method to detect autoantibodies which have

CC thyroid function stimulating activity.
 SQ Sequence 408 BP: 90 A: 110 C: 119 G: 89 T:
 Query Match 52.9% Score 200; DB 22; Length 408;
 Best Local Similarity 86.7%; Pred. No. 2.72e-116;
 Matches 254; Conservative 0; Mismatches 36; Indels 3; Gaps 2;
 Db 59 aggtcagctgcagagtcgagccagcagactggtgagaccccttcgagaccccttcgaccca 118
 QY 2 AGGTGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 61
 Db 119 cctgcactgtctctgtgactccatcagtagt--t-actactgagctgagtcgagcagc 175
 QY 62 CCGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 121
 Db 176 ccccaaggaaggaagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 235
 QY 122 CCGCAAG 181
 Db 236 actctcctcagagagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 295
 QY 182 ACCCATCCCTCAACGATGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTCC 241
 Db 296 taagctgagctgtgtgacccgtgagcagcagcagcagcagcagcagcagcagcagcag 348
 QY 242 TGAGGCTGAGCTCTGTGTGAGCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
 RESULT 14
 ID Q33035 standard: cDNA: 366 BP.
 AC Q33035;
 DT 06-MAY-1993 (first entry)
 DE MAB 1-3-1 variable region of heavy chain.
 KW Monoclonal antibody: hybridoma; PCR: variable region;
 KW constant region; heavy chain; light chain; ss.
 OS Synthetic
 PN EP-520499-A.
 PD 30-DEC-1992.
 PF 26-JUN-1992; 110841.
 PR 28-JUN-1991; JP-158860.
 PR 28-JUN-1991; JP-158860.
 PR 28-JUN-1991; JP-158861.
 PA (MITU) MITSUBISHI KASEI CORP.
 PI Hirakawa Y, Hosokawa S, Ito N, Nagaike K, Tagawa T;
 DR WPI: 93-001328/01.
 DR P-PSDB: R30145.
 PT Human monoclonal antibody specific for a cancer cell membrane
 PT surface antigen - prepd. from a hybridoma obt'd. by cell fusion
 PT between human lymphocytes derived from cancer patients and mouse
 PT myeloma cells
 PS Claim 17; Page 31 + 18; 37pp; English.
 CC A human MAb specifically binding to a surface antigen of cancer
 CC cell membrane comprises variable regions of the heavy and light
 CC chains having the amino acid sequences of R30145-46 respectively.
 CC encoded by DNA sequences Q33035-36 respectively.
 SQ Sequence 366 BP: 76 A: 105 C: 111 G: 74 T:
 Query Match 52.4% Score 198; DB 5; Length 366;
 Best Local Similarity 86.1%; Pred. No. 6.51e-115;
 Matches 254; Conservative 0; Mismatches 38; Indels 3; Gaps 2;
 Db 2 agctcagctgcagagtcgagccagcagactggtgagaccccttcgagaccccttcgaccca 61
 QY 2 AGGTGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 61
 Db 62 cctgcactgtctgtgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 121
 QY 62 CCGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 118
 Db 122 agccccaggaagggctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 181
 QY 119 AGCCCCCGGAGGAGGACTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 178



(TM)

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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 12:05:34 1998: Maxpar time 469.87 Seconds
Tabular output not generated
1142.715 Million cell updates/sec

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Scoring table: TABLE default
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Listing first 45 summaries

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1: BCT 2: FUN 3: GEN 4: HTO 5: HTO 6: HTO 7: HTO 8: HUM
9: HUM 10: HUM 11: INV 12: INV 13: INV 14: INV 15: VPT
16: PLN 17: PLN 18: PLN 19: PLN 20: SYN 21: SYN 22: VPT
genbank101
23: BCT 24: BCT 25: BCT 26: BCT 27: BCT 28: BCT 29: BCT
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36: GEN 37: GEN 38: GEN 39: GEN 40: GEN 41: GEN 42: HTO
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121: VPT 122: VPT 123: VPT 124: VPT 125: VPT
Database: genbank-new7
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138: VPT 139: VPT 140: VPT 141: VPT
Database: u-emb151_101
142: VPT 143: VPT

Statistics: Mean 10.163: Variance 4.887: scale 2.080
Pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	245	64.8	366	95	Human immunoglobulin	4,12e-180
2	244	64.6	432	91	H.sapiens mRNA for XL	3,61e-179
3	244	64.5	432	91	H.sapiens mRNA for XL	3,61e-179
4	243	64.3	294	96	Human V(H)IV family	2,24e-178
5	243	64.3	294	91	H.sapiens germline Ig	2,24e-178
6	243	64.3	308	99	Human Ig germline H-C	2,24e-178
7	243	64.3	317	96	Human anti streptococ	2,24e-178
8	243	64.3	363	95	Human immunoglobulin	2,24e-178
9	243	64.3	363	95	Human immunoglobulin	2,24e-178
10	243	64.3	414	91	H.sapiens mRNA for XL	2,24e-178
11	243	64.3	414	91	H.sapiens mRNA for XL	2,24e-178
12	243	64.3	465	91	H.sapiens germline im	2,24e-178
13	243	64.3	465	99	Human immunoglobulin	2,24e-178
14	239	63.2	364	95	Human immunoglobulin	6,57e-175
15	239	63.2	423	91	H.sapiens mRNA for XL	6,57e-175
16	239	63.2	423	91	H.sapiens mRNA for XL	6,57e-175
17	239	63.2	423	91	H.sapiens mRNA for XL	6,57e-175
18	239	63.2	423	91	H.sapiens mRNA for XL	6,57e-175
19	239	63.2	437	96	H.sapiens IG VH mRNA	6,57e-175
20	239	63.2	626	91	Human Ig heavy chain	6,57e-175
21	239	63.2	6036	90	H.sapiens DNA for BCL	6,57e-175
22	239	63.2	6036	137	H.sapiens DNA for BCL	6,57e-175
23	239	63.2	6036	8	H.sapiens mRNA for BCL	6,57e-175
24	237	62.7	420	91	H.sapiens mRNA for XL	3,55e-173
25	237	62.7	420	91	H.sapiens mRNA for XL	3,55e-173
26	235	62.2	294	96	Human V(H)IV family	1,92e-171
27	235	62.2	294	96	Human V(H)IV family	1,92e-171
28	235	62.2	294	91	Human Ig germline Ig	1,92e-171
29	235	62.2	312	99	Human Ig germline H-C	1,92e-171
30	235	62.2	466	91	H.sapiens germline im	1,92e-171
31	234	61.9	335	96	H.sapiens gene encodi	1,41e-170
32	234	61.9	426	91	H.sapiens germline im	1,41e-170
33	233	61.6	414	93	H.sapiens mRNA for Ig	1,03e-169
34	232	61.4	291	99	Human immunoglobulin	7,59e-169
35	232	61.4	426	91	H.sapiens germline im	7,59e-169
36	232	61.4	426	91	H.sapiens germline im	7,59e-169
37	230	60.8	365	95	Human immunoglobulin	4,09e-167
38	229	60.6	332	93	H.sapiens mRNA for Ig	3,00e-166
39	229	60.6	594	91	Human Ig heavy chain	3,00e-166
40	228	60.3	427	91	H.sapiens germline im	2,10e-165
41	227	60.1	375	92	H.sapiens germline im	1,91e-164
42	227	60.1	416	91	H.sapiens mRNA for XL	1,61e-164
43	227	60.1	416	91	H.sapiens mRNA for XL	1,61e-164
44	227	60.1	423	91	H.sapiens mRNA for XL	1,61e-164
45	227	60.1	423	91	H.sapiens mRNA for XL	1,61e-164

ALIGNMENTS

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RESULT LOCUS HSU80141 366 bp DNA PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V4-4b) gene.
partial cds.
ACCESSION U80141
NID 91791124
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 366)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient.
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 97182739

REFERENCE 2 (bases 1 to 366)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 TITLE Direct Submission
 JOURNAL Submitted (29-Nov-1996) Immunology, Virginia Mason Research Center,
 1000 Seneca Street, Seattle, WA 98101, USA

FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /note="CD19+ peripheral blood B cells obtained from a bone marrow transplant recipient 1 year post transplant; clone 66 in reference 1"
 /cell_type="CD19+ B cells"
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 /chromosome="14"
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 /db_xref="PID:g1791125"
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BASE COUNT 74 a 109 c 110 g 73 t

ORIGIN
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 Best Local Similarity 91.0%; Pred. No. 4,12e-180;
 Matches 272; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 2 aggtgcagctgcaggagtcggccaggagctggtgaagccttcggggaccctgtccctca 61
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Db 62 cctgcctctctgtgctcctcaccagcagtagtaactggtgagtggtggtccgcagc 121
 QY 62 CCTGCCTCTCTGTGCTCCTCACCAGCAGTAGTAAGTGGTGGTGGTGGTGGTGGTGG 121

Db 122 cccacaggaggagctggtgagtgattgggaaatctatcatagtgaggagcaccactaca 181
 QY 122 CCCACAGGAGGAGCTGGATGGAGAGTCTTTTATTAGTGAAGCACCATCTACA 181

Db 182 accgtccctcaagatcgagtcaccatcatcagtagacaagtcacgaaccagttctccc 241
 QY 182 ACCGTCCTCTCAAGATCGAGTCACCATCATCAGTAGACAGTCTTCTGTAGAACGTC 241

Db 242 tgaagctgagctgtgacccgcgggacacgcccgtgtattactgtgcgagagtcctccc 300
 QY 242 TGAGGCTGAGCTGTGACCGCGGGACACGCCCGTGTATTACTGTGCGAGATCTCCC 300

RESULT 2
 LOCUS HSIGHXX26 432 bp PNA PPT 07-DEC-1993
 DEFINITION H sapiens mRNA for XLA Ig heavy chain VDJ region (LE 4-56)
 ACCESSION X65908 S58699
 NID g395106
 KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region;
 variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 432)
 Schifff C.
 Direct Submission
 Submitted (08-APP-1992) C. Schifff, Centre d'Immunologie de
 Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
 REFERENCE 2 (bases 1 to 432)
 AUTHORS Milili,M., Le Velst,F., de Saint-Basile,G., Fischer,A.,

Fougereau,M. and Schifff,C.
 Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
 J. Clin Invest. 91 (4), 1616-1620 (1993)

FEATURES
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 /clone="LE 4-56"
 /chromosome="14"
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 sig_peptide 58..352
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BASE COUNT 88 a 126 c 123 g

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 Best Local Similarity 91.2%; Pred. No. 3,03e-179;
 Matches 270; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 59 aggtgcagctgcaggagtcggccaggagctggtgaagccttcggggaccctgtccctca 118
 QY 2 AGGTGCAGCTGCTCGAGTCGGGCCAGGACTGGTGAAGCTTCGGGGACCTGTCTCC 61

Db 119 cctgcctctctgtgctcctcaccagcagtagtaactggtgagtggtggtccgcagc 178
 QY 62 CCTGCCTCTCTGTGCTCCTCACCAGCAGTAGTAAGTGGTGGTGGTGGTGGTGGTGG 121

Db 179 cccacaggaggagctggtgagtgattgggaaatctatcatagtgaggagcaccactaca 238
 QY 122 CCCACAGGAGGAGCTGGATGGAGAGTCTTTTATTAGTGAAGCACCATCTACA 181

Db 239 accgtccctcaagatcgagtcaccatcatcagtagacaagtcacgaaccagttctccc 298
 QY 182 ACCGTCCTCTCAAGATCGAGTCTCATCTGTGTAGAACGTCATTAAGTGAAGTCTCC 241

Db 299 tgaactgagctgtgacccgcgggacacgcccgtgtattactgtgcgagagtcctccc 354
 QY 242 TGAGGCTGAGCTGTGACCGCGGGACACGCCCGTGTATTACTGTGCGAGATCTCC 297

RESULT 3
 ID HSIGHXX26 standard; RNA; HUM; 432 BP.
 AC X65908; S58699;
 NI g395106
 DT 13-JUL-1993 (Rel. 36, Created)
 DT 26-JUL-1997 (Rel. 52, Last updated, Version 8)
 DE H sapiens mRNA for XLA Ig heavy chain VDJ region (LE 4-56)
 KW diversity region; Ig heavy chain; immunoglobulin; joining region;
 KW variable region.
 OS Homo sapiens (human)
 OC Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 OC Homo.
 RN [1]
 RP 1-432
 RA Schifff C.;
 RT Submitted (08-APP-1992) to the EMBL/GenBank/CDR databases.
 PL C. Schifff, Centre d'Immunologie de Marseille, Case 906, 13288
 PL Marseille, Cedex 9, FRANCE
 RN [2]
 RP 1-432
 RT MEDLINE; 93232287.


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Best Local Similarity 91.5%; Pred. No. 2,24e-178;
Matches 268; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 2 aggtgcagctgcagagtcggccagagctggtagaagccttcgggaacccctgtccctca 61
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Db 62 cctgcactctctctggtggtccatcagcagctagtaactggtgagttgggtccgcagc 121
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Qy 62 CCTGCACCTCTCTGCTGCTCCATCAGGAGCAGTCTGCTGGTGGAGTTGGTCCGCGAGC 121

Db 122 ccccaaggaggggtgagtagattggggaattctatcatagtgaggagcacaactaca 181
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Qy 122 CCCACAGGGAAGGAGCTGAGAGTGGATTTGGAGAGTCTTTTTTAGTGGAGGACCACTATCA 181

Db 182 accgctccctcaagatcagtcacccatcagtagacaaatccaaagacagttctccc 241
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Qy 182 ACCCATCCCTCAACGATCGAGTCTTCATGCTGTGTAGACAAGTCCAAAGGACAGGTCTCC 241

Db 242 tgaagctgagctctgacccgcgaggacagcccgctgtattactgtgcgaga 294
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Qy 242 TGAGCTGAGCTCTGACGCGGCGGAGACAGCGCGCTGTATTACTGTGCGGAGA 294

RESULT 6 HUMIGHCAD 308 bp DNA PRI 09-NOV-1994
LOCUS Human Ig germline H-chain gene V4-region, partial cds.
DEFINITION
ACCESSION L10091
NID g185221
KEYWORDS V-region; germline; immunoglobulin heavy chain.
SOURCE Homo sapiens (tissue library: 3116 EMBL3) Male Adult blood DNA.
ORGANISM Homo sapiens
Eukaryotes; Eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 308)
AUTHORS Bull, A., and Milner, E.C.
Bull, A., and Milner, E.C.
Chromosomal organization of the human VH4 gene family. Location of
individual gene segments
J. Immunol. 150 (7), 2858-2868 (1993)
MEDLINE 93203606
FEATURES
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Best Local Similarity 91.5%; Pred. No. 2,24e-178;
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Db 70 cctgcactctctctggtggtccatcagcagctagtaactggtgagttgggtccgcagc 129
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Db 130 ccccaaggaggggtgagtagattggggaattctatcatagtgaggagcacaactaca 189
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Qy 122 CCCACAGGGAAGGAGCTGAGAGTGGATTTGGAGAGTCTTTTTTAGTGGAGGACCACTATCA 181

Db 190 accgctccctcaagatcagtcacccatcagtagacaaatccaaagacagttctccc 249
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Qy 182 ACCCATCCCTCAACGATCGAGTCTTCATGCTGTGTAGACAAGTCCAAAGGACAGGTCTCC 241

Db 250 tgaagctgagctctgacccgcgaggacagcccgctgtattactgtgcgaga 302
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Qy 242 TGAGCTGAGCTCTGACGCGGCGGAGACAGCGCGCTGTATTACTGTGCGGAGA 294

RESULT 7 HSU96389 317 bp mRNA PRI 12-MAY-1997
LOCUS Human anti-streptococcal/anti-mysin immunoglobulin heavy chain
DEFINITION variable region mRNA, partial cds.
ACCESSION U96389
NID g2078357
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 317)
AUTHORS Adderson, E. E., Shinkman, A. P., Ward, K. E., and Cunningham, M. W.
Molecular analysis of human anti-streptococcal/anti-mysin antibody
V region genes from rheumatic carditis
Unpublished
REFERENCE 2 (bases 1 to 317)
AUTHORS Adderson, E. E.
Direct Submission
TITLE Submitted (04-APR-1997) Pediatrics, University of Utah, 50 N.
Medical Drive, Salt Lake City, UT 84132, USA
JOURNAL
FEATURES
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BASE COUNT 66 a 86 c 105 g 60 t
ORIGIN
Query Match 64.3%; Score 243; DB 96; Length 317;
Best Local Similarity 91.5%; Pred. No. 2,24e-178;
Matches 268; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 2 aggtgcagctgcagagtcggccagagctggtagaagccttcgggaacccctgtccctca 61
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Db 62 cctgagcgtctctctgagtcctccatccacagtaactaactgtagtgtagtgcgcagc 121
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Db 182 accctccctcaagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 241
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QY 242 TGAGGCTGAGCTCTGTGAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 294
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RESULT 8 HSP80179 363 bp DNA PFI 19-FEB-1997
LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene,
DEFINITION partial cds.
ACCESSION U80179
NID g1791200
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo
REFERENCE 1 (bases 1 to 363)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 97182739
REFERENCE 2 (bases 1 to 363)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
FEATURES
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BASE COUNT 75 a 108 c 108 g 71 t
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Query Match 64.3%; Score 243, DB 95, Length 363,
Best Local Similarity 91.5%; Pred. No. 2,24e-178;
Matches 268, Conservative 0, Mismatches 25, Indels 0; Gaps 0.

Db 2 agtgcagctcagaaatccagccagagctcagaaatccagccagagctcagaaatccagaa 61
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Db 62 cctgagcgtctctctgagtcctccatccacagtaactaactgtagtgtagtgcgcagc 121
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RESULT 9 HSP80180 368 bp DNA PFI 19-FEB-1997
LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene,
DEFINITION partial cds
ACCESSION U80180
NID g1791202
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo
REFERENCE 1 (bases 1 to 368)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 97182739
REFERENCE 2 (bases 1 to 368)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
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Location/Qualifiers
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BASE COUNT 81 a 101 c 111 g 75 t
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Query Match 64.3%; Score 243, DB 95, Length 368;
Best Local Similarity 91.5%; Pred. No. 2,24e-178;
Matches 268, Conservative 0, Mismatches 25, Indels 0; Gaps 0.

Db 2 agtgcagctcagaaatccagccagagctcagaaatccagccagagctcagaaatccagaa 61
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QY 2 AGTGCAGCTCAGAAATCCAGCCAGAGCTCAGAAATCCAGCCAGAGCTCAGAAATCCAGAA 61
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Db 62 cctgagcgtctctctgagtcctccatccacagtaactaactgtagtgtagtgcgcagc 121
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immunoglobulin G: auto- and multi-reactivity, diverse VH gene

source 1...

immunoglobulin G: auto- and multi-reactivity, diverse VH gene

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BASE COUNT 78 a 106 c 108 g 72 t
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Query Match 63.2%; Score 239; DB 95; Length 364;
Best Local Similarity 91.1%; Pred. No. 6.57e-175;
Matches 265; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Db 62 cctgcgctgtctgtgactcctacagcagcagtagtaactggtgagtggtgcgcgcagc 121
QY 62 CCTGCAGCTGCTCTGTGTGCTCCATCAGGAGCAGTCACTGTGGAGTTGGGTCCGCCAGC 121
Db 122 cccagggaagggtgagtgatggggaaatctatcatagtgaggagaccacactaca 181
QY 122 CCCAGGGAAGGACTGGAGTGGATTGGAGAACTCTTTTATGTGGAAGCACCATCTACA 181
Db 182 accgctccctcaagctcagtcaccatcatcagtagacaagtcacaagaccagttctccc 241
QY 182 ACCATCCCTCAACGATCGAGTCTTCATGTTGTGTGAGCAAGTCCCAAGGACCAAGTCTCCC 241
Db 242 tgaagctgagctgtgacgcgcgcggacacgagcagtggtattactgtgcga 292
QY 242 TGAGGCTGAGCTGTGTGAGCGCGCGACACGCGCGTGTATTACTGTGCGA 292

RESULT 15
LOCUS HSIHXX20 423 bp RNA PRI 02-DEC-1993
DEFINITION H. sapiens mRNA for XLA Ig heavy chain VDJ region (LE 4-104).
ACCESSION X65902 S58671 S58672
NID g395100
KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region;
variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 423)
Schiff, C
Direct Submission
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE 2 (bases 1 to 423)
Millili, M., Le Deist, F., de Saint-Basile, G., Fischer, A.,
Fougereau, M. and Schiff, C.
Bone marrow cells in X-linked agammaglobulinemia express
pre-B-specific genes (lambda-like and V pre-B) and present
immunoglobulin V-D-J gene usage strongly biased to a fetal-like
repertoire
J. Clin. Invest. 91 (4), 1616-1629 (1993)
J232287
FEN:RES Location/Qualifiers

source 1..423
/organism="Homo sapiens"
/tissue_type="bone marrow"
/cell_type="pre-B"
/clone_lib="LE library"
/clone="LE 4-104"
/chromosome="14"
1..57
sig_peptide 58..352
misc_feature /note="variable region"
353..376
misc_feature /note="diversity region"
377..423
misc_feature /note="joining region"
BASE COUNT 89 a 117 c 120 g 97 t
ORIGIN
Query Match 63.2%; Score 239; DB 91; Length 423;
Best Local Similarity 90.8%; Pred. No. 6.57e-175;
Matches 266; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Db 59 aggtgcagctgcaggagtcggcccgagcactggtgaagccttcggggaccctgtccctca 118
QY 2 AGGTGCAGCTGCTCGAGTCGGGCGCCAGGACTGGTGAAGCCTTCGGGGACCCGTGCCCTCA 61
Db 119 cctgcgctgtctgtgactcctacagcagcagtagtaactggtgagcactggtgcgcgcagc 178
QY 62 CTTGACTGCTCTGTGCTCCATCAGGAGCAGTCACTGTGAGTGGAGTGGGTCCGCCAGC 121
Db 179 cccagggaagggtgagtgatggggaaatcttcatagtgaggagaccacactaca 238
QY 122 CCCAGGGAAGGACTGGAGTGGATTGGAGAACTCTTTTATGTGGAAGCACCATCTACA 181
Db 239 accgtccctcaagagtcgagtcaccatataatagacaagtcacaagaccacttctccc 298
QY 182 ACCCATCCCTCAACGATCGAGTCTTCATGCTGTAGACAAGTCCCAAGGACCAAGTCTCCC 241
Db 299 tgaagctgagctgtgacgcgcgcggacacgagcagtggtattactgtgcga 351
QY 242 TGAGGCTGAGCTGTGTGAGCGCGCGACACGCGCGTGTATTACTGTGCGAGA 294

Search completed: Tue Feb 24 12:25:36 1998
Job time : 1202 secs.

strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.

/clone="741181"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1...266

Query Match 12.9%, Score 47, DB 54; Length 266;
Best Local Similarity 72.8%; Pred. No. 4.47e-44;
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 38 aggcagagtcacccctgacacaggacacgtccacagacacactctacatgggctgagca 97
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 182 AGGCCGATTTCGTCCTCAGAGACAATCCAGGACACGCTGTTCTGAGATGAGCA 241
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98 gctgagatctgagacagccctctattactgtgcaaga 140
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 242 GCCTGAGACTCGAGGACACGGCTGCTATTACTGTGCGACAGA 284

RESULT 6
LOCUS AA505044 238 bp mRNA EST 02-JUL-1997
DEFINITION aa63901.r1 NCI_CGAP_CCB1 Homo sapiens cDNA clone 825648 5' similar to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
ACCESSION AA505044
NID 92241204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
REFERENCE 1 (bases 1 to 238)
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..238
/organism="Homo sapiens"
/note="Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CREF). cDNA synthesis was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGCGGCTTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.

/clone="825648"
/clone_lib="NCI_CGAP_CCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
<1...238

BASE COUNT 57 a 69 c 66 g 46 t
ORIGIN

Query Match 9.6%; Score 35; DB 35; Length 238;
Best Local Similarity 67.3%; Pred. No. 4.12e-24;
Matches 68; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Db 20 cccggggagtcctgagatctctctgagactctctgagacgtttaccacagcactgg 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 28 CCGGGAGGTCCTGAGACTCTCTGTGCGAGCGTCTACCTTCACAGCGTATGGC 87
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 atccactgggtgcgcagatgcccgaggaaagaactctagt 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 88 ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGCGTGGAGTG 128

RESULT 7
ID HS1300461 standard; RNA; EST: 238 BP.
AC AA505044;
NI 92241204;
DT 04-JUL-1997 (Rel. 52, Created)
DT 04-JUL-1997 (Rel. 52, Last updated, Version 1)
DE aa63901.r1 NCI_CGAP_CCB1 Homo sapiens cDNA clone 825648 5' similar to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
RN 1
RP 1-238
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center
NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Trace considered overall poor quality Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 1.
Location/Qualifiers
1..238
/organism="Homo sapiens"
/note="Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CREF). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGGCTTTTCTTTTCTTTT 3'] Double-stranded cDNA was ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
1 (bases 1 to 511)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)

CONTACT: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from AmerSham
High quality sequence stop: 414.
Location/Qualifiers
1..511
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCGAAGTGGAGCGCCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Patima Bonaldo."
/clone="810397"
/tissue="ovary; Soares ovary tumor NbHOT"
/sex="Female"
/lab_host="DH10B (ampicillin resistant)"
/db_xref="GDB:6040750"
106 a 169 c 124 g 112 t
mRNA
41..>511

Query Match 7.4%; Score 27; DB 17; Length 511;
Best Local Similarity 90.9%; Pred. No. 4,23e-12;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 388 tggggccaggagacactggtcacctctctca 420
||||||| ||| |||||||||||||||||
QY 331 TGGGGCCAGGAACCTGGTCCCGTCTCTCA 363

RESULT 11
ID HS1214338 standard; RNA; EST; 551 BP.
AC AA418907;
NI 92080726
DT 14-MAY-1997 (Rel. 51, Created)
DE 2w01g09.s1 Soares NhMPu S1 Homo sapiens cDNA clone 768064 3'
DE similar to gb:K03191 CYTOCHROME P450 1A1 (HUMAN);.
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
White Y., Wylie T., Waterston R., Wilson R.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
RC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -41ml3 fwd. ET from AmerSham High
CC quality sequence stop: 261.
FH Key Location/Qualifiers
FH 1..551
FT source
FT /organism="Homo sapiens"
FT /note="Organ: mixed (see below); Vector: pT73D-Pac
FT (Pharmacia) with a modified polylinker; Site_1: Not I;
FT Site_2: Eco RI; Equal amounts of plasmid DNA from three
FT normalized libraries (melanocyte 2NBHM, pregnant uterus
FT NBHP0, and fetal heart NDH19W) were mixed, and ss circles
FT were made in vitro. Following HAP purification, this DNA
FT was used as tracer in a subtractive hybridization reaction
FT
FT The driver was PCR-amplified cDNAs from pools of 5,000
FT clones made from the same 3 libraries. The pools consisted
FT of I.M.A.G.E. clones 250232-255223, 340488-345479, and
FT 484488-489479."
FT /clone="768064"
FT /tissue="Pooled human melanocyte, fetal heart, and
FT pregnant uterus"
FT /lab_host="DH10B"
FT complement(<1..>551)
FT mRNA
SQ Sequence 551 BP; 147 A; 127 C; 123 G; 154 T; 0 other;
Query Match 6.6%; Score 24; DB 56; Length 551;
Best Local Similarity 78.6%; Pred. No. 5.15e-08;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 224 gaaataccccccctcactccagccctagtctggtgcttg 265
||||||| ||| ||||||||||| ||||| |||||
Cp 143 GAAATACCTGCCACCCACTCCAGCCCTTGGCTGGAGGCTGG 102

RESULT 12
LOCUS AA488043 259 bp mRNA EST 24-JUN-1997
DEFINITION ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613
5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);.
ACCESSION AA488043
NID 92215474
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 259)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-Merck human EST Project
Unpublished (1997)
TITLE JOURNAL
COMMENT

CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from AmerSham.
Location/Qualifiers
1..259
source
/organism="Homo sapiens"
/note="Organ: lung; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned into: pGEM-11; Primer:

Oligo dT, normal lung. Average insert size: 1.0 kb;
 Uni-ZAP XP Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' -
 /clone="840613"
 /sex="male"
 /dev_stage="72 years"
 /lab_host="SOLR cells (kanamycin resistant)"
 <1..>259

mrna
 BASE COUNT 51 a 99 c 71 g 38 t
 ORIGIN

Query Match 6.3%; Score 23; DB 30; Length 259;
 Best Local Similarity 96.0%; Pred No 1.01e-06;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gggaacgtggtcacccgtctctca 25
 ||||| ||||| ||||| ||||| |||||
 QY 339 GCGAACCTGGTCACCGTCTCTCA 363

RESULT 13
 ID HS1281117 standard; RNA; EST: 259 BP.
 AC AA488043;
 NI 92215474
 DT 27-JUN-1997 (Rel. 52, Created)
 DE ab12f07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840613
 DE 5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);
 KW EST.
 OS Homo sapiens (human)
 OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominidae;
 OC Homo.
 RN [1]
 RP 1-259
 RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
 RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
 RA Martin J., Moore P., Scheinberg K., Steptoe M., Tan F.,
 RA Theising B., White Y., Wylie T., Waterston P., Wilson P.;
 RT "WashU-NCI human EST Project";
 RL Unpublished.
 CC Contact: Wilson RK Washington University School of Medicine 4444
 CC Forest Park Parkway, Box 9501, St. Louis, MO 63108 Tel: 314 286
 CC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is
 CC available royalty-free through LBNL; contact the IMAGE Consortium
 CC (info@image.llnl.gov) for further information Seq primer: -28m13
 CC rev1 ET from Amersham.
 FH Location/Qualifiers
 FT 1..259
 FT /organism="Homo sapiens"
 FT /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI

FT Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
 FT normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
 FT Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'
 FT adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' -
 FT /clone="840613"
 FT /sex="male"
 FT /dev_stage="72 years"
 FT /lab_host="SOLR cells (kanamycin resistant)"
 FT <1..>259
 mrna
 SQ Sequence 259 BP; 51 A; 99 C; 71 G; 38 T; 0 other;

Query Match 6.3%; Score 23; DB 66; Length 259;
 Best Local Similarity 96.0%; Pred No 1.01e-06;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gggaacgtggtcacccgtctctca 25
 ||||| ||||| ||||| ||||| |||||
 QY 339 GCGAACCTGGTCACCGTCTCTCA 363

RESULT 14
 LOCUS
 DEFINITION

P melanogaster STS determined from European Mapping Project
 cosmid.
 ACCESSION 270880
 NID 91263754
 KEYWORDS sequence tagged site.
 SOURCE fruit fly.

ORGANISM
 Drosophila melanogaster

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Arthropoda;
 Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 (Bases 1 to 156)
 European Drosophila Mapping Consortium.
 Direct Submission
 Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,
 Downing St., Cambridge CB2 3EH, England

COMMENT

STS name = Dm36D7S
 clone_name = 36D7
 STS_from_promoter = SP6
 vector_class = cosmid, Lorist 6
 origin_of_clone = Oregon-R
 in_situ_site_primary = 98C
 BLAST program = BLASTN
 database_searched = EMBL
 database_version = 45.0 and updates till date_of_search
 date_of_search = 08-01-1996
 BLAST program = BLASTX
 database_searched = SWISSPROT
 database_version = 32.0
 date_of_search = 15-12-1995.

FEATURES
 source

1..156
 /organism="Drosophila melanogaster"
 /strain="Oregon-R"
 /clone="36D7"

BASE COUNT 28 a 37 c 30 g 27 t 34 others
 ORIGIN

Query Match 6.1%; Score 22; DB 1; Length 156;
 Best Local Similarity 14.7%; Pred. No. 1.83e-05;
 Matches 5; Conservative 23; Mismatches 5; Indels 0; Gaps 0;
 Db 22 sksrrgrcrrkgagksksrrrkkrrk 55
 QY 100 GGTATAGGTTCAGGCAAGGCGCTGAGTGGGTGG 133

RESULT 15

ID HS1259169 standard; RNA; EST: 189 BP.

AC AA465361;

NI 92191528

DT 19-JUN-1997 (Rel. 52, Created)

DE aaz3c11 s1 NCI-CGAP; Hom sapiens cDNA clone 814100 3' similar

DE to gb:D90209 DNA-BINDING PROTEIN TAXPER67 (HUMAN);

KW EST.

OS Homo sapiens (human)

OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP 1-189

RA NCI-CGAP;

RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

RT Tumor Gene Index";

RL Unpublished.

CC Contact: Robert Strausberg, Ph.D. Tel: (401) 464-1650 Email:

CC Robert.Strausberg@nih.gov This clone is available royalty-free

CC through LBNL; contact the IMAGE Consortium (info@image.llnl.gov)

CC for further information. Seq primer: -41m13 fwd. ET from Amersham.

FH Location/Qualifiers

```

FH source
FT 1..189
FT /organism="Homo sapiens"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT was prepared from human tonsillar cells enriched for
FT germinal center B cells by flow sorting (CD20+, IgD-),
FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
FT primed with a Not I - oligo(dT) primer
FT [5'-TGTACCAATCTCAAGTGGAGCGCGCCGCTCAATTTTTTTTTTTTTT-
FT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (
FT Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified pT73 vector. Library wen
FT t
FT through one round of normalization, and was constructed by
FT Bento Soares and M. Fatima Bonaldo."
FT /clone="814100"
FT /clone_lib="NCI_CGAP_GCB1"
FT /tissue_type="germinal center B cell"
FT /lab_host="DH10B"
FT complement(<1..>189)
FT mRNA
FT SQ Sequence 189 BP; 32 A; 68 C; 59 G; 30 T; 0 other;

Query Match
Best Local Similarity 5.8%; Score 21; DB 63; Length 189;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 119 gcacgcgagcgtctcggggacacccaagcaagaccacgcgctccc 163
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 56 GCACAGGAGAGTCTCAGGAGACTCCCGAGGCTGGACACGCGCTCCC 12

```

Search completed: Tue Feb 24 12:05:08 1998
Job time : 452 secs.

Release 2 ID: John F. Collins, Biocomputing Research Unit
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

```
MPsrch_nnn n a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:48:27 1998, MasPar time 112.83 Seconds
907.284 Million cell updates/sec
Tabular output not generated
```

```

Title:
Description:
Perfect Score:
N.A. Seq:
Comp:
>US-08-844-215-25
(1-363) : from US08B44215.seq
363
1 GATCGACTGCGGGGCAAGGGT
GATCGACTGCGGGGCAAGGGT
CGGACCACTCGGACAGCACT
CGCTGTGTAAGGCTGTGTAAGG

```

```

Scoring table:  TABLE default
               gap 5

Nmatch      STD :  Dbase 0:  Query 0

Searched:    397346 seqs, 141010104 bases x 2

Post-processing:  Minimum Match 0%
                  Listing first 45 summaries

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Database: EST-C

1	EST197	2	EST198	3	EST199	4	EST200	5	EST201	6	EST202
7	EST203	8	EST204	9	EST205	10	EST206	11	EST207	12	EST208
13	EST209	14	EST210	15	EST211	16	EST212	17	EST213	18	EST214
19	EST215	20	EST216	21	EST217	22	EST218	23	EST219	24	EST220
25	EST221	26	EST222	27	EST223	28	EST224	29	EST225	30	EST226
31	EST227	32	EST228	33	EST229	34	EST230	35	EST231	36	EST232
37	EST233	38	EST234	39	EST235	40	EST236	41	EST237	42	EST238
43	EST239	44	EST240	45	EST241	46	EST242	47	EST243	48	EST244
49	EST245	50	EST246	51	EST247	52	EST248	53	EST249	54	EST250
55	EST251	56	EST252	57	EST253	58	EST254	59	EST255	60	EST256
61	EST257	62	EST258	63	EST259	64	EST260	65	EST261	66	EST262
67	EST263	68	EST264	69	EST265	70	EST266	71	EST267	72	EST268
73	EST269	74	EST270	75	EST271	76	EST272	77	EST273	78	EST274
79	EST275	80	EST276	81	EST277	82	EST278	83	EST279	84	EST280
85	EST281	86	EST282	87	EST283	88	EST284	89	EST285	90	EST286
91	EST287	92	EST288	93	EST289	94	EST290	95	EST291	96	EST292
97	EST293	98	EST294	99	EST295	100	EST296	101	EST297	102	EST298

90:EST225 100:EST206 101:EST297 102:EST298 103:EST299
104:EST300 105:EST301 106:EST302 107:EST303 108:EST304
109:EST305 110:EST306 111:EST307 112:EST308 113:EST309
114:EST310 115:EST311 116:EST312 117:EST313 118:EST314
119:EST315

Statistics: Mean 9.837; Variance 1.898; scale 5.183

100

SUMMARIES

Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	14	34	25	AA255703	EST100902 Pancreas tis	5,22e-198
2	99	27	34	AA365029	EST63410 Lymph node	1.40e-146
3	98	27	34	AA325955	EST30457 Colon I Homo	1.39e-144
4	97	26	27	AA303982	EST13889 Testis tumor	1.47e-142
5	85	23	31	AA314630	EST18648 Lung Homo sa	2.41e-120
6	68	18	7	AA291381	EST44702 r1 Soares ova	5.77e-85
7	55	15	21	AA3377061	EST83641 Small intest	2.72e-60
8	48	13	2	AA378312	EST91017 Synovial sar	1.78e-47
9	47	12	9	AA4025647	EST47107 r1 Soares ova	1.11e-45
10	47	12	9	AA352777	EST60616 Activated T-	1.11e-45
11	47	12	9	AA300571	EST13661 Testis tumor	1.11e-45
12	44	12	21	AA377128	EST89660 Small intest	2.37e-40
13	41	11	3	AA360195	EST63374 Lymph node I	4.01e-35
14	39	10	7	AA3377074	EST85603 Small intest	1.05e-31
15	35	9	6	AA327972	EST30322 Colon I Homo	4.98e-25
16	35	9	6	AA330045	EST13823 Testis tumor	4.98e-25
17	34	9	4	AA300605	EST13453 Testis tumor	2.11e-23
18	33	9	1	AA428970	EST49022 r1 Soares ova	8.55e-22
19	33	9	1	AA295045	EST100185 Pancreas tis	8.55e-22
20	32	8	3	AA327241	EST30532 Colon I Homo	3.31e-20
21	29	8	0	AA381085	EST94138 Activated T-	1.43e-15
22	26	8	0	AA329249	EST4709 r1 Soares ova	1.43e-15
23	26	7	3	AA337565	EST30921 Colon I Homo	4.49e-14
24	24	7	4	AA383972	EST94225 Rhyms I Ho	1.32e-12
25	25	6	2	AA385989	EST970708 Pancreas tum	3.65e-11
26	25	5	9	AA300999	EST13049 Testis tumor	9.38e-10
27	25	6	9	AA377311	EST89659 Small intest	9.38e-10
28	24	6	6	AA360197	EST63376 Lymph node I	2.23e-08
29	24	6	5	AA175689	EST54502 r1 Soares mon	2.23e-08
30	24	6	5	AA419907	EST14091 r1 Soares NIH	2.23e-08
31	23	6	3	AA301099	EST14127 Testis tumor	4.87e-07
32	22	6	1	AA116663	EST23607 r1 Barstead M	9.71e-06
33	21	5	8	AA361096	EST63375 Lymph node I	1.75e-04
34	21	5	8	AA04273	Human Heart cDNA, c10	1.75e-04
35	21	5	8	AA146478	EST5507 r1 Soares mon	1.75e-04
36	20	5	5	AA323223	EST25551 Adipose tiss	2.84e-03
37	20	5	5	AA2448782	EST19231 seq.F Human fet	2.84e-03
38	20	5	5	AA05553	Human Heart cDNA, c10	2.84e-03
39	20	5	5	AA05176	Human Heart cDNA, c10	2.84e-03
40	20	5	5	AA026196	Human Heart cDNA, c10	2.84e-03
41	20	5	5	AA456765	EST27605 r1 Soares ova	2.84e-03
42	20	5	5	AA347670	EST57636 r1 KO mouse c	2.84e-03
43	20	5	5	AA343631	EST90631 r1 Soares mon	2.84e-03
44	20	5	5	AA4542318	EST48102 r1 Soares tes	2.84e-03
45	20	5	5	AA427605	EST47407 r1 Soares mon	2.84e-03

ALIGNMENTS

1	341 bp	mfna	EST	10 APR-1997
LOCUS	AA995703			
DEFINITION	ESR-0902 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to similar to human g-cb1b mu heavy chain, V region.			
ACCESSION	AA995703			
NID	g1948048			
KEYWORDS	EST			
SOURCE	Human			
ORGANISM	Homo sapiens			
OTYPOG	mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 341)			
AUTHORS	Adams M.D., Kerlavage A.P., Fleischmann P.D., Fuldner P.A., But.C.U., Lee N.H., Kirknes E.P., Weinstock X.G., Geyrhofer J.D., White O., Sutton G., Blake J.A., Brandon P.C., Man-Wai C., Clayton P.A., Cline T.P., Cotton M.D., Farle-Rughes I., Fine L.D., Fitzgald L.M., Fitzhugh W.M., Fitchman J.L., Geoghagen N.S., Glodex A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle P.S., Jr.,			

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
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 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M13 Reverse

FEATURES
 source
 Location/Qualifiers
 1..341
 /organism="Homo sapiens"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
 /clone_lib="Pancreas tumor I"
 /dev_stage="adult"
 <1..341
 mpNA
 BASE COUNT 74 a 79 c 100 g 83 t 5 others
 ORIGIN

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 Matches 182; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
 Db 99 ggtccgcagccagccagcgaagggctgagtgctgagcagttatccatnaccgtag 158
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 96 GTCCGCCAGGCTCCAGGCAAGGGGCTGAGTGGGTGGCAGGTATTCGTTCATGGAAG 155
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 Db 159 tcaacaattatgcagattccgtgaaggccgattcatctccagagacgattccaa 218
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 QY 156 TAACCAATATTACGAGACTCCGTGAAGGGCGGATTCAATGCTCCAGACAAATTCAG 215
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 Db 219 gaacacagctcttntgcaaatnaacagcctgacatctgagacacgggtgctttattg 278
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 QY 216 GCACAGGGTTCGTGCAGATCAGACGCTCAGACTCGAGGACAGCGCTGCTATTACTG 275
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 Db 279 tctcagagacccgacccggaggacctgctgctggtgtracactagaatactgggg 338
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 QY 276 TCGCAGACAGGGTTCCTCTTTGGCTGCAATTAAGGGGCGTACTACCTTGAAATTTGGG 335
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 339 cca 341
 |||||
 QY 336 cca 338
 |||||

RESULT 2 AA360289 240 bp mpNA EST 21-APP-1997
 LOCUS
 DEFINITION EST69410 Lymph node, subtracted Homo sapiens cDNA 5' end similar to
 similar to immunoglobulin gamma heavy chain, V(III) region
 (GB:U04494)
 ACCESSION AA360289
 NID g2012607
 EST.
 KEYWORDS EST.
 * SOURCE human
 ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 240)
 Adams, M.D., Kerlavage, A.R., Fleischmann, P.D., Fuldner, P.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, C., Blake, J.A., Brandon, P.C., Man-Wai, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 FitzGerald, L.M., Fitch, W.M., Fritchman, J., Geoghagen, N.S.,
 Glodzik, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
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 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
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 Fraser, C.M., and Venter, J.C.
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 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M13 Reverse

FEATURES
 source
 Location/Qualifiers
 1..240
 /organism="Homo sapiens"
 /note="Organ: lymph node; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
 /clone_lib="Lymph node, subtracted"
 /dev_stage="adult"
 <1..240
 mpNA
 BASE COUNT 64 a 56 c 56 g 53 t 1 others
 ORIGIN

Query Match 27.3% Score 99; DB 52; Length 240;
 Best Local Similarity 78.9% Pred. No. 1.30e-146;
 Matches 135; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Db 1 aaggggctgagtggtttcattacattagcagtggttagtagtaccataactacacagac 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 115 AAGGGGCTGAGTGGGCGAGGTATTTGTTGATGGAAGTAACCAATATTACGACAG 174
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 tctgtgaaggccgattccaccatctccagagacacgccaagaactcactgtatctgcaa 120
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 QY 175 TCGGTGAAGGCGCGATTCATCGTCTCCAGAGAACAAITCCAGGACACAGGCTGAG 234
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 Db 121 atgaacagcctgacagccgacgacagcggctgtgtattactgtcgagagag 171
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 235 ATGACGACGCTGAGACTCGAGGACAGCGGTGCTGTATTACTGTGCGACAGAG 285
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RESULT 3 AA326955 280 bp mpNA EST 20 APR-1997
 LOCUS
 DEFINITION EST30467 Colon 1 Homo sapiens cDNA 5' end similar to immunoglobulin
 mu heavy chain, VDJC regions.
 ACCESSION AA326955
 NID g1979434
 EST.
 KEYWORDS EST.
 SOURCE human.

ORGANISM	Human sapiens	OPGANISM	Human sapiens
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 280) Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brannon, P. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Springs, I. A., Utterback, T. P., Weidman, J. F., Li, Y., Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Fertie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P. S., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, I., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Posen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.	AUTHORS	1 (bases 1 to 273) Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brannon, P. C., Man-Wai, C., Clayton, R. A., Cline, T. P., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Springs, I. A., Utterback, T. P., Weidman, J. F., Li, Y., Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. F., Fertie, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P. S., Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, I., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Posen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)	JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE	96026280	MEDLINE	96026280
COMMENT	Other ESTs: THC167575 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tadb/hgi/hgi.html) Seq primer: M13 Reverse.	COMMENT	Other ESTs: THC179200 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tadb/hgi/hgi.html) Seq primer: M13 Reverse.
FEATURES	Source 1..280 /organism="Homo sapiens" /note="Organ: colon; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XbaI" /clone_lib="Colon 1" /dev_stage="adult" <1..>280	FEATURES	Source 1..273 /organism="Homo sapiens" /note="Organ: testis; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XbaI" /clone_lib="Testis tumor" /sex="male" /dev_stage="adult" <1..>273
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ORIGIN	Query Match 27.0%; Score 98; DB 37; Length 280; Best Local Similarity 88.1%; Pred. No. 1.39e-144; Matches 118; Conservative 0; Mismatches 15; Indels 1; Gaps 1.	ORIGIN	Query Match 26.7%; Score 97; DB 26; Length 273; Best Local Similarity 84.8%; Pred. No. 1.49e-142; Matches 117; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Db 134	gattctggggaggagctgtctcagctggagagctgagagctctctgtctgtacagctctt 193	Db 127	gagtcgggggggggggtttgttgaagcctgggggggagccctgaactctctgtgtctct 186
QY 4	GAGTCGGGGGAGGGGTGTCTCAGCTGGAGAGCTCTCTGTCTGTACAGCTCTT 63	QY 4	GAGTCGGGGGAGGGGTGTCTCAGCTCTCTGTCTGTGTGTGTGTGTGTGTGTGT 63
Db 194	ggattcaccttccgtatattatctatcacactgggtccgcagagctccagggagggcg 253	Db 187	gggttcaacttttagagactatagcctatgagctgggtccgcagagctccagggagggcg 246
QY 64	GCATTACCTTTAAACAGCTATGSCATGACTGGGTCTGCCAGGGCTCCAGGCTG 123	QY 64	GGAATCACCCTTCAAGACGTAIGGTAIGTACATGAGTCTGGTCTGAGAGCTCTG 123
Db 254	gnaataggtgagcaq 267	Db 247	gagtgaggtctcaggcatt 264
QY 124	G-AGTGGGTGGCAG 136	QY 124	GAGTGGGTGGCAGGTATT 141
RESULT	4 AA300982 273 bp mRNA EST 18-APR-1997	RESULT	5 AA314630 284 bp mRNA EST 19-APR-1997
LOCUS	EST13889 Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain gene, VDJC regions (38:M34024).	LOCUS	EST18648 Lung Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, V region.
DEFINITION	AA300982	DEFINITION	AA314630
ACCESSION	AA300982	ACCESSION	AA314630
NID	q195335	NID	q195335
KEYWORDS	EST.	KEYWORDS	EST

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NID      g1966978
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 294)
Adams,M.D., Kerlavage,A.R., Fleischmann,P.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
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96026280

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Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1..294
/organism="Homo sapiens"
/clone_lib="Lung"
/dev_stage="adult"
<1..>294

BASE COUNT 57 a 68 c 92 g 76 t 1 others
ORIGIN
Query Match 23.7%; Score 86; DB 31; Length 294;
Best Local Similarity 85.2%; Pred. No. 2,128-120;
Matches 109; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Db 136 gaatctgggggggagctgctgaagccggggggggtccctnagaactctctctgtgagcctct 195
QY 4 GAGTCGGGGGGGCGGTGGTCCAGCTCGAGAGCTCTCTGAGACTCTCTCTGTGCGAGCTCT 63

Db 196 ggaattcattttcaacagttacagatgaactggttcccccag-ctccagggaaggagctg 254
QY 64 GGATTCACCTTCAAGACGATATGGCATGACTGGTCCCGCCAGGCTCCAGGCAAGGGGCTG 123

Db 255 cagtgaggt 262
QY 124 GAGTGGGT 131

RESULT 6
LOCUS A291381 379 bp mRNA EST 16-MAY-1997
DEFINITION nt44202.r1 Soares ovary tumor NbHCT Homo sapiens cDNA clone 725234
5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION

(HUMAN):
AA291381
g1939359
EST.
human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 379)
Hiller,L., Allen,M., Rowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,R.,
White,Y., Wylie,T., Waterston,R., and Willson,R.
WashU-Merck EST Project 1997
Unpublished (1997)

Contact: Willson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amerisham
High quality sequence stop: 361.
Location/Qualifiers
1..379
/organism="Homo sapiens"
/clone_lib="Soares ovary tumor NbHCT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>379

BASE COUNT 85 a 82 c 121 g 91 t
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Query Match 18.7%; Score 68; DB 99; Length 379;
Best Local Similarity 63.9%; Pred. No. 5,778-85;
Matches 156; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Db 84 tgagggtctctgttaagacctctgtttacacctttggcacttttggtatcaactgagtc 143
QY 41 TGAGACTCTCTGTGCGAGCGCTGGATTTCACCTTCAGACGCTATGCGCTGCTGGTCC 100

Db 144 ggcagggccctggacaaggccttgagtggtggtggtggtggtggtggtggtggtggtg 203
QY 101 GCCAGGCTCCAGGCTCAAGGCGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 150

Db 204 caaactttgaggaggagtttttcaggagcagagctgagctgtgaccactgacacatccagata 263
QY 161 AATATTAAGTCAAGTCTGTAAGGCGGCGGATGATGATGATGATGATGATGATGATGATG 270

Db 264 cagcctacatgagctgagaaacctagatctcaacacagcccatattactatgaca 323
QY 221 GGGTGTTCCTGATATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 280

Db 324 gaga 327
QY 281 CAGA 284

```


[illegible]



WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.

MPsrch_nnn a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:34:56 1999, MacPar time 217 14 seconds
Tabular output not generated 825 544 Million cell updates/sec

Title: XUS-09-844-215-25
Description: (1-363) from US08844215.seq
Perfect Score: 363
N A Sequence: 1 CTGAGTGGGGAGAGCTT... GACACAGTGGGAGAGAGT
Comp: GAGTCAGCCCCCGCTCGCA

Scoring table:
Gap 5
TABLE default

Nmatch STD : Dbase 0: Query 0

Searched: 565703 seqs, 246912890 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-A

1. EST1 2. EST2 3. EST3 4. EST4 5. EST5 6. EST6 7. EST7 8. EST8
9. EST9 10. EST10 11. EST11 12. EST12 13. EST13 14. EST14
15. EST15 16. EST16 17. EST17 18. EST18 19. EST19 20. EST20
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27. EST27 28. EST28 29. EST29 30. EST30 31. EST31 32. EST32
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Database: EST-B

99. EST99 100. EST100 101. EST101 102. EST102 103. EST103
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179: EST179 180: EST180 181: EST181 182: EST182 183: EST183
184: EST184 185: EST185 186: EST186 187: EST187 188: EST188
189: EST189 190: EST190 191: EST191 192: EST192 193: EST193
194: EST194 195: EST195 196: EST196

Statistics: Mean 9.877 Variance 1.909 scale 5 200

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	195	53.7	419 90	H73816	Y51801.r1 Homo sapiens	0.00e+00
2	174	47.9	430 35	H72787	Y51809.r1 Homo sapiens	0.00e+00
3	147	40.5	823 196	AA170256	MS87410.r1 Soares mem	1.86e+246
4	134	36.9	330 123	SSC1210	S-scfofa mRNA: exons	4.64e+219
5	133	35.6	297 58	T27858	EST18962 Homo sapiens	5.03e+217
6	123	33.9	303 51	H43139	Y51803.r1 Homo sapiens	3.80e+196
7	82	22.6	422 59	H43252	Y51805.r1 Homo sapiens	2.13e+112
8	64	17.6	485 29	H43774	Y51804.r1 Homo sapiens	3.77e+77
9	53	14.6	147 59	H42647	Y51812.r1 Homo sapiens	2.04e+56
10	48	13.2	329 63	H22008	Y51808.r1 Homo sapiens	2.79e+47
11	47	13.0	294 59	T28438	EST18186 Homo sapiens	1.76e+45
12	39	10.7	478 60	H43753	Y51801.r1 Homo sapiens	1.80e+31
13	38	10.5	287 58	T27609	EST10334 Homo sapiens	8.92e+30
14	38	10.5	299 58	T27277	EST13874 Homo sapiens	8.92e+30
15	37	10.2	238 58	T29570	EST89669 Homo sapiens	4.26e+28
16	36	9.9	412 64	H27044	Y51802.r1 Homo sapiens	1.96e+26
17	36	9.6	446 34	R71741	Y51811.r1 Homo sapiens	1.96e+26
18	35	9.6	437 116	HSU53085	Human clone 7/24 mRNA	8.71e+25
19	34	9.4	331 58	T27715	EST13381 Homo sapiens	3.71e+23
20	34	9.4	385 51	R35288	Y51809.r1 Homo sapiens	3.71e+23
21	31	8.5	194 70	H61365	Y51801.r1 Homo sapiens	2.19e+18
22	31	8.5	222 89	H58593	Y51801.r1 Homo sapiens	2.19e+18
23	31	8.5	369 63	H22104	Y51804.r1 Homo sapiens	2.19e+18
24	31	8.5	437 116	HSU53086	Human clone 8/24 mRNA	2.19e+18
25	29	8.0	200 65	H27476	Y51803.r1 Homo sapiens	2.79e+15
26	29	8.0	408 60	H42300	Y51803.r1 Homo sapiens	2.79e+15
27	29	7.2	397 69	H47711	Y51801.r1 Homo sapiens	5.18e+11
28	25	6.9	309 65	H27957	Y51803.r1 Homo sapiens	1.72e+09
29	25	6.9	318 114	HSCNH041	H. sapiens partial CD	1.72e+09
30	25	6.9	367 3	T60311	Y51807.r1 Homo sapiens	1.72e+09
31	25	6.9	410 65	H30111	Y51804.r1 Homo sapiens	1.72e+09
32	24	6.6	228 63	H26004	Y51806.r1 Homo sapiens	4.69e+08
33	24	6.6	351 68	H39077	Y51802.r1 Homo sapiens	4.69e+08
34	23	6.3	253 68	T26641	EST89449 Homo sapiens	8.96e+07
35	23	6.3	350 51	R85072	Y51803.r1 Homo sapiens	8.96e+07
36	23	6.3	471 69	H45128	Y51801.r1 Homo sapiens	8.96e+07
37	22	6.1	233 166	AA091940	chr00720 seq F. Fetal	1.79e+05
38	22	6.1	340 1	S00144	Y51801.r1 Homo sapiens	1.79e+05
39	22	6.1	354 29	R45498	Y51801.r1 Homo sapiens	1.79e+05
40	22	6.1	417 14	R08595	Y51801.r1 Homo sapiens	1.79e+05
41	22	6.1	508 59	H42836	Y51806.r1 Homo sapiens	1.79e+05
42	22	6.1	769 105	W27712	3935 Human retina cDN	1.79e+05
43	21	5.8	429 21	H02756	Y51803.r1 Homo sapiens	3.23e+04
44	21	5.8	458 182	AA054153	2554308.s1 Soares ret	3.23e+04
45	21	5.8	626 189	AA054771	2554312.s1 Soares ret	3.23e+04

ALIGNMENTS

RESULT 1 H73816 419 bp mRNA EST 31-OCT-1995
LOCUS Y51801.r1 Homo sapiens cDNA clone 214442.5 similar to 4L162726
DEFINITION IG HEAVY CHAIN V-III REGION (HUMAN):
ACCESSION H73816
NID g1046750
KEYWORDS EST
SOURCE human clone:214442 primer-M13RP1 library:Soares fetal liver spleen

SULT	2	R72787	430 bp	mpNA	EST	02-JUN-1995
ICUS		via109	ri	Homc	staple's cDNA clone 156161 5'	similar to gb-M62726
DEFINITION					IG HEAVY CHAIN V-III REGION (HUMAN),	
CESSION		R72787				
D*					9846819	

RESULT
LOGS
DEFINITION

Accession	Size (bp)	Species	Library	EST
AA170256	823	mouse	mpna	
U08710.1		mouse	mdms	Mus musculus
				CHAIN PRECURSOR
				for immunoglobulin
				gb:V00821
				Mouse mpna fragment

16-FEB-1997

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGAGGAGCCGCCCCCTTTTTTTTTTTTTTTT ;],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M. Fatima Bonaldo.

ORGANISM

Homo sapiens

Phylogeny: Metazoa, Eumetazoa, Bilateria, Coelomata:
Eukaryotomia; Chordata: Vertebrata: Gnathostomata: Osteichthyes;
Sarcopterygii: Chonata: Tetrapoda: Amniota: Mammalia: Theria:
Eutheria: Archonta: Primates: Catarrhini: Hominoidea: Homo
1 (bases 1 to 303)
1

REFERENCE
AUTHORS

Hollan M., Clark N., Dubuque T., Ellison K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra, M.,
Parsons, J., Rifkin L., Rohlfing T., Soares M., Tan, F.,
Trevisan S. E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 111
Source: IMAGE Consortium, LLNL

<hr/>					
FEATURES					
source					
		1	303		
		location/Qualifiers			
		/organism="Homo sapiens"			
		/clone="187156"			
USE COUNT	62 a	65 c	91 g	76 t	9 others
IGIN					

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Query Match      33.9%;   Score 123;   DB 51;   Length 303;
Best Local Similarity 82.0%;   Pred. No. 3,80e-196;
Matches 146;   Conservative 0;   Mismatches 32;   Indels 0;   Gaps 0;

      126  gadtctggggaggagggtggtccagcctgggagggttcctgagactctctgtgagagctct 185
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      4  GAGTCGCGCGGAGCGCTGTCTTCAGCTGGAGAGTCTCTGAAATCTCTCTGTCAGCTCT 63

      186  ggaattcaccttcagtgggatgtggcaggcactgggtctcccccacgacgacgaagagggtctg 245
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      64  GGATTCAACCTTCAAGACGCTATGGCATGCTACTGGGTCTGGCCAGCTCCAGCAAGCGGCTG 123

      246  gaatnggtgtcatttatcatcatatnnnagaaataataataactaccacnacttctga 303
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      124  GAGTGGGTGGCAGGTATTCGTTTCGTGGAGTAACCAATATTACGACACTCCGTGA 181

RESULT 7 H43952 422 bp mRNA EST 31-JUL-1995
ACU5 y07ag05_r1 Homo sapiens cDNA clone 183320 5' similar to gb:555735
DEFINITION IG ALPHA-1 CHAIN C REGION (HUMAN)..
GENE IG ALPHA-1
VERSION H43952

```

EST.
SOURCE
human clone=183320 library=Soares breast 3NDHst vector=pT7T3D
(Pharmacia) with a modified polylinker host=DHO10B (ampicillin
resistant) primer=M13pI Psite=Not I Psite2=EcoRI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'.
TGTTACCACTGAGTCGGGACGCCGCCCTTTTTTTTTTTT-3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Patima Bonaldo.

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1

Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality.

FEATURES

source
 1..147
 /organism="Homo sapiens"
 /clone="187294"

BASE COUNT
 ORIGIN

19 a 35 c 48 g 40 t 5 others

Query Match 14.6%; Score 53; DB 69; Length 147;

Best Local Similarity 85.9%; Pred. No. 2.04e-56; Length 147;
 Matches 61; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 71 gactcggggagcttagctcagctcgggggtccctgagactctcctgtgcagcctnt 130

QY 4 GAGTCGGGGGAGGGGCTGCTCCAGCCTGGAGGTCCTCTGAGACTCTCCTGTGCAGCGTCT 63

Db 131 ggaattcctnt 141

QY 64 GGATTCACCTT 74

RESULT 10 H2208 329 bp mRNA EST 06-JUL-1995
 LOCUS Y138e08_r1 Homo sapiens cDNA clone 160550 5' similar to
 DEFINITION gb-S71043_rnal IG ALPHA-2 CHAIN C REGION (HUMAN);
 ACCESSION H2208
 NID g989093
 KEYWORDS EST
 SOURCE human clone-160550 library-Soares breast 3nbHBst vector-pt7T3D
 (Pharmacia) with a modified polylinker host-DH10B (ampicillin
 resistant) primer-M13R1 psiTel-Nrt I PsiE2-Eco RI Adult human
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGGGCGGCCCTTTTITTTTTTTTITTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned into the Not I and Eco RI sites of a
 modified pT73 vector (Pharmacia). Library went through one round
 of normalization to a Cot = 20 Library constructed by Bento Soares
 and M. Fatima Bonaldo.

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 329)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson PK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

High quality sequence stops: 177
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information

FEATURES

source

1..329

/organism="Homo sapiens"
 /clone="160550"

BASE COUNT 74 a 99 c 84 g 61 t 11 others
 ORIGIN

Query Match 13.2%; Score 48; DB 63; Length 329;

Best Local Similarity 73.5%; Pred. No. 2.79e-47;

Matches 75; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 1 gcaattccacattctcaagagatgactcaagaccacgctgtatctgtacatgagacagc 60

QY 185 GCCGATTCATCTCTTCAGAGACAATTCAGAGACATGRTGTTCACAGATCAGTACT 244

Db 61 tgaaccgagagacacacgctgtattctgtgtgtgtggaagg 102

QY 245 TGAGACTCGAGGACACGCTGCTCAITACTGTGGACAGAGG 286

RESULT 11

LOCUS

T28938 209 bp mRNA EST 06-SEP-1995
 DEFINITION EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu
 heavy chain, VDJ regions (GB:M17751) (HT:3055).

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

EST.
 human primer-M13 Reverse library=Human white blood cells.
 Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 209)
 Adams, M.D., Kerlavage, A.R., Fleischmann, P.D., Fuldner, R.A.,
 Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
 Clayton, P.A., Cline, P.T., Coffey, M.P., Earle-Hughes, E., Fine, L.D.,
 Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.T., Geoghagen, N.S.M.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, Jr, P.S.,
 Kelley, J.M., Kimek, K.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M.,
 Merrick, J.M., Moreno-Parlanques, P.F., McDonald, L.A., Nguyen, D.T.,
 Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.I.,
 Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
 Waldman, J.F., Li, Y., Bednarik, D.P., Rao, L., Cepeda, M.A.,
 Coleman, T.A., Collins, E.J., Dimke, D., Feng, P., Ferrie, A.,
 Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
 Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
 Weissner, P.S., Olsen, H., Raymond, R., Wei, Y.-F., Wind, J., Xu, C.,
 Yu, G.-L., Rubin, S.M., Dillon, P.J., Pannon, M.P., Rosen, J.C.,
 Hasegawa, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)

Contact: Venter, J.C.

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org).

FEATURES

source

mRNA

BASE COUNT

ORIGIN

43 a 62 c 48 g 55 t 1 others

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Score 47; DB 58; Length 209;

Pred. No. 1.76e-45;

0; Mismatches 34; Indels 0; Gaps 0;

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RESULT	13				
LOCUS	T27509	287 bp	mRNA	EST	06-SEP-1995
DEFINITION	EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain, VJJC regions (GR-M19512) (HT-3056)				
ACCESSION	T27509				
NID	9609707				
KEYWORDS	EST.				
SOURCE	human	primer=M13	Reverse library=Human	Pancreas.	
ORGANISM	Homo sapiens				
	Eukaryotae:	Metazoa:	Eumetazoa:	Bilateria:	Ceolomata:
	Deuterostomia:	Chordata:	Vertebrata:	Gnathostomata:	Osteichthyes
	Sarcopterygii:	Chonata:	Tetrapoda:	Amniota:	Mammalia:
	Eutheria:	Archonta:	Primates:	Catarrhini:	Hominidae:
REFERENCE	1 (bases 1 to 287)				

White, O., Sutton, G., Blake, J. A., Brandon, R. C., Chiu, M. W., Clayton, P. A., Cline, P. T., Cotton, M. D., Earle-Hughes, J., Fine, L., Fitzgerald, L. M., FitzHugh, W. M., Fritchman, I. L., Geobachsen, N. S., Glodde, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle Jr, P. S., Kelley, J. M., Kline, K. M., Kelley, J. C., Liu, L. I., Marnaros, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T., Pellegrino, S. M., Phillips, C. A., Pyder, S. E., Scott, J. J., Saudek, D. M., Shirley, P., Small, K. V., Springs, T. A., Utterback, J. Weidman, J. F., Li, Y., Bednarek, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dinke, D., Feng, P., Ferris, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Li, Gruber, J., Hudson, P., Kim, A., Korzak, D. L., Kusch, C. J., H. H., Li, Messner, P. S., Olsen, H., Raymond, I., Wei, Y. F., Wang, J., Xu, C., Yu, G. L., Ruben, S. M., Dillon, P. J., Pannoc, M. P., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million basepairs of cDNA Sequence
(Unpublished (1995))

JOURNAL

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)

Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR database
 (tdbinfo@tdb.tigr.org).

BASE COUNT	62 a	77 c	85 g	50 t	3 others
ORIGIN					
Query Match	10.5%				
Best Local Similarity	64.0%				
Matches	Pred. No. 8 92e-30;				
87: Conservative	0: Mismatches 49; Indels 0; Gaps				

Query Match	10.5%	Score 38:	DB 58:	Length 287:
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Db	147	gatagccttcaccgactactatatacctgatttcagagggccctggacaaagctctg	206	
QY	65	GATTCACCTTCAGACGCTATGGCATGATCTGGCTTCGGCAGGCTCTCAAGCAAGAGGCTGG	124	

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Db 207 aatggatggatgat 222
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QY 125 AGTGGGTGGCAGGTAT 140

RESULT 14
LOCUS 272727 299 bp mRNA EST 06-SEP-1995
DEFINITION EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu
(chain gamma) heavy chain, V(I)DJC regions (H1:3057).
ACCESSION T272727
NID q609825
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human Testis.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 299)
REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Chiu,M.-W.,
Clayton,R.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,J.M., FitzHugh,W.M., Fritchman,J.L., Georhagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,Jr,P.S.,
Kelley,J.M., Kline,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.P., Rosen,C.A.,
Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org).
FEATURES
source 1..299
Location/Qualifiers
/organism="Homo sapiens"
mRNA <1..>299
BASE COUNT 61 a 84 c 82 g 68 t 4 others
ORIGIN
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Query Match 10.5%; Score 38; DB 58; Length 299;
Best Local Similarity 65.1%; Pred No 8 92e-10;
Matches 82; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 4 GAGTCGGGGGAGGGCGGTGCTCCAGCTGAGAGCTCTCTGAGACTCTCTGTCAGCTCT 63
| | | | | | | | | |
Db 154 ggtgggtccatcagtagtactactgactgagctgattccggcagcccccaggaaggactg 213
| | | | | | | | | |
QY 64 GGATTACCTTCAAGACGATATGCCATGCTACTGCGCTCCAGGCTCCAGGAGGCGTG 123
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Db 214 cagtgg 219
| | | | |
QY 124 GAGTGG 129
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```

Search completed: Tue Feb 24 11:48:05 1998
Job time : 789 secs.

WORLD (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 15:39:10 1998: Maspar time 23.60 Seconds
707.450 Million cell updates/sec
Tabular output not generated

Title: >US-08-844-215-25
Description: (1-363) from US0844215.seq
Perfect Score: 363
N.A. Sequence: 1 CTCGAGTGGGGGAGGGGTCCCTGGTCACGGTCTCTCA 363
Comp: GAGTCACGCCCTCCGCA.....GGGACGAGTGGCAGAGGT

Scoring table: TABLE default
Gap 5

Nmatch STD: Dbase 0: Query 0

Searched: 87531 seqs, 22996021 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1-back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PT90 9:PT91
10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 7.667: Variance 4.010: scale 1 912

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description	Pred. No.
1	219	60.3	US-08-259-	Sequence 1, Applicatio	4,876-152
2	219	60.3	US-08-458-	Sequence 1, Applicatio	4,876-152
3	210	57.9	US-08-305-	Sequence 1, Applicatio	8,166-145
4	205	56.5	PCT-US93-1	Sequence 45, Applicati	8,336-141
5	190	52.3	PCT-US93-1	Sequence 43, Applicati	8,426-129
6	187	51.5	PCT-US93-1	Sequence 47, Applicati	2,106-126
7	185	51.0	PCT-US93-1	Sequence 41, Applicati	8,306-125
8	184	50.7	US-08-326-	Sequence 1, Applicatio	5,226-124
9	183	50.4	PCT-US93-1	Sequence 3, Applicati	3,286-123
10	179	49.3	PCT-US93-1	Sequence 19, Applicati	5,086-120
11	179	49.3	PCT-US93-1	Sequence 21, Applicati	5,086-120
12	179	49.3	US-08-264-	Sequence 13, Applicati	5,086-118
13	177	48.8	PCT-US93-1	Sequence 2, Applicati	2,006-118
14	177	48.8	PCT-US93-1	Sequence 23, Applicati	2,006-118
15	177	48.8	PCT-US93-1	Sequence 33, Applicati	2,006-118
16	174	47.9	PCT-US93-1	Sequence 31, Applicati	4,906-116
17	174	47.9	PCT-US93-1	Sequence 29, Applicati	4,906-116
18	174	47.9	PCT-US93-1	Sequence 35, Applicati	3,066-115
19	173	47.7	PCT-US93-1	Sequence 42, Applicati	2,916-111

20 173 47.7 360 11 PCT-US93-1 Sequence 39, Applicati 3,066-115
21 168 46.3 366 11 PCT-US93-0 Sequence 42, Applicati 2,916-111
22 158 45.7 376 11 PCT-US93-1 Sequence 2, Applicatio 2,916-111
23 156 45.7 389 11 PCT-US93-0 Sequence 11, Applicati 1,136-109
24 154 45.2 389 11 PCT-US93-0 Sequence 13, Applicati 4,406-108
25 154 42.4 393 7 US-08-468- Sequence 3, Applicatio 3,756-100
26 154 42.4 393 6 US-08-259- Sequence 3, Applicatio 3,756-100
27 153 42.1 369 5 US-08-199- Sequence 3, Applicatio 2,326-99
28 148 40.8 354 11 PCT-US93-0 Sequence 9, Applicatio 2,066-95
29 147 40.5 405 13 PCT-US95-0 Sequence 38, Applicati 1,296-94
30 147 40.5 444 5 US-07-826- Sequence 7, Applicatio 1,296-94
31 145 39.9 405 13 PCT-US95-0 Sequence 3, Applicatio 4,916-93
32 143 39.4 1347 1 5455030-2 Patent No. 5455030
33 142 39.1 417 7 US-08-398- Sequence 21, Applicati 1,146-90
34 142 39.1 417 7 US-08-398- Sequence 21, Applicati 1,146-90
35 142 39.1 756 7 US-08-398- Sequence 29, Applicati 1,146-90
36 142 39.1 756 7 US-08-398- Sequence 29, Applicati 1,146-90
37 141 38.8 752 1 5455030-12 Patent No. 5455030
38 140 38.6 339 4 US-07-789- Sequence 9, Applicatio 4,326-89
39 139 39.3 3343 1 5453363-2 Patent No. 5453363
40 138 38.0 357 7 US-08-207- Sequence 26, Applicati 1,626-87
41 138 38.0 711 1 5455030-8 Patent No. 5455030
42 138 38.0 923 12 PCT-US94-0 Sequence 1, Applicatio 1,626-87
43 137 37.7 357 7 US-08-331- Sequence 21, Applicati 1,626-87
44 137 37.7 375 7 US-08-331- Sequence 59, Applicati 9,956-87
45 137 37.7 717 12 PCT-US94-1 Sequence 58, Applicati 9,956-87

ALIGNMENTS

RESULT 1
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08259372A.
CC Sequence 1, Application US/08259372A
CC Patent No. 5565354
CC GENERAL INFORMATION:
CC APPLICANT: Ostberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
N
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.50
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/38/259,372A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196

CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO. 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 423 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
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Matches 250; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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DT 01-JAN-1900
DE Sequence 1, Application US/08468671.
CC Sequence 1, Application US/08468671.
CC Patent No 5648077
CC GENERAL INFORMATION:
CC APPLICANT: Ostberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
N
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA

CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/468,671
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/259,372
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CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
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CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO. 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 423 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
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CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC CELL TYPE: Hybridoma
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Query Match 60.3%; Score 219; DB 7; Length 423;
Best Local Similarity 89.0%; Pred. No. 4,87e-152;
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CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
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CC OTHER INFORMATION: /product= "Immunoglobulin Variable Region"
CC OTHER INFORMATION: /standard_name= "Humab L612 Heavy Chain Variable
CC OTHER INFORMATION: Region Sequence"
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 148..162
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CC FEATURE:
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CC LOCATION: 271..300
CC OTHER INFORMATION: /function= "Complementary
CC OTHER INFORMATION: determining region 2 (CD#2)"
CC FEATURE:
CC NAME/KEY: misc_feature
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CC OTHER INFORMATION: /function= "Complementary determining
CC OTHER INFORMATION: region 3 (CD#3)"
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Matches 232; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
Db 73 GATCTGGGGAGGCTTGTAGACTGGGGGGTGGCTGAGACTCTCTCTGCGAGCTCT 132
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QY 124 GAGTGGGTCTCAGCTATTAGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 183
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 37, Application PC/TUS9310555.
CC Sequence 37, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY PESTICIDED ANTIBODIES
CC THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA

TES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 37:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 369 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: SpA2-08
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..369
SQ Sequence 369 BP: 79 A: 97 C: 115 G: 78 T: 0 other:
Query Match 50.4%: Score 183; DB 11; Length 369;
Best Local Similarity 82.3%: Prod No 3,28e-123;
Matches 233; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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QY 1 CTGAGAGTGTGGGGAACCTTGGTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
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QY 51 CTGAGAGTGTGGGGAACCTTGGTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 130
Db 133 CTGAGAGTGTGGGGAACCTTGGTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 192
QY 121 CTGAGAGTGTGGGGAACCTTGGTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 193 AAGGGGCTATTACCATCTCCAGAGCAACGGCTGTGTGTGTGTGTGTGTGTGTGTGT 252
QY 181 AAGGGGCTATTACCATCTCCAGAGCAACGGCTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 253 AGTCTGAGAGCGGAGGACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 295
QY 241 AGTCTGAGAGCGGAGGACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 283
RESULT 10
ID PCT-US93-10555-19 STANDARD: DNA: UNC: 360 BP
AC xxxxxx
DT 01-JAN-1900
DE Sequence 19, Application PC/TUS9310555.
CC Sequence 19, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.

CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
 CC TES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: FD-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 360 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC IMMEDIATE SOURCE:
 CC CLONE: SpA3-02
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1..360
 CC Sequence 360 BP; 76 A; 97 C; 110 G; 77 T; 0 other;

Query Match 49.3%; Score 179; DB 11; Length 360;
 Best Local Similarity 82.1%; Pred. No. 5,08e-120;
 Matches 229; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 13 CTCGAGTCTGGGCGAGGATGGTACAGCTGGGGGTGCTCTAGACTCTCTCTGTGCAGCC 72
 QY 1 CTCGATCGGGGAGAGGAGGATGATGAGCTGGGAGGATGCTGAGACTCTCTGTGAGAG 60
 Db 73 TCTGGATTCACCTTTTAGCAGCATGATGATGATGATGATGATGATGATGATGATGATG 132
 QY 61 TCTGGATTCACCTTTTAGCAGCATGATGATGATGATGATGATGATGATGATGATGATG 120
 Db 133 CTCGATGAGGTCCTTACATATATGATGATGATGATGATGATGATGATGATGATGATG 192
 QY 121 CTCGATGAGGTCCTTACATATATGATGATGATGATGATGATGATGATGATGATGATG 180
 Db 193 AAGGCGCGGTTCCACATCTCCAGAGCAATTCAGAGACACCTCTATTTCGAAATGAC 252
 QY 181 AAGGCGCGGTTCCACATCTCCAGAGCAATTCAGAGACACCTCTATTTCGAAATGAC 240
 Db 253 AGCCTGAGAGCGGAGACACACCGGCTTATTACTGTGG 291
 QY 241 AGCCTGAGAGCGGAGACACACCGGCTTATTACTGTGG 279

RESULT 11
 ID PCT-US93-10555-21 STANDAPC DNA UNC: 360 BP
 AC xxxxxx
 DT 01-JAN-1900

DE Sequence 21, Application PC/THS9310555.
 CC Sequence 21, Application PC/THS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
 CC TES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: FD-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 21:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 360 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC IMMEDIATE SOURCE:
 CC CLONE: SpA3-08
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1..360
 CC Sequence 360 BP; 75 A; 97 C; 111 G; 77 T; 0 other;

Query Match 49.3%; Score 179; DB 11; Length 360;
 Best Local Similarity 82.1%; Pred. No. 5,08e-120;
 Matches 229; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 13 CTCGAGTCTGGGCGAGGATGGTACAGCTGGGGGTGCTCTAGACTCTCTCTGTGCAGCC 72
 QY 1 CTCGATCGGGGAGAGGAGGATGATGAGCTGGGAGGATGCTGAGACTCTCTGTGAGAG 60
 Db 73 TCTGGATTCACCTTTTAGCAGCATGATGATGATGATGATGATGATGATGATGATGATG 132
 QY 61 TCTGGATTCACCTTTTAGCAGCATGATGATGATGATGATGATGATGATGATGATGATG 120
 Db 133 CTCGATGAGGTCCTTACATATATGATGATGATGATGATGATGATGATGATGATGATG 192
 QY 121 CTCGATGAGGTCCTTACATATATGATGATGATGATGATGATGATGATGATGATGATG 180
 Db 193 AAGGCGCGGTTCCACATCTCCAGAGCAATTCAGAGACACCTCTATTTCGAAATGAC 252
 QY 181 AAGGCGCGGTTCCACATCTCCAGAGCAATTCAGAGACACCTCTATTTCGAAATGAC 240
 Db 253 AGCCTGAGAGCGGAGACACACCGGCTTATTACTGTGG 291
 QY 241 AGCCTGAGAGCGGAGACACACCGGCTTATTACTGTGG 279

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RESULT 12
ID US-08-264-093-13 STANDARD; DNA: UNC; 360 BP
AC xxxxxx
DT 01-JAN-1900
DE Sequence 13, Application US/08264093
CC Sequence 13, Application US/08264093
CC Patent No. 5639863
CC GENERAL INFORMATION:
CC APPLICANT: Michael D. Dan
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CC TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
CC TITLE OF INVENTION: ANTIGEN
CC NUMBER OF SEQUENCES: 25
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ridout & Maybree
CC STREET: 2300 Richmond-Adelaide Centre
CC STREET: 101 Richmond Street West
CC CITY: Toronto
CC STATE: Ontario
CC COUNTRY: Canada
CC ZIP: M5H 2J7
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: MS-DOS 6.00
CC SOFTWARE: ASCII Editor
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/264,093
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA: No. 5639863 applicable
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lake, James R.
CC REGISTRATION NUMBER: 31081
CC REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (416) 868-1482
CC TELEFAX: (416) 362-0823
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 360 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
CC Sequence 360 BP; 85 A; 76 C; 106 G; 93 T; 0 other:

Query Match 49 3%; Score 179; DB 7; Length 360;
Best Local Similarity 82 5%; Pred. No. 5 08e-120;
Matches 227; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Db 1 GGGGGAGGCTGGTCCAGGCTGGGGGGTCCCTGAGACTCTCTGTTCAGGCTCTGGATTG 60
QY 10 GGGGGAGGCTGGTCCAGGCTGGGGGGTCCCTGAGACTCTCTGTTCAGGCTCTGGATTG 60
Db 61 ACCTTCAGTAGCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 120
QY 70 ACCTTCAGGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 120
Db 121 GTTTCGGCTATTAGTAGTAAATGAGGAGTACATATAGTACAGACTCTGGTGAAGGCTAGA 180
QY 130 GTGGCAGGTAATTCGTTTCATGAGTAAAGCAATATATAGGAGAGTCTGGTGAAGGCTAGA 180
Db 181 TTCACCATCTCCAGAGACAATTCAGAGACAATTCAGAGACAATTCAGAGACAATTCAGAG 240
QY 190 TTATCGTCTCCAGAGACAATTCAGAGACAATTCAGAGACAATTCAGAGACAATTCAGAG 240
Db 241 GCTGAGGACACGCTCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 275
QY 250 CTCGAGGACACGCTCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 284

*RESULT 13
ID PCT-US93-10555-27 STANDARD; DNA: UNC; 360 BP
AC xxxxxx
DT 01-JAN-1900
DE Sequence 27, Application PC/TUS9310555.
CC Sequence 27, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
CC TES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 27:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 360 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: SpA3-16
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..360
CC Sequence 360 BP; 75 A; 97 C; 111 G; 77 T; 0 other:

Query Match 48 8%; Score 177; DB 11; Length 360;
Best Local Similarity 81 7%; Pred. No. 2 00e-118;
Matches 228; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 13 CTCGAGTCTGAGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 72
QY 1 CTCGAGTCTGAGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 72
Db 73 TTGGATTCAGCTTTAGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATG 132
QY 61 TTGGATTCAGCTTTAGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATG 120
Db 133 CTGGAGTGGTCTCAGATATTAGTCCGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 192
QY 121 CTGGAGTGGTCTCAGATATTAGTCCGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
Db 193 AAGGGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 252
QY 181 AAGGGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Db 253 AGCCTGAGAGCGGAGAGACGGCTTATATGCTGCTG 291
QY 241 ACCCTGAGACTCTGAGAGACGGCTTATATGCTGCTG 279

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Db 193 AAGGGCGGTTTCAGCATCTCCAGAGACAATCCAAAGAACACGCTGTATTTGCAAAATGAAC 252
||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 AAGGGCCGATTTCATGCTCTCCAGAGACAATCCAGGAGACACGCTGTGTTTCTGCAGATGAGC 240
||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 AGCCTGAGAGCCGGAAGACACGCGCCTTATATTACTGTGCG 291
||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 AGCCTGAGACTCGAGGACACGCGCTGTCTATTACTGTGCG 279
||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: Tue Feb 24 15:41:13 1998
Job time : 123 secs.

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      WQSELEH
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      (TM)

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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:31:49 1998: Maspar time 53.66 Seconds
Tabular output not generated.

Title: >US-08-844-215-25
Description: (1-363), from US08844215.seq
Perfect Score: 363
N.A. Sequence: 1 CTCGAGTCGGGGGAGGGGT.....GCTGTGTCACCGTCTGCTCA 363
Comp: GAGCTCAAGCCGCCCTCCGCA.....GGGACCAAGTGGCAGAGAGT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0: Query 0
Searched: 159651 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.049; Variance 4.621; scale 1.742

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description Pred. No.
1	232	53-9	909 7 Q43772 Sequence encoding the 1.40e-146
2	231	63-6	583 13 Q78971 Human immunoglobulin 7.54e-146
3	228	62-8	336 2 Q11957 Anti-human RHD HAM-B 1.18e-143
4	227	62-5	512 13 Q78968 Human immunoglobulin 6.37e-143
5	226	62-3	339 2 Q11956 Anti-human RHD REG-A 3.44e-142
6	225	62-0	369 33 T60380 Anti-TGF beta-1 scFv 1.85e-141
7	224	61-7	732 25 T44089 Ulcerative colitis-as 9.97e-141
8	222	61-2	345 33 T50369 Anti-TGF beta-2 scFv 2.89e-139
9	221	60-9	369 33 T50381 Anti-TGF beta-1 scFv 1.56e-138
10	221	60-9	1521 2 Q11880 Encodes heavy chain v 1.56e-138
11	219	60-3	337 28 T50122 Coding sequence for h 4.50e-137
12	219	60-3	423 24 T46128 Monoclonal antibody p 4.50e-137
13	219	60-3	423 33 T85838 Monoclonal antibody p 4.50e-137
14	219	60-3	429 10 Q64050 Sequence of the VH re 4.50e-137
15	215	59-5	350 33 T60370 Anti-TGF beta-2 scFv 7.00e-135

15	216	59-5	357 28 T60116 Coding sequence for h 7.00e-135
17	216	59-5	699 25 T44088 Ulcerative colitis-as 7.00e-135
18	216	59-5	342 2 Q11953 Anti-human RHD HAM-B 7.00e-134
19	214	59-0	369 33 T60382 Anti-TGF beta-1 scFv 2.02e-133
20	212	58-4	342 2 Q11955 Anti-human RHD GAD-2 5.83e-132
21	211	58-1	657 6 Q36133 MH47 Mab heavy chain 3.13e-131
22	210	57-9	426 32 T80758 64-863 antibody H5vef 1.68e-130
23	209	57-6	925 2 Q12839 Variable region of u 9.00e-130
24	203	55-9	339 10 Q64855 SPA-reactive VH regio 2.13e-125
25	202	55-6	423 14 Q87236 Anti-interleukin-1a1 1.14e-124
26	201	55-4	357 28 T60118 Coding sequence for h 6.11e-124
27	197	54-3	357 28 T60120 Coding sequence for h 4.90e-121
28	194	53-4	375 1 Q03608 Sequence encoding 461 7.60e-119
29	194	53-4	456 1 Q03610 Sequence encoding 461 7.60e-119
30	183	53-2	514 13 Q78961 Human immunoglobulin 4.06e-118
31	182	52-9	453 29 T42619 Heavy chain transcrip 2.16e-117
32	181	52-6	402 30 T43529 DNA encoding anti-lym 1.15e-116
33	181	52-6	1576 8 Q49944 Human anti-HBs heavy 1.15e-116
34	180	52-3	354 33 T72129 CEA-specific antibody 6.15e-116
35	189	52-1	705 1 N81639 Sequence of genomic D 3.28e-115
36	189	52-1	743 13 Q78986 Human immunoglobulin 3.28e-115
37	188	51-8	372 10 Q64854 SPA-reactive VH regio 1.75e-114
38	187	51-5	294 10 Q64856 SPA-reactive VH regio 9.31e-114
39	187	51-5	519 13 Q78959 Human immunoglobulin 9.31e-114
40	185	51-0	345 10 Q64953 SPA-reactive VH regio 2.64e-112
41	185	51-0	649 13 Q79002 Human immunoglobulin 2.64e-112
42	185	51-0	877 13 Q78945 Human immunoglobulin 2.64e-112
43	183	50-4	264 14 Q89332 DP54 VH gene 7.46e-111
44	183	50-4	369 10 Q64851 SPA-reactive VH regio 7.46e-111
45	182	50-1	432 12 Q71717 Monoclonal antibody L 3.97e-110

ALIGNMENTS

```

RESULT 1
ID Q43772 standard: CDNA: 909 BP.
AC Q43772:
DT 01-OCT-1993 (first entry)
DE Sequence encoding the heavy chain variable region (VH) of human
DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line
DE 88BV59, ATCC CPT 10634
KW B-cell; immunoglobulin g; cancer; tumour; ss.
OS Homo sapiens.
FH Key
FT CDS
FT /tag= a
FT CDS
FT /tag= b
FT /product= VAR
FT /note= "1st AA of VAR is denoted AA#1"
FT CDS
FT /tag= c
FT /product= CDR 1
FT CDS
FT /tag= d
FT /product= CDR 2
FT CDS
FT /tag= e
FT /product= CDR 3
FT CDS
FT /tag= f
FT /product= CH 1
FT CDS
FT /tag= g
FT /product= Hinge
FT CDS
FT /tag= h
FT /product= FAB'
PN EP-546634-A.
PD 16-JUN-1993.
PF 09-DEC-1992. 203827.
PR 13-DEC-1991. US-807300.
PA (ALKU) AKZO NV.

```


CC The DNA sequence of eleven monoclonal antibodies are
CC represented in Q19145-57. Synthetic genes, for both heavy and
CC light chains may be created by combining selected CDR 1, 2, and 3
CC regions, which may be selected from different antibody mols. having
CC varied binding specificity. The chimaeric anti-RhD antibodies can be
CC used for diagnosis and therapy, and are capable of providing blood-
CC typing reagents of high specificity and reliability. They can also
CC be used in passive immunisation to prevent haemolytic disease of the
CC newborn.
SQ Sequence 336 BP; 76 A; 77 C; 108 G; 74 T;

Query Match 62.9%; Score 238; DB 2; Length 336;
Best Local Similarity 90.4%; Pred. No. 118e-143;
Matches 253; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

Db 1 ggrrggcgtgtccagcctggaggtccctgagactctctctgacagcgttggaattcac 60
QY 12 GGGAGGCGTGGTCCAGCCTGGCAGGTGCTGAGACTCTCTCTGAGCCTCTGGATTTCAC 71

Db 61 ctcccaactatgcatgcatgctgaggtccgcagactccagcgaaggcctggagtgggt 120
QY 72 CTTCAGAGCGTATGCGATGCACTGGGTGGCCAGGCTCTCAGGGCAGGGGCTGGAGTGGGT 131

Db 121 ggcagttatttggtatgaggaagtaataataactatgcagactccgtggaaggccgatt 180
QY 132 GGCAGGTATTGCTTTGATGGAAGTATACCAATATTACCGAGACTCCCTGTAAGGCGCGATT 191

Db 181 caccattctccagagacaattcccaagaacgcgtgtatctgcaaatgaacagcctggaagc 240
QY 192 CATCGTCTCCAGAGACAATTCAGGAGACAGCGTGTCTTCGAGATGAGCAAGCTCTGAGACT 251

Db 241 caagagacagcgtgtgtattactgtccagagaaattact 280
QY 252 CGAGAGACAGCGTGTGTATTATATGTGCGACAGAGGCTCTT 291

RESULT 4
ID Q78968 standard; DNA; 512 BP.
AC Q78968;
DT 03-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #30.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid, placenta; vector, pJB81, E.coli; mammalian, ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS
FT /tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 56..155
FT /tag= b
FT /misc_signal 462..464
FT /tag= c
FT /note= "miscellaneous signal, does not conform to
FT terminator or splice site sequence"
PN W09426895-A.
PD 24-NOV-1994.
PE 10-MAY-1993; J00603.
PR (NIBS) JAPAN TOBACCO INC.
PA Honjo T, Matsuda F.
PI WPI: 95-006791/01.
DR P-PSR: P66321
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Claim 38; Page 69-70; 130pp; Japanese.
CC A series of genes (Q78939-79002) encoding human immunoglobulin variable
CC heavy chains. The genes were isolated and cloned from a series of cosmid
CC constructs. Y202, Y103, Y21, Y5, Y24, 3-31, M84, M18 and M31, by PCR
CC amplification using primers Q78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with *NotI* restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions

CC were collected. The fragments were ligated with *ClaI*-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 512 BP; 120 A; 108 C; 159 G; 125 T;

Query Match 62.5%; Score 227; DB 13; Length 512;
Best Local Similarity 90.4%; Pred. No. 6.37e-143;
Matches 254; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 183 gggctctggggagggcgtgtccagcctggaggtccctgagactctctctgacagcctct 242
QY 4 GASTGGGCGGAGGCGTGGTGGAGAGCTTGGAGAGTCTCTCTGAGACTCTCTCTGAGAGCTCT 63

Db 243 ggaattcaacttcaagacgtatggcattggaatggaatggaatggaatggaatggaatgga 302
QY 54 GAAITCACTTCAAGACGCTATGGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 123

Db 303 gattgggtggcaggttatcatcatgatggaatggaatggaatggaatggaatggaatgga 362
QY 124 GASTGGGCGGAGGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 183

Db 363 gggcgtatccaccatctccagagacaattcccaagaacgcgtgtatctgcaaatggaacgc 422
QY 184 GGGCGATTTCATCGTCTCCAGAGACAATTCAGGAGACAGCGTGTCTCTGAGACTCTCTGAG 243

Db 423 ctgagagcgtggagcagcagcgtgtattactgtgagagaga 463
QY 244 CTGAGAGCTGGAGCAACGGCTGTCTATTACTGTGCGACAGA 284

RESULT 5
ID Q11956 standard; DNA; 339 BP.
AC Q11956;
DT 15-AUG-1991 (first entry)
DE Anti-human RhD REG-A MAB (Vh chain).
KW Monoclonal antibody; rhesus D; blood-typing; CDR;
KW haemolytic disease of the newborn; HDN; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 68..82
FT /tag= a
FT /label= CDR1
FT /misc_feature 125..175
FT /tag= b
FT /label= CDR2
FT /misc_feature 272..322
FT /tag= c
FT /label= CDR3
PN W09107492-A.
PD 30-MAY-1991.
PE 13-NOV-1990; E01964.
PR 13-NOV-1989; GB-025590.
PA (BLAO-) CENT BLOOD LAB AUTH.
PI Hughes- Jones N;
DR WPI: 91-178104/24.
DR P-PSDB: R12274.
PT DNA encoding complementary determining regions - of human
PT anti-rhesus D antibodies, useful in prodn of monoclonal
PT antibodies and for passive immunisation
PS Disclosure: Fig 13; 32pp; English
CC The DNA sequence of eleven monoclonal antibodies are
CC represented in Q119145-57. Synthetic genes, for both heavy and
CC light chains may be created by combining selected CDR 1, 2, and 3
CC regions, which may be selected from different antibody mols. having
CC varied binding specificity. The chimaeric anti-RhD antibodies can be
CC used for diagnosis and therapy, and are capable of providing blood-
CC typing reagents of high specificity and reliability. They can also
CC be used in passive immunisation to prevent haemolytic disease of the
CC newborn.
SQ Sequence 339 BP; 62 A; 80 C; 102 G; 75 T;

Query Match 62.3%; Score 226; DB 2; Length 339;
 Best Local Similarity 90.4%; Pred. No. 3,44e-142;
 Matches 253; Conservative 0; Mismatches 27; Indels 0; Gaps 0.

Db 1 gggagcgtgggtccagcctggagagtcctcagacactcctcgtgcagcgtcgtgattcac 60
 QY 12 GGGAGCGTGGTCCAGCCTGGAGGTCCTCCTGAGACTCTCTGTCAGCGTCTGGATTAC 71

Db 61 ctccaataattatggcattgcacatgggtccgcagagctccagcgaaggcgtggagtggt 120
 QY 72 CTTCAAGCGTATGCGATGCGATGGTCTGGAGGTCCTGAGACTCTCTGTCAGCGTCTGGATTAC 131

Db 121 ggcatttatatgatgatgaagtaataaaaaactatcacacatccgtgaaaggccgatt 180
 QY 132 GGCAGGTATTCGTTTGTATGGAAGTAACCATATTACGACACTCCCGTGAAGGCGCCGATT 191

Db 181 caccatctccagagacaattccaaaacacgcgtgtatcgaatgaacagcctgagagc 240
 QY 192 CATCGCTCTCCAGAGACAATTCAGGAGACACGCGTGTCTGTCGATGAGCACTCTGAGACT 251

Db 241 cgaagacacgcgtgtattactatgctcagagaaacgtact 280
 QY 252 CGAGGACACGGCTGTCTATTACTGTCCACACAGCGGTCT 291

RESULT 6
 ID T60380 standard; DNA; 369 BP.
 AC T60380;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scfv antibody 1-B2 VH gene.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scfv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy; ss.
 OS Homo sapiens.
 GN GB2305921-A.
 PN GB2305921-A.
 DT 23-APR-1997.
 PF 19-OCT-1996; 020920
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DR WPI: 97-215360/20.
 DR P-PSDB; W15534.
 DR PT Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and inflammatory disease
 PT Example 1: Fig la(i); 184pp: English.
 PS This DNA sequence comprises the gene encoding the VH domain (W15534) of human scfv antibody 1B2 (also known as 7A3), which is specific for transforming growth factor (TGF) beta-1. It was isolated by panning a phage antibody library produced from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (1) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are

CC highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for neutralisation. 115 G. 81 T;
 SQ Sequence 369 BP, 87 A, 86 C, 115 G, 81 T;

Query Match 62.0%; Score 225; DB 33; Length 369;
 Best Local Similarity 90.6%; Pred. No. 1.85e-141;
 Matches 251; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 16 gagttcggggggagcgtggtccagcctgggaggtccctgagacactcctcgtgcacacctct 75
 QY 4 GAGTGGGGGGAGGAGGAGTGTGAGCTGGAGAGTGTGTGACACACACACACACACACAC 63

Db 76 ggattcaccttcagtagctatggcattgcactgggtccgcagaggtccgcgaaggagctg 135
 QY 64 GGAATTCACCTTCACAGCGTATGGCATGTGGGTGGCGAGGCTTCAGGCAAGAGGCTG 123

Db 136 gagtggtgggcagttatatcatatgatggaagtataataactatgcagactccgtgaaag 195
 QY 124 GAGTGGGTGGTGGAGTATTTGCTTTTATGCAAGTAACTAATATTACGAGACTCCGTGAAG 183

Db 196 gcccaattcacacatctccagagacaattccaaagacacgcgtgtatctgcaaatgaacagc 255
 QY 184 GCGCGATTATCGTCTCCAGAGACAAATTCACGGGACACGGTGTTCCTGCAGATAGCAGC 243

Db 256 ctgagagctgagggacacgcgtgtgttactactgtgcga 292
 QY 244 CTGAGACTCGAGGACACGGCTGTCTATTACTGTGCGA 280

RESULT 7
 ID T44089 standard; cDNA; 732 BP.
 AC T44089;
 DT 27-FEB-1997 (first entry)
 DE ulcerative colitis-associated PANCA Fab 5-4 heavy chain cDNA.
 KW ulcerative colitis; anti-neutrophil cytoplasmic antibody; ANCA;
 KW PANCA; UC-PANCA; antibody engineering; phage display; diagnosis;
 KW cyclic; ds.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT /tag= a
 FT /product= UC-associated ANCA IgG heavy chain
 FT misc_RNA
 FT /tag= b
 FT /product= N-terminal tag
 FT misc_RNA
 FT /tag= c
 FT /label= FR1
 FT /note= "framework region 1"
 FT misc_RNA
 FT /tag= d
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT misc_RNA
 FT /tag= e
 FT /label= FR2
 FT /note= "framework region 2"
 FT misc_RNA
 FT /tag= f
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT misc_RNA
 FT /tag= g
 FT /label= FR3
 FT /note= "framework region 3"
 FT misc_RNA
 FT /tag= h
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT misc_RNA
 FT /tag= i
 FT /label= FR4
 FT /note= "framework region 4"

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FT misc_RNA 394...684
FT /tag- j
FT /label- CH1
FT /note- "heavy chain constant region"
FT misc_RNA 685...711
FT /tag- k
FT /label- Hinge
FT /note- "partial hinge segment of the heavy chain"
FT misc_RNA 712...732
FT /tag- l
FT /label- Hex-HTAG
FT /note- "hexahistidine tag"
FT misc_RNA 16...684
FT /tag- m
FT /label- Fd
FT /note- "heavy chain Fd"
FT misc_RNA 16...297
FT /tag- n
FT /label- VHSEGMENT
FT /note- "heavy chain variable segment"
FT misc_RNA 298...363
FT /tag- o
FT /label- D
FT /note- "diversity segment"
FT misc_RNA 364...408
FT /tag- p
FT /label- JH
FT /note- "heavy chain joining segment"
FT misc_RNA 16...408
FT /tag- q
FT /label- VHDOMAIN
FT /note- "heavy chain variable domain"
PN W09639186-AL.
PD 12-DEC-1996.
PF 05-JUN-1996: 008756.
PP 06-JUN-1995: US-472698.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PA (PFGC ) UNIV CALIFORNIA.
PI Braun J., Eggena MP., Targan SR;
DR WPI: 97-042866/04.
DR P-PSDB: W07614.
DR Antibody material associated with ulcerative colitis - comprising
PT anti-neutrophil cytoplasmic antibody, characterised by perinuclear
PT neutrophil staining pattern
PS Disclosure: Page 113-114: 145pp: English.
CC A cDNA clone (T44089) derived from human gut-associated lymphoid
CC tissue codes for the heavy chain (W07614) of recombinant UcpANCA
CC Fab clone 5-4. Anti-neutrophil cytoplasmic antibody characterised
CC by perinuclear neutrophil staining pattern (pANCA) associated with
CC ulcerative colitis (UC) was recombinantly produced and
CC characterised using a phase display technique. Libraries of VH-
CC and VL-encoding DNA homologues having the immunoreactivity of
CC UcpANCA antigen were created. Recombinant UcpANCA Fab clones 5-3
CC and 5-4 were generated (see also W07613-16). These can be used in
CC methods for screening for UcpANCA and for isolating UcpANCA
CC antirens.
SQ Sequence 732 BP. 169 A. 227 G. 124 G. 142 T.

Query Match 61.7%; Score 224; DB 25; Length 732;
Best Local Similarity 89.4%; Pred No. 9, 97A-141;
Matches 254; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 1 ctgagctggggagggagctgggtccagcctgggaagctccctgaagactctcctgtgacgcc 60
QY 1 CTCGAGTCGGGGGAGGGGAGCTGGTGTCTGAGCTTGGGAGGAGGCTTGGAGCTTCTGTGTGATGG 60
Db 61 tctgattcaaccttcagcaactatgcatgactgggtccgacgctccaggtccagggcgaagg 120
QY 61 TCTGATTCACTTCAAGAGCATGTCATGTCATGCTGGGTCCGACAGGCTCCAGGGCAAGGG 120
Db 121 ctgagtgagtgacaggtattcctctgatacaaaaaaaagtatatgtagactccgtg 180
QY 121 CTGATGAGTGTACAGGTATTTCCTTTGATGGAATTAACCAATATTACAGACTCCGTG 180

Db 181 aagggccgattcttcattccagagacaaattccagagacacaccttatctatctatgaac 240
QY 181 AAGGGCCGATTCTTCATTCCAGAGACAAATTCAGAGACACACCTTATCTATCTATCTATGAG 240
Db 241 accctgagagctgagacacagctctctattactctacgaaga 284
QY 241 ACCCTGAGAGCTGAGAGACAGCTCTCTATTACTTACTCTACGAAGA 284

RESULT 8
ID T60369 standard; DNA: 345 BP.
AC T60369.
DT 27-NOV-1997 (first entry)
DE Anti-TGF beta-2 scFv antibody 2A-H11 VH gene.
KW Transforming growth factor beta-2; TGF-beta-2; human;
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy; ss.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
PN GB2305921-A.
PD 23-APR-1997.
PF 07-OCT-1996: 020920.
PP 19-JAN-1996: GB-001081.
PP 06-OCT-1995: GB-020486
PA (CAME-) CAMERIDGE ANTIBODY TECHNOLOGY.
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
DR WPI: 97-215360/20.
DR P-PSDB: W15522.
DR Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
PS Example 1; Fig 2a(i); 184pp: English.
CC This DNA sequence comprises the gene encoding the VH domain
CC (W15522) of human scFv antibody 2A-H11 (also known as 6H1), which
CC is specific for transforming growth factor (TGF) beta-2. It was
CC isolated by panning a phage antibody library produced from cloned
CC germline V genes and synthetic CDRs. The antigen-binding domains
CC of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can
CC be used to counter the adverse effects of TGF beta, such as (i)
CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
CC fibrosis, arterial injury, proliferative retinopathy, retinal
CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,
CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
CC arthritis, macrophage deficiency diseases or macrophage pathogen
CC infection). Nucleic acids encoding human antibody VH and VL can be
CC used for prodn. of recombinant antigen-binding domains. These are
CC highly specific, have low dissociation constants (pref. less than 5
CC nM) and low IC50s for neutralisation.
SQ Sequence 345 BP. 75 A. 83 C. 112 G. 74 T.

Query Match 61.2%; Score 222; DB 33; Length 345;
Best Local Similarity 90.5%; Pred No. 2, 49e-139;
Matches 248; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 16 gagctctggggagggagctgggtccagcctgggaagctccctgaagactctcctgtgacgcc 75
QY 4 GAGCTCGGGGAGGGAGGCTGGTGTCTGAGCTTGGGAGGAGGCTTGGAGCTTCTGTGTGATGG 63
Db 76 gaattcaccttcagtagctatgcatgactgggtccgacgctccaggtccagggcgaaggct 135
QY 76 GATTTCACCTTCAGTAGCTATGTCATGTCATGCTGGGTCCGACAGGCTCCAGGGCAAGGGCT 135

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QY 64 GGATTCACCTTCAGACGATGATGCGATGCGGTGCGGCTCCAGGCTCCAGGCAAGGGGCTG 123
Db 136 gattgagtgacgtatgatggtatggaagtaataatactatgcagactccgtgaag 195
QY 124 GATGGGGGCGCAGGTATTTCGTTTGATGGAAGTAACCAATATTACGACACTCCGTGAAG 183
Db 196 ggcgattaccatctccagagacaattccaagaacacgctgtatctgcaaatggacagc 255
QY 184 GGCCGATTATCTCTCCAGAGACAATCCAGGGACACGGTGTCTTCGAGATGAGCAGC 243
Db 256 ctgagagccagagacgcccgtgtattactgtg 289
QY 244 CTGAGACTCGAGGACACGGCTGTCTATTACTGTG 277

RESULT 9
ID T60381 standard: DNA; 369 BP.
AC T60381;
DE Anti-TGF beta-1 scfv antibody 31G9 VH gene.
KW Transforming growth factor beta-1; TGF-beta-1; human;
KW antibody engineering; scfv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy; ss.
OS Homo sapiens.
PN GR230521-A.
PD 23-APR-1997.
PF 07-OCT-1996; 020920.
PR 19-JAN-1996; GB-001081.
PR 06-OCT-1995; GB-020486.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
DR WPI: 97-215360/20.
DR P-PSDB: W15535.
PT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
PS Example 1: Fig 1a(ii); 184pp; English.
CC This DNA sequence comprises the gene encoding the VH domain
CC (W1535) of human scfv antibody 31G9, which is specific for
CC transforming growth factor (TGF) beta-1. It was isolated from
CC a large single chain Fv library. The antigen-binding domains
CC of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can
CC be used to counter the adverse effects of TGF beta, such as (i)
CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
CC fibrosis, arterial injury, proliferative retinopathy, retinal
CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,
CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
CC arthritis, macrophage deficiency diseases or macrophage pathogen
CC infection). Nucleic acids encoding human antibody VH and VL can be
CC used for prodn. of recombinant antigen-binding domains. These are
CC highly specific, have low dissociation constants (pref. less than 5
CC nM) and low IC50s for neutralisation.
SQ Sequence 369 BP; 83 A; 88 C; 117 G; 81 T;

Query Match 60.98; Score 221; DB 33; Length 369;
Best Local Similarity 90.28; Pred. No. 1.56e-138;
Matches 248; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 17 agtctggggagcggtggtccacccctggaggtccctgagactctctgtcagctctg 76
QY 5 AGTCGGGGGGAGCGGTGTCAGGCTGGGAGGTCCCTGAGACTCTCTCTTGACAGGCTT 64
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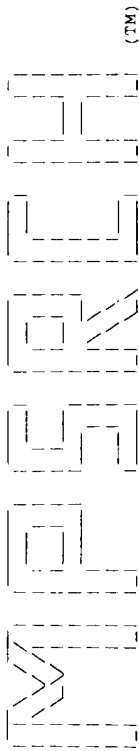
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Db 77 gattcacttcagtagctatggtgcatgcactgggtccgccaggctccagacaaaggactgg 136
QY 65 GATTCACCTTCAGACGATGATGCGATGCGGTGCGGCTCCAGGCTCCAGGCAAGGGGCTG 124
Db 137 agtgggtggcagttatcatatgatggaagtattaaatactatgcagactccgtgaaag 196
QY 125 AGTGGGTGGGAGGTATTTCGTTTGATGGAAGTAACCAATATTACGACAGACTCCGTGAAG 184
Db 197 ggcgattaccatctccagagacaattccaagaacacgctgtatctgcaaatgaaacagc 256
QY 185 GCCGATTATCTCTCCAGAGACAATCCAGGGACACGGTGTCTTCGAGATGAGCAGC 244
Db 257 tgagagctgagagacacgctgtgtattactgtg 291
QY 245 TGAGACTCGAGGACACGGCTGTCTATTACTGTGCG 279

RESULT 10
ID Q11880 standard: DNA; 1521 BP.
AC Q11880;
DE 01-AUG-1991 (first entry)
DE Encodes heavy chain variable region for 4B9 human monoclonal Ab.
KW immunoglobulin G; heavy chain; variable region; duplication;
KW passive immunity; group B streptococci; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_RNA 450..57
FT /tag= a
FT /note= "octamer"
FT sig_peptide 583..628
FT /tag= b
FT /note= "leader"
FT misc_RNA 732..1107
FT /tag= c
FT /product= heavy chain variable region
PN W09106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-153947/22.
DR P-PSDB: P12132, P12133, P12134.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Claim 44; Fig 18; 104pp; English.
CC The leader peptide and the L/V region are encoded in different
CC reading frames. The L/V region corresponds to the last three amino
CC acids of the leader peptide and the variable region gene.
CC See also Q11878 and Q11879.
SQ Sequence 1521 BP; 349 A; 376 C; 425 G; 371 T;

Query Match 60.98; Score 221; DB 2; Length 1521;
Best Local Similarity 89.38; Pred. No. 1.56e-138;
Matches 251; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 756 gattctgggggagcggtggtccagcctggaggtccctgagactctctgtcagctct 815
QY 4 GAGTCGGGGGGAGGCGGTGTCAGGCTGGGAGGTCCCTGAGACTCTCTCTTGACAGGCTC 63
Db 816 ggaattcccttcagagagactatggcactggtggtccgccaggtccagcagaggggctg 875
QY 64 GGATTCACCTTCAGACGATGATGCGATGCGGTGCGGCTCCAGGCAAGGGGCTG 123
Db 876 gattgggtggcagttatcatctgtatggaagtgttgactactatgcagactccgtgaaag 935
QY 124 GAGTGGGTGGCAGGTATTTCGTTTGATGGAAGTAACCAATATTACGACAGACTCCGTGAAG 183
Db 936 ggcgattaccatctccagagacaattccaagaacacgctgtatctgcaaatgaaacagc 995
QY 184 GGGGATTTCATCTCTTCAGAGACAATCCAGGGACACGGTGTCTTCGAGATGAGCAGC 243
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(TM)

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MPsearch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:59:04 1998: MasPar time 459.90 Seconds
Tabular output not generated. 1121.143 Million cell updates/sec

Title: >US-08-844-215-25
Description: (1-363) from US08844215 seq
Perfect Score: 363
N.A. Sequence: 1 CTCGAGTGGGGGAGGGG.....CCCTGGTACCGGCTCTCTCA 363
Comp: GAGCTCAGCCCGCCCTCCGCA

Scoring table: TABLE default
Gap 6
Nmatch STD: Dbase 0: Query 0
Searched: 430261 seqs. 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1: BCT 2: FUN 3: GEN 4: HTG1 5: HTG2 6: HTG3 7: HTG4 8: HUM1
9: HUM2 10: HUM3 11: INV1 12: INV2 13: ORG 14: NAM 15: VRT
16: PLN 17: PRL 18: PRC 19: RCD 20: SYN 21: UNC 22: VIF
Database: genbank101

23: BCT1 24: BCT2 25: BCT3 26: BCT4 27: BCT5 28: BCT6 29: BCT7
30: BCT8 31: BCT9 32: BCT10 33: BCT11 34: BCT12 35: BCT13
36: GEN1 37: GEN2 38: GEN3 39: GEN4 40: GEN5 41: GEN6 42: HTG1
43: HTG2 44: HTG3 45: HTG4 46: HTG5 47: INV1 48: INV2 49: INV3
50: INV4 51: INV5 52: INV6 53: INV7 54: INV8 55: INV9 56: INV10
57: INV11 58: INV12 59: MAM1 60: MAM2 61: MAM3 62: VRT1
63: VRT2 64: VRT3 65: VRT4 66: PAT1 67: PAT2 68: PAT3 69: PAT4
70: PAT5 71: PAT6 72: PAT7 73: PHG 74: PLN1 75: PLN2 76: PLN3
77: PLN4 78: PLN5 79: PLN6 80: PLN7 81: PLN8 82: PLN9 83: PLN10
84: PLN11 85: PLN12 86: PRL1 87: PRL2 88: PRL3 89: PRL4
90: PRL5 91: PRL6 92: PRL7 93: PRL8 94: PRL9 95: PRL10
96: PRL11 97: PRL12 98: PRL13 99: PRL14 100: PRL15 101: PRL16
102: PRL17 103: RCD1 104: RCD2 105: RCD3 106: RCD4 107: RCD5
108: RCD6 109: RCD7 110: RCD8 111: RCD9 112: STE 113: SYN
114: UNA
Database: genbankb101

115: VRL1 116: VRL2 117: VRL3 118: VRL4 119: VRL5 120: VRL6
121: VRL7 122: VRL8 123: VRL9 124: VRL10 125: VRL11
Database: genbank-new7
126: BCT 127: GEN 128: HTG1 129: HTG2 130: INV 131: MAM
132: VRT 133: PHG 134: PLN1 135: PLN2 136: PRL1 137: PRL2
138: RCD 139: SYN 140: UNA 141: VRL
Database: u-emb151.101
142: part1 143: part2

Statistics: Mean 9.942: Variance 4.310: scale 2.305
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Prod. No.
1	246	67.8	375	9	HSHAMRH	H sapiens mRNA for Hg
2	246	67.8	375	91	HSHAMRH	H sapiens mRNA for Hg
3	245	67.5	375	92	HSLD140	H sapiens mRNA for im
4	243	66.9	378	9	HSPEGAR	H sapiens mRNA for p
5	243	66.9	378	93	HSPEGAR	H sapiens mRNA for p
6	242	66.7	377	95	HSU80162	Human immunoglobulin
7	239	65.8	375	92	HSLD1110	H sapiens mRNA for va
8	238	65.6	373	101	HUMVH3J	Human mRNA for immuno
9	238	65.6	373	95	HSU43759	Human immunoglobulin
10	236	65.0	378	95	HSU80104	Human immunoglobulin
11	235	64.7	454	99	HUMIGVDJ2	Homo sapiens IgH chai
12	234	64.5	375	95	HSU80105	Human immunoglobulin
13	234	64.5	375	95	HSU80102	Human immunoglobulin
14	231	63.6	341	99	HUMIGHYABK	Human Ig germline H-c
15	231	63.6	341	99	HUMIGHYABN	Human Ig germline H-c
16	231	63.6	341	99	HUMIGHYABL	Human Ig germline H-c
17	231	63.6	342	91	HSIHCVDI1	H sapiens mRNA for re
18	231	63.6	359	96	HSVH3132	H sapiens rearranged
19	231	63.6	360	99	HUMIGHYAAS	Human Ig germline H-c
20	231	63.6	366	96	HSVH31348	H sapiens rearranged
21	231	63.6	384	90	HSBP94H	Homo sapiens mRNA for
22	231	63.6	399	91	HSIGVHC28	H sapiens rearranged
23	231	63.6	412	99	HUMIGHYAAC	Homo sapiens germline
24	231	63.6	412	91	HSIGVHB28	H sapiens germline im
25	231	63.6	412	99	HUMIGHYAAE	Homo sapiens germline
26	231	63.6	583	98	HUMIGH333X	Human immunoglobulin
27	230	63.4	333	91	HSIHCVDA	H sapiens mRNA for re
28	230	63.4	355	99	HUMIGHYAAM	Human Ig germline H-c
29	230	63.4	355	99	HUMIGHYAAT	Human Ig germline H-c
30	230	63.4	355	99	HUMIGHYAAT	Human Ig germline H-c
31	230	63.4	355	99	HUMIGHYAAU	Human Ig germline H-c
32	230	63.4	257	102	S70739	Ig VH-anti-DNA mAb WR
33	230	63.4	363	95	HSU80108	Human immunoglobulin
34	230	63.4	366	91	HSIG040VH	H sapiens mRNA for Ig
35	230	63.4	378	94	HSU00519	Human immunoglobulin
36	230	63.4	411	90	HSACVPC	H sapiens mRNA for m
37	229	63.1	294	91	HSIGDP50	H sapiens germline Ig
38	229	63.1	294	91	HSIGVH277	H sapiens germline im
39	229	63.1	341	99	HUMIGHYABP	Human Ig germline H-c
40	229	63.1	341	99	HUMIGHYABQ	Human Ig germline H-c
41	229	63.1	360	92	HUMIGHYAAX	Human Ig germline H-c
42	229	63.1	363	95	HSU80161	Human immunoglobulin
43	229	63.1	412	99	HUMIGHVAAD	Homo sapiens germline
44	229	63.1	450	90	HSBEL29	H sapiens rearranged
45	229	63.1	523	99	HUMIGHCJCM	Human Ig chain VJCC

ALIGNMENTS

RESULT 1
ID HSHAMRH standard: RNA: HUM: 375 BP.
AC X64154;
NI 938353
DT 06-MAR-1993 (rel 35, Created)
TT 26-JUL-1997 (rel 52, Last updated, Version 6)
DE H.sapiens mRNA for HamB heavy chain variable Ig domain
KW heavy chain, Ig heavy chain;
KW immunoglobulin heavy chain variable region, variable region.
OS Homo sapiens (human)
OC Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
OC Homo.
RN [1]
RP 1-375
RA Hughes-Jones N.C.;

RL Submitted (08-JAN-1992) to the EMBL/GenBank/DBJ databases.
 PL N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research,
 RN Babraham Hall, Cambridge CB2 4AT, UK
 RP [2]

RX MEDLINE: 93107334.
 RA Bve J.M., Carter C., Cui Y., Gorick B.D., Songsivilai S.,
 PA Winter G., Hughes-Jones N.C., Marks J.D.;
 RT "Germline variable region gene segment derivation of human
 RT monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation
 RT by somatic hypermutation and repertoire shift";
 PL J. Clin. Invest. 90:2481-2490(1992).
 DR IMGT/HLIM: X64154; Release 97.06.
 CC See also X64148-69

Key Location/Qualifiers

FT source 1..375
 FT /organism="Homo sapiens"
 FT /cell_type="B-lymphocytes"
 FT /cell_line="HAM-B"
 FT /isolate="blood donor Ha"
 FT /chromosome="14"
 FT misc_feature 1..23
 FT /note="PCR primer"
 FT misc_feature 1..375
 FT /note="VDJ region"
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 FT /note="Vh region"
 FT misc_feature 91..106
 FT /note="CDR1 region"
 FT misc_feature 148..198
 FT /note="CDR2 region"
 FT misc_feature 295..324
 FT /note="D region"
 FT misc_feature 295..342
 FT /note="CDR3 region"
 FT misc_feature 325..375
 FT /note="J region"
 FT misc_feature 360..375
 FT /note="PCR primer"
 FT SQ Sequence 375 bp; 81 A; 88 C; 122 G; 81 T; 3 other;

Query Match 67.8%; Score 246; DB 9; Length 375;
 Best Local Similarity 83.5%; Pred. No. 1.30e-201;
 Matches 299; Conservative 3; Mismatches 56; Indels 0; Gaps 0;

Db 16 sagtcrgggggggcgtggtcagcctggaggctccctgagactctcctgtgcagcgtct 75
 QY 4 GAGTCGGGGGAGGCGGTGGTCCAGCCTGGGAGGTCCTGTGACACTCTCCTGTGCAGCGTCT 63
 Db 76 ggattcaccttcagtagctatggcctgggtccgcagcgtcccgcaaggggctg 135
 QY 64 GGATTCACCTTCAAGACGATGGCATGCTGGTCCGCCAGGCTCCAGGCAAGGGGTG 123
 Db 136 gadtgggtggcagttatttgggtatgatgaagataataatactatgcagactccctgaag 195
 QY 124 GAGTGGGTGGCAGGTATTTCTGTTGATGGAAGTAACCAATATTATACGCAGACTCCGTGAAG 183
 Db 196 ggcgcattaccatctccagagacaattcccaagaacagcgtctatcgaataaagacgc 255
 QY 184 GGCCTGATTCATCTCTCCAGACAAATCCAGGGACACAGGTGTTTCTGCAGATGACAGC 243
 Db 256 ctgagagccgagagacggcgtgtgtattactgtgcagagagaagttactatggttcgggga 315
 QY 244 CTGAGACTCGAGACACGGCTGTCTATTACTGTGCGACAGAGGGTTCCTTCCTTGGCTCG 303
 Db 316 gttaggcgttactacggtatgacgtctgtggcccgagggaccacaggtcacggtctcct 373
 QY 304 AITTAAGGGCGTTTACTACCTTGAAATTTGGGGCCAGGGAACTTGTGTACCGTCTCTCT 361

RESULT 2
 LOCUS HSHAMBH 375 bp RNA PRI 10-MAR-1993

DEFINITION H. sapiens mRNA for HAMBH heavy chain variable Ig domain.
 ACCESSION X64154
 NID g38353
 KEYWORDS heavy chain; Ig heavy chain; immunoglobulin heavy chain variable region; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; mitochondria; eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 375)
 AUTHORS Hughes-Jones, N.C.
 TITLE Direct Submission
 JOURNAL Submitted (08-JAN-1992) N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research, Babraham Hall, Cambridge CB2 4AT, UK

REFERENCE 2 (bases 1 to 375)
 AUTHORS Bve J.M., Carter C., Cui Y., Gorick B.D., Songsivilai S., Winter G., Hughes-Jones N.C. and Marks J.D.
 TITLE Germline variable region gene segment derivation of human monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation by somatic hypermutation and repertoire shift
 J. Clin. Invest. 90 (6), 2481-2490 (1992)

MEDLINE 93107334
 COMMENT See also X64148-69.

FEATURES
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 /organism="Homo sapiens"
 /isolate="blood donor Ha"
 /cell_type="B-lymphocytes"
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 /chromosome="14"
 1..23
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 1..375
 /note="VDJ region"
 1..294
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 91..106
 /note="CDR1 region"
 148..198
 /note="CDR2 region"
 295..342
 /note="CDR3 region"
 295..324
 /note="D region"
 325..375
 /note="J region"
 360..375
 /note="PCR primer"

BASE COUNT 81 a 88 c 122 g 81 t 3 others
 ORIGIN
 Query Match 67.8%; Score 246; DB 91; Length 375;
 Best Local Similarity 83.5%; Pred. No. 1.30e-201;
 Matches 299; Conservative 3; Mismatches 56; Indels 0; Gaps 0;

Db 16 sagtcrgggggggcgtggtcagcctggaggctccctgagactctcctgtgcagcgtct 75
 QY 4 GAGTCGGGGGAGGCGGTGGTCCAGCCTGGGAGGTCCTGTGACACTCTCCTGTGCAGCGTCT 63
 Db 76 ggattcaccttcagtagctatggcctgggtccgcagcgtcccgcaaggggctg 135
 QY 64 GGATTCACCTTCAAGACGATGGCATGCTGGTCCGCCAGGCTCCAGGCAAGGGGTG 123
 Db 136 gadtgggtggcagttatttgggtatgatgaagataataatactatgcagactccctgaag 195
 QY 124 GAGTGGGTGGCAGGTATTTCTGTTGATGGAAGTAACCAATATTATACGCAGACTCCGTGAAG 183
 Db 196 ggcgcattaccatctccagagacaattcccaagaacagcgtctatcgaataaagacgc 255
 QY 184 GGCCTGATTCATCTCTCCAGACAAATCCAGGGACACAGGTGTTTCTGCAGATGACAGC 243
 Db 256 ctgagagccgagagacggcgtgtgtattactgtgcagagagaagttactatggttcgggga 315

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QY 244 CTGAGACTCGAGGACAGCGGTGCTTACTTACTGTGCGACAGAGGGTCTCTCTTTGGCTCG 303
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Db 316 gttaggcgttactacagtgatggagcgtctgggcccagggagccacagtcacagctccct 373
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QY 304 ATTAAGGGGGTTTACTACCTTGAATAATTGGGCGCAGGGAACCCCTGGTCACCGCTCTCCT 361
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RESULT 3
LOCUS HSLD140 375 bp RNA PRI 11-SEP-1996
DEFINITION H.sapiens mRNA for immunoglobulin heavy chain, clone LD1-40.
ACCESSION Y07816
NID g1536906
KEYWORDS heavy chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata,
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 375)
AUTHORS Miescher, S.M.
JOURNAL Unpublished
AUTHORS Miescher, S.M.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1996) S. M. Miescher, Institute of Immunology And
Allergology, University Of Bern, Sahli Haus 2, Inselspital, CH-3010
Bern, SWITZERLAND

FEATURES
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/organism="Homo sapiens"
/isolate="donor D"
/notes="peripheral; anti-Rhesus D"
/cell_type="B lymphocyte"
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/dev_stage="adult"
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<1..>375
/codon_start=1
/product="immunoglobulin heavy chain"
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/translation="QVKLESQGVVQFSLPLSCIASGFTLPLNHYAMHWKAPSKG
LEWAGIWFDSGNKAYADSVKGRFTISPDNSKNTLFLNLSLPEDTAVVYCAPEPAA
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BASE COUNT 89 a 91 c 114 g 81 t
ORIGIN

Query Match 67.5% Score 245. DB 92. Length 375.
Best Local Similarity 83.7% Pred. No. 1.19e-200;
Matches 304; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Db 13 ctgagtcggggagcgtgttcacagcctggaggtccctcagacactctctgtatagcg 72
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QY 1 CTCAGTCGGGGGAGCGGTGCTCCAGCGCTGGAGGTCCTGAGACTCTCCTGTGCAGCG 60
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Db 73 tctgattccacctcaggaattatgcctgactggttcgcccaggtccagcagggg 132
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QY 61 TCTGGATTACCTTCACAGAGGTATGCGATGCGCTGGCTCCAGGCTCCAGGCAAGGGG 120
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Db 133 ctgagtggtggcaggtatattggtttgtaggaagtaacaaaactatgcagactccgtg 192
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QY 121 CTGAGTGGGTGGCAGGTATTTCTGTTGATGGAAGTAACCAATATACCGACACTCCGTG 180
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Db 193 aagggcattaccattccagagacaattccaaagaacacgctgtttctgcaactgaac 252
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QY 181 AAGGCTCGATTCATGCTCTCCAGAGACAAATCCAGGAGACAGCGTGTTCTGCGAGTAGGC 240
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Db 253 agcctgagagacagagacagcagctgtgtattattgtgcagagagagcagcagcagtggt 312
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QY 241 AGCCTGAGACTCGAGGACACGGCTGTCTATTACTGTGCGACAGAGGGTCTCTCTTTGGC 300
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Db 313 attctaggttctattactacatgaacgtctgtgggcaagggagccacaggtccacgtctcc 372
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QY 301 TCGATTAAAGGGGGTITACTACTACTTGAATAATTGGGCGCAGGGAACCCCTGGTCACCGCTCTCCT 360
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Db 373 cca 375
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QY 361 TCA 363
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RESULT 4
ID HSPGAGH standard: PNA: HUM; 378 BP.
AC X64157;
NI g38356
DI 06-MAR-1993 (Rel. 35, Created)
DT 26-JUL-1997 (Rel. 52, Last updated, Version 6)
DE H.sapiens mRNA for REGAH heavy chain variable Ig domain
KW heavy chain; Ig heavy chain;
KW immunoglobulin heavy chain variable region; variable region.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OC Homo.
RN [1]
PP 1-378
RA Hughes-Jones N.C.;
RT Submitted (08-JAN-1992) to the EMBL/GenBank/DBJ databases.
RL N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research,
RL Babraham Hall, Cambridge CB2 4AT, UK
RN [2]
RP 1-378
RX MEDLINE: 93107334.
RA Bye J.M., Carter C., Cui Y., Corrick R.D., Songvilai S.,
FA Winter G., Hughes-Jones N.C., Marks J.D.;
RT "Germline variable region gene segment derivation of human
monoclonal anti-Rh(n) antibodies: Evidence for affinity maturation
by somatic hypermutation and repertoire shift";
PL J. Clin. Invest. 90:2481-2490(1992)
DR TMGT/LIGM: X64157; Release 97.06.
CC See also X64148-69
FH Key Location/Qualifiers
FH source 1..378
FT /organism="Homo sapiens"
FT /cell_type="B-lymphocytes"
FT /cell_line="Reg-A"
FT /isolate="blood donor Re"
FT /chromosome="14"
FT misc_feature 1..23
FT /note="PCR primer"
FT misc_feature 1..378
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FT misc_feature 91..105
FT /note="CDR1 region"
FT misc_feature 148..198
FT /note="CDR2 region"
FT misc_feature 295..333
FT /note="D region"
FT misc_feature 295..345
FT /note="CDR3 region"
FT misc_feature 334..378
FT /note="J region"
FT misc_feature 363..378
FT /note="PCR primer"
SQ Sequence 378 BP, 87 A, 92 C, 114 G, 83 T, 2 other,
Query Match 66.9% Score 243. DB 9. Length 378;
Best Local Similarity 85.1% Pred. No. 1.00e-198;
Matches 308; Conservative 2; Mismatches 49; Indels 3; Gaps 3;

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Db 17 agtctggggaggcgtgtgtccagcctggaggtccctgcagactctctgtgcagcgtctg 76
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Db 77 gattcaccctcaataatattgcatgcactgggtcccccaggtccaggcaaggcgtgg 136
Qy 65 GATTCAACCTTCAACAGCTATGGCATGGCTGGGTCCCGCCAGGCTCCAGGCAAGGGCTGG 124

Db 137 agtgggtggcgttatgtatggaagtataaaactatgcagactccgtgaagg 196
Qy 125 AGTGGGTGGCAGGATTTTCGTTTATGGAAGTAACCAATATTAGCGAGACTCCGTGAAGG 184

Db 197 gccattcaccatctccagagacaattcccaagaacacgctgtatctgcgaataaaacggc 256
Qy 185 GCCGATTTCATCGTCTCCAGACACAAATTCACAGGACACGSGTGTTCCTGCAGATGAGTAGCC 244

Db 257 tgagagccgagacacggcgtgtattactgtgcgagagaacgtactacgatctcggag 316
Qy 245 TGAGACTCGAGACACGGCTGTCTATTACTGTGGACAGAGGGTTCCTCT-T-T-TGGCT 301

Db 317 tgatcattcctcgcggtattttgactactggggccagggaacccgggtcacgctctcmt 376
Qy 302 CGATTAGGGCGGTACTACTCTTGAAAATTGGGGCCAGGGAACCCCTGGTCACCGTCTCCT 361

Db 377 cm 378
Qy 362 CA 363

RESULT 5
LOCUS HSREGAH 378 bp PNA PPI 10-MAR-1993
DEFINITION H.sapiens mRNA for RegAH heavy chain variable Ig domain.
ACCESSION X64157
NID 938356
KEYWORDS heavy chain; Ig heavy chain; immunoglobulin heavy chain variable
region; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 378)
AUTHORS Hughes-Jones, N.C.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992) N.C. Hughes-Jones, Inst of Animal
Physiology and Genetics Research, Babraham Hall, Cambridge CB2 4AT,
UK
REFERENCE 2 (bases 1 to 378)
AUTHORS Bye, J.M., Carter, C., Cui, Y., Gorick, B.D., Songsivilai, S.,
Winter, G., Hughes-Jones, N.C. and Marks, J.D.
TITLE Germine variable region gene segment derivation of human
monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation
by somatic hypermutation and repertoire shift
JOURNAL J Clin. Invest. 90 (5), 2481-2490 (1992)
MEDLINE 93107334
COMMENT See also X64148-69.
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/isolate="blood donor Re"
/cell_type="B-lymphocytes"
/line="Reg-A"
/chromosome="14"
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1..378
misc_feature /note="VDJ region"
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misc_feature /note="CDR2 region"
295..345

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misc_feature /note="CDR3 region"
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misc_feature /note="D region"
334..378
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BASE COUNT 87 a 92 c 114 g 83 t 2 others
ORIGIN
Query Match 66.9%; Score 243; DB 93; Length 378;
Best Local Similarity 85.1%; Pred. No. 1.00e-198;
Matches 308; Conservative 2; Mismatches 49; Indels 3; Gaps 3;
Db 17 agtctggggaggcgtgtgtccagcctggaggtccctgcagactctctgtgcagcgtctg 76
Qy 5 AGTCGGGGAGGCGTGTGTCAGCGTCGGAGGTCCTCGAGACTCTCTGTCAGCGCTCTG 64

Db 77 gattcaccctcaataatattgcatgcactgggtcccccaggtccaggcaaggcgtgg 136
Qy 65 GATTCAACCTTCAACAGCTATGGCATGGCTGGGTCCCGCCAGGCTCCAGGCAAGGGCTGG 124

Db 137 agtgggtggcgttatgtatggaagtataaaactatgcagactccgtgaagg 196
Qy 125 AGTGGGTGGCAGGATTTTCGTTTATGGAAGTAACCAATATTAGCGAGACTCCGTGAAGG 184

Db 197 gccattcaccatctccagagacaattcccaagaacacgctgtatctgcgaataaaacggc 256
Qy 185 GCCGATTTCATCGTCTCCAGACACAAATTCACAGGACACGSGTGTTCCTGCAGATGAGTAGCC 244

Db 257 tgagagccgagacacggcgtgtattactgtgcgagagaacgtactacgatctcggag 316
Qy 245 TGAGACTCGAGACACGGCTGTCTATTACTGTGGACAGAGGGTTCCTCT-T-T-TGGCT 301

Db 317 tgatcattcctcgcggtattttgactactggggccagggaacccgggtcacgctctcmt 376
Qy 302 CGATTAGGGCGGTACTACTCTTGAAAATTGGGGCCAGGGAACCCCTGGTCACCGTCTCCT 361

Db 377 cm 378
Qy 362 CA 363

RESULT 6
LOCUS HSU80162 377 bp DNA PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V3-33) gene,
partial cds.
ACCESSION U80162
NID g1791166
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotae, mitochondrial eukaryotes; Metazoa, Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 377)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 97182739
REFERENCE 2 (bases 1 to 377)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
FEATURES
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1..377 Location/Qualifiers
/organism="Homo sapiens"
/note="CD19+ peripheral blood B cells obtained from a
healthy subject; clone 87 in reference 1"
/cell_type="CD19+ B cells"
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BASE COUNT 82 a 89 c 116 g 90 t

Query Match 66.7%; Score 242; DB 95; Length 377;

Best Local Similarity 84.8%; Pred. No. 9,18e-198;

Matches 307; Conservative 0; Mismatches 53; Indels 2; Gaps 2;

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Db 15 gattctggggagagctgtctcagctggagagctccctcgaactctctctgagcgcgtct 75
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Db 76 gattcaccttcagtagctatgagctgagctgagctgagctgagctgagctgagctg 135
QY 64 GATTCACTTCAAGACGTATGCGATGCACTGGGTCCGCCAGGCTCCAGGCGGCTG 123
Db 136 gattgggtggcagttatggttatgagatgaatgaatgaatgaatgaatgaatgaatga 195
QY 124 GAGTGGGTGGCAGGTATTCGTTTGAAGTAACCAATATTAAGCAAGCTCCGTTGAAG 183
Db 196 gcccgtaccattccagagacattccagagacattccagagacattccagagacattcc 255
QY 184 GGCCTGATTCATGCTCTCCAGACAAATCCAGGACACGGGTCTTCTGCAATGAGCAGC 243
Db 256 ctgaagccgagagacacgtctgtattactgtgcagatatacagatttttgagtggttaa 315
QY 244 CTAGAACTGAGGACACGCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 303
Db 316 tcttttagcccgagagcgtttagctactgagcagcagcagcagcagcagcagcagcagc 375
QY 304 A-TTAAAGGGGGCTTACTACTTT-GAAATTTGGGGCCAGGAACTGCTGACCGTCTCT 361
Db 376 ca 377
QY 362 CA 363

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RESULT 7
LOCUS HSLD1110 375 bp RNA PRI 19-SEP-1996
DEFINITION H.sapiens mRNA for variable region of immunoglobulin G heavy chain,
clone-LD1-110.
ACCESSION Y08180
NID q1552279
KEYWORDS heavy chain; IgG; immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Homidae; Homo
1 (bases 1 to 375)
Miescher, S.M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 375)
Miescher, S.M.
AUTHORS Direct Submission
TITLE Submitted (11-SEP-1996) S.M. Miescher, Institute Of Immunology And
Allergy, University Of Bern, Sahli Haus 2, Inselspital, CH-3010
Bern, SWITZERLAND
FEATURES
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/organism="Homo sapiens"
/isolate="donor D"

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CDS

BASE COUNT 94 a 92 c 114 g 75 t

Query Match 65.8%; Score 239; DB 92; Length 375;

Best Local Similarity 82.9%; Pred. No. 7.03e-195;

Matches 301; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Db 13 ctccagctctggggagcgcgtgtccagcctggagagctccctcgaactctctctgataagc 72
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QY 61 TCTGATTCACTTCAAGACGTATGCGATGCACTGGGTCCGCCAGGCTCCAGGCGGCTG 120
Db 133 ctggagctgggtggcaggttatggtttgagagacacacacacacacacacacacacac 192
QY 121 CTCGAGTCGGTCGCGAGGCTATTCGCTTTCATGCAACTAACCAATATTACGCAATGCTG 180
Db 193 agggcccgattcacctctccagagacacacacacacacacacacacacacacacacacac 252
QY 181 AAGGGCCGATTCTATGCTCTCCAGACAAATTCAGGACACGGGTCTTCTGCAATGAGC 240
Db 253 agcctgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 312
QY 241 AGCCTGAGACTCGAGGACACGGGTCTGCTATTAATTAATTAATTAATTAATTAATTA 300
Db 313 atcagtagatatacattactacatgagcgtctgggagcagcagcagcagcagcagcagc 372
QY 301 TCATTAAGGGGCTTACTACTTT-GAAATTTGGGGCCAGGAACTGCTGACCGTCTCT 360
Db 373 tca 375
QY 361 TCA 363

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RESULT 8
LOCUS HUMVH37 373 bp mRNA PRI 06-MAR-1997
DEFINITION Human mRNA for immunoglobulin M (IgM), partial cds (VH1-N-D-N-1H4);
clone H2-27E.
ACCESSION D83684
NID q1213573
KEYWORDS IgM; immunoglobulin M.
SOURCE Homo sapiens Blood B-cell rearranged cDNA to mRNA, clone H2-27E.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Homidae;
Homo.
1 (bases 1 to 373)
AUTHORS Hakoda, M., Kametani, N., Hayashimoto-Kurumada, S., Silverman, G.,
Yamanaka, H., Terai, C. and Kashiwazaki, S.
TITLE Differential binding avidities of human IgM for staphylococcal
protein A derive from specific germline VH3 gene usage
JOURNAL Unpublished (1996)
REFERENCE 2 (bases 1 to 373)
AUTHORS Hakoda, M.
TITLE Direct Submission

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[illegible]

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Db 247 ggcgattcaccatctccagagacaattccaagaacacgcgtgtatctgcaaatgaacagc 306
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RESULT 12 HSU80105 375 bp DNA PRI 19-FEB-1997
LOCUS Human immunoglobulin heavy chain variable region (V3-30) gene,
DEFINITION partial cds.
ACCESSION U80105
NID 91791052
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin Exp Immunol 107 (2), 372-380 (1997)
MEDLINE 97182739
REFERENCE
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE Direct Submission
JOURNAL Submitted (26-Nov-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
FEATURES
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/tissue_type="peripheral blood"
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LEWAVISYDGSNKYYADSVKGRFTISPDNSKNTLYQMNSLRAEDTAVYYCAPDPNK
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BASE COUNT 89 a 97 c 113 g 76 t
ORIGIN

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Best Local Similarity 82.5%; Pred. No. 4.47e-190;
Matches 297; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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QY 4 GAGTCGGGGGAGGGCGGGTGGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 63
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QY 184 GCGGATTTCATCGTCCAGAGACAAATCCAGGACACGCGTGTTCGACATGAGCAGC 243
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QY 304 ATTAAGGGCGGTACTACCTTGAAATTTGGGCGCAGGGAACCTTGCTCAGCTCTCTCA 363
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RESULT 13 HSU80102 375 bp DNA PRI 19-FEB-1997
LOCUS Human immunoglobulin heavy chain variable region (V3-30) gene,
DEFINITION partial cds
ACCESSION U80102
NID 91791046
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin Exp Immunol 107 (2), 372-380 (1997)
MEDLINE 97182739
REFERENCE
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-Nov-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
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BASE COUNT 83 a 92 c 117 g 83 t
ORIGIN

Query Match 64.5%; Score 234; DB 95; Length 375;
Best Local Similarity 82.5%; Pred. No. 4.47e-190;
Matches 297; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Db 16 gactctggggagggcgtgctcagactggagagtcctcctgagactctcctgtgacgctct 75
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QY 4 GAGTCGGGGGAGGGCGGGTGGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 63
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 Db 316 qttcagcttctactacatgagctctgaggaagaaagagacacagctgacagctctctct 375
 QY 304 ATTAAGGGGGGTATACCTTAAATTTGGGGGAGGAAAGGCTGCTACCGCTCTCTCTCA 363

RESULT 14 HUMIGHYABK 341 bp DNA PRI 03-JAN-1995
 LOCUS Human Ig germline H-chain gene V-region, Clones b9-12,33,35.
 DEFINITION M77333
 ACCESSION g185761
 NID
 KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain
 SOURCE Homo sapiens (individual isolate Baji) adult DNA.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 341)
 AUTHORS Wu, J., Kozin, F., Carson, D. A. and Chen, P. P.
 TITLE Molecular basis of an autoantibody-associated restriction fragment length polymorphism that confers susceptibility to autoimmune diseases
 JOURNAL J. Clin. Invest. 88 (1), 193-203 (1991)
 MEDLINE 91277280
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 QY 4 GAGTCGGGGGAGGGGTGGTCCAGCTTGGAGGTCCTGAGACTCTCTCTGTCAGCTCT 63

Db 116 gattacccttcagtagctatgcatgacatgggtccgcagcgtccacagcaagggttg 175
 QY 64 GGATTCACCTTCACAGACGTATGGCAIGCATGGCTGGCTCCAGGCTCCAGGCAAGGGGCTG 123
 Db 176 gactgggtggcagttatctatcatatgatggaagtaataataactatgcagactccgtgaaag 235
 QY 124 GAGTGGGTGGCAGGTATTTCTGTTGATGGAAGTAACCAATATTACGCGAGACTCCGTGAAG 183
 Db 236 ggcattaccatctccagagacaattccaaagacacagctgtatctgcaaatgaaacac 295
 QY 184 GGCCATTTCATCGTCTCCAGAGCAATTCAGGACACAGGCTGTTCTTCGACATGACAGC 243
 Db 256 ctgagagctgagacacagctgtgtattactgtgcagagatattccacaggggggttatg 336
 QY 244 CTGAGACTCGAGGACAGCGCTGTCTATTACTGTCCGACAGC 284

RESULT 15 HUMIGHYABN 341 bp DNA PRI 03-JAN-1995
 LOCUS Human Ig germline H-chain gene V-region, Clone b13,15.
 DEFINITION M77336
 ACCESSION g185767
 NID
 KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain.
 SOURCE Homo sapiens (individual isolate Baji) adult DNA.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 341)
 AUTHORS Wu, J., Kozin, F., Carson, D. A. and Chen, P. P.
 TITLE Molecular basis of an autoantibody-associated restriction fragment length polymorphism that confers susceptibility to autoimmune diseases
 JOURNAL J. Clin. Invest. 88 (1), 193-203 (1991)
 MEDLINE 91277280
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 Db 56 gactctgggagggcgtggtccagctggaaggtccctgagactctctgtgacagctct 115
 QY 4 GAGTCGGGGGAGGGGTGGTCCAGCTTGGAGGTCCTGAGACTCTCTCTGTCAGCTCT 63

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Db 116 ggattcaaccttcagtagctatggaatgcactgggtccgccaggctccaggccaaggggctg 175
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Db 176 gagggtggcaggttatcatatgatggaagtaataataactacgcagactccgtggaag 235
QY 124 GAGTGGGTGGCAGGTATTTCGTTTGATGGAAGTAACCNATATTACGCAGACTCCGTGAAG 183
Db 236 ggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagc 295
QY 184 GGCCGATTTCATCGTCTCCAGACACAATTCCAGGGACACGGTGTCTTCTGCAGATGAGCAGC 243
Db 296 ctgagagctgagacacgctgtgtattactgtacgagaga 336
QY 244 CTGAGACTCGAGGACACGGCTGTCTATTACTGTGCGACAGA 284

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Search completed: Tue Feb 24 11:31:27 1998
Job time : 1343 secs.

WASHU

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit
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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 11:00:51 1998; Maspar time 117.90 Seconds
Tabular output not generated. 795.384 Million cell updates/sec

Title: >US-08-844-215-24
Description: (1-372) from US0844215 seq
Perfect Score: 372
N.A. Sequence: 1 CTCACGACGCTGCGGGTGA
Comp: GAGCTCGTACGCTGGACCT

Scoring table: TABLE default
Gap 5

Nmatch STD : Dbase 0; Query 0

Searched: 332433 seqs, 12614548 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
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Statistics: Mean 9.902; Variance 1.949; scale 5.081

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES			
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6	30	8.1	597.24	AA472093	vh10a05.r1 Soares mod	1.15e-16
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8	27	7.3	511.17	AA464794	zx83h07.r1 Soares ova	3.29e-12
9	23	6.2	471.7	C23101	human STS WI-14557	8.97e-07
10	22	5.9	156.1	DM36D7S	D. melanogaster STS d	1.57e-05
11	22	5.9	435.80	HSAA4475	nh76c05.s1 NCI_CGAP_B	1.67e-05
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13	21	5.6	259.66	HS1281117	ab31f07.r1 StrataGene	2.80e-04
14	21	5.6	259.33	AA488043	ab31f07.r1 StrataGene	2.80e-04
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ALIGNMENTS

RESULT 1
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AC AA02547;
NI 92056386
DT 01-MAY-1997 (Pel. 51, Created)
DT 22-MAY-1997 (Pel. 51, Last updated, Version 2)
DE zu47h07.r1 Soares ovary tumor NHEKt Homo sapiens cDNA clone 741181
DE 5. similar to gb:U817789 IG GAMMA-1 CHAIN C REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; mitochondria; euKaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-256
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisler C., Jost S.,
RA Kuraba T., Lacy M., Le N., Lennon G., Martin J.,
PA Moore R., Scheinberg P., Strefee M., Tan F., Theising B.,
RA White Y., Wylie T., Waterston P., Wilson P.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63104 Tel.: 314 296 1900 Fax: 314 296 1810 Email:
CC estw@wustl.edu This clone is available royalty-free through
CC LNL, contact the IMASE Consortium (info@imase.net) for
CC further information. Seq primer: 28m13 rev2 ET from AmerSham.

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FH Key Location/Qualifiers
FH source
FT 1..266
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FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified
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FT strand cDNA was primed with a Not I - oligo(dT) primer [5',
FT TGTTACCAATCGAAGTGGAGGCGGGGTTTTTTTTTTTTTTT 3'],
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Bonaldo."
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FT /sex="female"
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FT /lab_host="DH10B (ampicillin resistant)"
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FT mRNA
SQ Sequence 266 BP; 54 A; 90 C; 70 G; 52 T; 0 other;

Query Match 22.3%; Score 83; DB 54; Length 266;
Best Local Similarity 83.2%; Pred. No. 7 20p-112;
Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 17 caaggtacacagagtgctccaggcagagtcacccctgaccaggacagctccacagca 76
QY 164 CAAACTCCGCACAGAGTTCAGGGGACAGTCTCGATTACCGCGGAGCAATCCGCGAGCA 223
Db 77 cactctacatggctgagcagctgagatctgagacacgcccctgtattactgtgcga 136
QY 224 CAGCCTACATGAGCTGAGTACCTGAGCTGAGTACCGGAGACAGGCCATCTATTACTGTGCGA 283
Db 137 gagac 141
QY 284 AAGAC 288

RESULT 2
LOCUS AA505044 238 bp mRNA EST 02-JUL-1997
DEFINITION aa63g01.r1 NCI-CGAP_GCB1 Homo sapiens cDNA clone 825648 5' similar
to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
ACCESSION AA505044
NID 92241204
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalia, Eutheria, Primates; Catarrhini; Homiidae,
Homo.
1. (bases 1 to 238)
NCI-CGAP
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel. (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.

FEATURES
source
Location/Qualifiers
1..238
/organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CREP). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCGAAGTGGAGGCGGGCTCTCAITTTTTTTTTTTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/clone="825648"
/clone_lib="NCI-CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
<1..>238
mRNA
BASE COUNT 57 a 66 g 46 t
ORIGIN
Query Match 10.2%; Score 38; DB 35; Length 238;
Best Local Similarity 65.8%; Pred. No. 3.16e-29;
Matches 79; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 8 gaggttaaaagaccggggagtgctctgagatctctctgagactcttgatacagcttt 67
QY 19 GAGGTGAAGAGGCTGGTCTCTCAGTGAAGTCTCTCTGCAAGGCTTCIGAGAGCACTTTC 78
Db 68 accagcgactggatccactgggtgctgcccagatgcccggaagaacatcagtgatagag 127
QY 79 AAGCGGCAATGTTATCAGCTGGGTGGACAGGCGGCTTGGACAGGGGCTTATGATGATGGG 138

RESULT 3
ID HS1300461 standard; RNA; EST; 238 BP.
AC AA505044;
NI 92241204
DT 04-JUL-1997 (Rel. 52, Created)
DE aa63g01.r1 NCI-CGAP_GCB1 Homo sapiens cDNA clone 825648 5' similar
to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;
KW EST.
OS Homo sapiens (human)
OC Eukaryote; mitochondrial eukaryotes, Metazoa, Chordata;
OC Vertebrata, Mammalia, Eutheria; Primates; Catarrhini; Homiidae;
OC Homo.
RN [1]
RP 1-238
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
RT Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel. (301) 496-1550 Email:
CC Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,
CC M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library
CC Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA
CC Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone distribution:
CC NCI-CGAP clone distribution information can be found through the
CC I.M.A.G.E. Consortium/ILNL at:
CC www-bio.llnl.gov/bbrp/image/image.html Trace considered overall
CC poor quality Possible reversed clone: similarity on wrong strand
CC Seq primer: -28m13 rev1 ET from Amersham High quality sequence
CC stop: 1.
FH Key Location/Qualifiers
FH source
FT 1..238
FT /organism="Homo sapiens"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified

```



```

mrna      /lab_host="DH10B"
BASE COUNT 94 a 128 c 112 g 101 t
ORIGIN

Query Match      5.6%  Score 22. DB 40. Length 435.
Best Local Similarity 70.0%  Pred. No. 1.67e-05.
Matches 38; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 209 ccactctgaacccctccctgagctggagcgggaaccccaactcatgcctgcgtgt 262
      ||||| || || || || || || || || || || || || || || || || || ||
Cc 132 CCACCTCAAGCCCTTTCAGAGGCGCTCTGTCACCCAGTGTATACATGCGCGCT 79

RESULT 13
ID HS1281117 standard: RNA: EST: 259 BP.
AC AA488043;
NI 92215474
DT 27-JUN-1997 (Rel. 52, Created)
DE ab12f07.r1 StrataGene lung (#937210) Homo sapiens cDNA clone 840613
DE 5' similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);..
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
OC Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Homnidae;
OC Homo.
RN [1]
RP 1-259
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
RA Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
RA Theising B., White Y., Wylie T., Waterston R., Wilson R.;
RA "WashU-NCI human EST Project";
RA Unpublished.
RL
CC Contact: Wilson RK Washington University School of Medicine 4444
CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
CC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is
CC available royalty-free through LNL: contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. Seq primer: -28m13
CC rev1 ET from Amersham.
FH Key Location/Qualifiers
FH source
FH 1..259
FH /organism="Homo sapiens"
FH /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
FH ;
FT FT
FT Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT
FT normal lung Average insert size: 1.0 kb; Uni-ZAP XP
FT Vector: -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'
FT adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
FT /clone="840613"
FT /clone.lib="StrataGene lung (#937210)"
FT /sex="male"
FT /dev_stage="72 years"
FT /lab_host="SOLP cells (kanamycin resistant)"
FT <1 >259
FT mrna
FT Sequence 259 BP; 51 A; 99 C; 71 G; 38 T; 0 other;

Query Match      5.6%  Score 21. DB 30. Length 259;
Best Local Similarity 92.0%  Pred. No. 2.80e-04;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 gggaacgctgctcaccgtctctca 25
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cc 348 GGGACACCTGTGTCACCGTCTCTCA 372

RESULT 15
ID HS1214338 standard: RNA: EST: 551 BP.
AC AA418907;
NI 92080726
DT 14-MAY-1997 (Rel. 51, Created)
DT 24-MAY-1997 (Rel. 52, Last updated, Version 2)
DE zw19g09.s1 Soares NHMPV S1 Homo sapiens cDNA clone 768064 3'
DE similar to gb:K03191 CYTOCHROME P450 1A1 (HUMAN);..
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
OC Vertebrata, Eutheria, Primates, Catarrhini, Homnidae; Homo.
RN [1]
RP 1-551
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Wylie T., Waterston R., Wilson R.;
RA "WashU-Merck EST Project 1997";
RA Unpublished.
RL
CC Contact: Wilson RK WashU-Merck EST Project, Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1910 Email:

```

US-08-844-215-24.rstc

Thu Feb 26 07:05:28 1998

est@watson.wustl.edu This clone is available royalty-free through
CC LNL : contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -41m3 fwd. ET from Amersham High
CC quality sequence stop: 261.

CC Key Location/Qualifiers

FH source 1.551
FH /organism="Homo sapiens"
FH /note="Organ: mixed (see below); Vector: pT7T3D-Pac
FH (Pharmacia) with a modified polylinker; Site.1: Not I;
FH Site.2: Eco RI; Equal amounts of plasmid DNA from three
FH normalized libraries (melanocyte 2NBHM, pregnant uterus
FH NBHPU, and fetal heart NBH19W) were mixed, and ss circles
FH were made in vitro. Following HAP purification, this DNA
FH was used as tracer in a subtractive hybridization reaction

FT The driver was PCR-amplified cDNAs from pools of 5,000
FT clones made from the same 3 libraries. The pools consisted
FT of I.M.A.G.E. clones 260232-265223, 340488-345479, and
FT 484488-489479.

FT /clone="768064"
FT /clone_lib="Soares NBHMPu S1"
FT /tissue_type="Pooled human melanocyte, fetal heart, and
FT pregnant uterus"
FT /lab_host="DH10B"
FT complement(<1..>551)

FT mRNA Sequence 551 BP; 147 A; 127 C; 123 G; 154 T; 0 other;

SQ Query Match 5.6%; Score 21; DB 56; Length 551;

Best Local Similarity 80.0%; Pred. No. 2 80e-04;

Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 230 cccccccctcactccagccctagtcctggtgcctg 264
||||| ||||| ||||| ||||| |||||

Cp 140 CCCCCCATCCACTCAAGCCCTTGCCAGGGGCGCTG 106

Search completed: Tue Feb 24 11:08:37 1998
Job time : 466 secs.

WWP

(TW)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPSrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 10:35:43 1998 MasPar time 21: 02 Seconds
Tabular output not generated. 870 550 Million cell updates/sec

Title: >US-08-844-215-24
Description: (1-372) from US0844215.seq
Perfect Score: 372 1 CTCACGACGCTGCGCTGCA
N A Sequence: GAAGCTGTGAGACCTGGAGACT
Comp: GCGACGACGCTGCGCTGCA 372

Scoring table:
Gap 6
TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 665703 seqs, 245912890 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-A

1: EST1 2 EST2 3 EST3 4 EST4 5 EST5 6 EST6 7 EST7 8 EST8
9: EST9 10: EST10 11: EST11 12: EST12 13: EST13 14: EST14
15: EST15 16: EST16 17: EST17 18: EST18 19: EST19 20: EST20
21: EST21 22: EST22 23: EST23 24: EST24 25: EST25 26: EST26
27: EST27 28: EST28 29: EST29 30: EST30 31: EST31 32: EST32
33: EST33 34: EST34 35: EST35 36: EST36 37: EST37 38: EST38
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Database: EST-B

1: EST1 2: EST2 3: EST3 4: EST4 5: EST5 6: EST6 7: EST7 8: EST8
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57: EST57 58: EST58 59: EST59 60: EST60 61: EST61 62: EST62
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174: EST174 175: EST175 176: EST176 177: EST177 178: EST178

Statistics: Mean 9.947; Variance 1.937; scale 5.135

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
C 1	121	32.5	209 59	T28938	EST1186 Homo sapiens	3.96e-189
2	109	29.3	287 59	T27609	EST10134 Homo sapiens	1.23e-164
3	104	28.0	238 58	T29670	EST18669 Homo sapiens	1.66e-154
4	84	22.6	385 51	P86288	Y12509 r1 Homo sapie	1.54e-114
5	61	16.4	330 123	SSG1D10	S. scrofa mRNA: exons	3.47e-70
6	58	15.6	419 90	H73816	YSL1B01 r1 Homo sapie	1.37e-64
7	57	15.3	97 69	H47711	YP20E11 r1 Homo sapie	9.80e-63
8	57	15.3	823 196	AA170256	msa7q10 r1 Soares mou	9.80e-63
9	49	13.2	430 35	P72787	Y101B09 r1 Homo sapie	3.61e-48
10	47	12.6	267 58	T27868	EST18962 Homo sapiens	1.20e-44
11	45	12.1	169 4	T64512	Y224506 r1 Homo sapie	4.31e-41
12	43	11.6	308 51	P83134	YF11A03 r1 Homo sapie	1.29e-37
13	40	10.8	422 69	H43952	Y070G05 r1 Homo sapie	1.75e-32
14	33	8.9	346 116	HSU53085	Human clone 7/24 mRNA	4.95e-21
15	31	8.3	223 89	H68593	Y069E06 r1 Homo sapie	6.40e-18
16	31	8.3	318 114	HSC2NH041	H. sapiens partial cD	6.40e-18
17	31	8.3	446 34	R71741	Y185D11 r1 Homo sapie	6.40e-18
18	30	8.1	331 58	T27715	EST11381 Homo sapiens	2.14e-16
19	23	7.8	362 23	H22104	Y134704 r1 Homo sapie	6.75e-15
20	29	7.8	408 59	H42180	Y063A08 r1 Homo sapie	6.75e-15
21	29	7.8	485 29	P54774	Y175F04 r1 Homo sapie	6.75e-15
22	28	7.5	299 58	T27727	EST11874 Homo sapiens	2.01e-13
23	27	7.3	209 55	H27976	Y162B09 r1 Homo sapie	5.64e-12
24	27	7.3	329 63	H22208	Y138E08 r1 Homo sapie	5.64e-12
25	27	7.3	412 64	H27044	Y165F02 r1 Homo sapie	5.64e-12
26	26	7.0	477 116	HSU53086	Human clone 8/24 mRNA	1.48e-10
27	25	6.7	199 70	H61166	Y041C01 r1 Homo sapie	3.61e-09
28	25	6.7	309 65	H27953	Y162C09 r1 Homo sapie	3.61e-09
29	25	6.7	478 59	H43753	Y021A01 r1 Homo sapie	3.61e-09
30	24	6.5	367 3	T60021	Y01A07 r1 Homo sapie	8.14e-08
31	23	6.2	359 51	P86072	Y062E03 r1 Homo sapie	1.69e-06
32	23	6.2	431 30	P60711	Y02B10 s1 Homo sapie	1.69e-06
33	23	6.2	471 69	H45128	Y066F01 r1 Homo sapie	1.69e-06
34	22	5.9	182 19	T50230	Y044F07 r1 Homo sapie	3.20e-05
35	22	5.9	223 64	T20661	EST0440 Homo sapiens	3.20e-05
36	22	5.9	351 116	MPS538EV	M. musculus mRNA (clon	3.20e-05
37	22	5.9	285 69	H42308	Y067E04 r1 Homo sapie	3.20e-05
38	22	5.9	404 123	AA146862	Y043A10 r1 Soares mou	3.20e-05
39	22	5.9	430 33	P67273	Y01A09 s2 Homo sapie	3.20e-05
40	21	5.6	420 133	W73236	Y043D11 s1 Soares fel	5.48e-04
41	21	5.6	461 39	H12800	Y14B06 r1 Homo sapie	5.48e-04
42	21	5.6	468 74	N22795	Y041B07 s1 Homo sapie	5.48e-04
43	21	5.6	469 74	N22794	Y041B06 s1 Homo sapie	5.48e-04
44	21	5.6	538 45	H16098	Y123A02 r1 Homo sapie	5.48e-04
45	21	5.6	795 104	W22154	52F7 Human retinas CN	5.48e-04

ALIGNMENTS

RESULT 1
LOCUS T28938
DEFINITION EST0186 Homo sapiens cDNA for end similar to immunoglobulin mu heavy chain, VDJ regions (GB:M17951) (HT:3055).
ACCESSION T28938
NID 9611036
KEYWORDS EST,
SOURCE human, primor=113 Reverse library: Human White blood cells.
06-SEP-1995

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 209)
REFERENCE AUTHORS
Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,P.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.I., Geodhagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,P.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.P., Posen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

FEATURES
source 1..209
mRNA <1..>209
BASE COUNT 43 a 62 c 48 g 55 t 1 others
ORIGIN
Query Match 32 5%, Score 121, DP 58, Length 209,
Best Local Similarity 79.4%, Pred. No. 3, 96e-189;
Matches 162; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Db 1 cggatgttcccttgtaagtgaactctgcccctgggaactctgtataattttgtgtac 60
Cp 217 CGGATTCTCGCGGTAAATCGAGACTCGCCCTGGAACTTCTGTGCGGAGTTTGATGTGC 158
Db 61 cattgcagcgttgatccatccatccatcaagcctttgtccggggcctggcgaccc 120
Cp 157 CAACAAGAGATACCTCCGCCATCCATCAAGCCTTGTCCAGGGGCTGTGCGACCC 98
Db 121 aatgcatacatagctagtagtgatgtatccagaagccttgaggaaaccttcactgagg 180
Cp 97 AGCTGATAACATGGCCGCTGAAGTGCTCCAGAAGCCTTCAGAGACCTTCACTGAGG 38
Db 181 cccagacgtcttcacctcagccc 204
Cp 37 ACCAGGCTTCTTACCTCAGCCC 14

RESULT #2
LOCUS T27609 287 bp mRNA EST 06-SEP-1995
DEFINITION EST01034 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512) (HT:3056).
ACCESSION T27609
NID g609707
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Pancreas.
ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 287)
REFERENCE AUTHORS
Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,P.A., Cline,P.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.I., Geodhagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,P.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.P., Posen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

FEATURES
source 1..287
mRNA <1..>287
BASE COUNT 62 a 77 c 85 g 60 t 3 others
ORIGIN
Query Match 29 3%, Score 109, DP 58, Length 287,
Best Local Similarity 79.7%, Pred. No. 1, 23e-164,
Matches 145; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Db 80 ctggtgcagctcgtgggtgaggtgaagagcctggggtcagtggaaggtctctctgaag 139
Cp 1 CTCGAGCAGCTCTGGGGTCTAGGTTGAAGAGCTTGAGTCTTAAAGTTTCTTAAAG 60
Db 140 actctgggtacgcttcacggactactatataactgattgacagggcctgggacaa 194
Cp 61 GCTTCTGGAGGACCTTCACCGGCTATGTTATCACTGGTGGACACAGCTTGGACAA 120
Db 200 ggcttgaatgatggatggatgaacccctgcagctgagtcacaaacctctctacgaag 259
Cp 121 GGGCTTCACTGGATGGGGGGAGTATCTCTTTCTTGGTACATCAAACTTGGACAGAG 180
Db 260 tt 261
Cp 181 TT 182

RESULT 3
LOCUS T29670 238 bp mRNA EST 06-SEP-1995
DEFINITION EST09669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain V region (GB:X61012) (HT:3230).
ACCESSION T29670
NID g611768
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Small intestine.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Contact: Wilson RK
 WashU-Merck EST Project
 Unpublished (1995)

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

Location/Qualifiers

1..97

/organism="Homo sapiens"

/clone="189012"

BASE COUNT 25 a 23 c 21 g 18 t 10 others

ORIGIN

Query Match 15.3% Score 57: DB 69: Length 97:

Best Local Similarity 74.2% Pred. No. 9,80e-63:

Matches 72: Conservative 0: Mismatches 25: Indels 0: Gaps 0:

Db 1 agatgttcnngggcagatcctnaccaggnacacgtncacacactctacatgg 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 176 AGAATTCAGGCGAGAGTCGATACCGGAGGAAATCCGAGCAGAGCTACATGG 235

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 actaatgacatcctnagacacggccatata 97

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 236 AGCTGAGTACCTGAGATCGGAGGACGCGCATCTA 272

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8 AAL70256 823 bp mRNA EST 16-FEB-1997

LOCUS ms27410.r1 Soares mouse 3NDMS Mus musculus cDNA clone 618534.5

DEFINITION similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION (HUMAN);

gb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the

C-terminus (MOUSE);

ACCESSION AAL70255

NID q1748794

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;

Mus.

REFERENCE 1 (bases 1 to 823)

AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,

Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,

Schellenberg K., Steptoe M., Tan F., Underwood K., Moore S.,

Theising B., Wylie I., Lennon G., Soares B., Wilson R. and

Waterston R.

Waterston R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

PM1379418

Putative full length read

vector to vector length is 867

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 492.

Location/Qualifiers

1..823

/organism="Mus musculus"

/strain="C57BL/6J"

/note="Vector: pT730-Pac (Pharmacia) with a modified

FEATURES

source

polylinker, Site 1, Not I, Site 2, Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGAGGGGGCGGCGTCTTTTTTTTTTTTTTTTTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo.

/clone="618594"

/clone.lib="Soares mouse 3NDMS"

/sex="male"

/tissue_type="Spleen"

/dev_stage="4 weeks"

/lab_host="DH10B"

<1..>823

BASE COUNT 200 a 208 c 202 g 213 t

ORIGIN

Query Match 15.3% Score 57: DB 196: Length 823:

Best Local Similarity 59.9% Pred. No. 9,80e-63:

Matches 172: Conservative 0: Mismatches 115: Indels 0: Gaps 0:

Db 127 ctgtgtgactctgtgggaagggttagtgagcctggagggtccctgaaactctctgtcca 186

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1 CTCGAGCAGCTCTGGGCTGAGGTGAAGAGCTGGTCTCAGTGAAGGTCTCTGCAAG 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 187 gctctggtatcaatttcagtagtaccatgtcttggttcgccagactcccaagaag 246

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GUTTTGSAAGGACCTTCAGGCGGCAATGTTATCAGCTGGTGGGACAGGCGGCCCC 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 247 agcgtggaatgggtctgcatacattagtagtggtggtgattacattactatgcagacact 306

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 GGGCTTGAATGTAATGAGGAGGAGATATCTCTCTTTTGGTCAATCAAACTGGGACAGAAG 180

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 307 gtaagggccgattccacatctccagagacaaatgccagagacacccctctacactccaaatg 366

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 TTCCAGGGCAGAGTCTCGATTTACGCGGAGGAAATGCGSAGCAAGGCTTATGACATG 240

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 367 agcagctgaagtctgagagacacacccatgtattactatcaagaaga 413

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 AGTAGCTCAGATCGGAGGACAGCGCCATCTATTACTGTGGGAAAGA 287

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9 R72787 430 bp mRNA EST 02-JUN-1995

LOCUS VJ91h09.r1 Homo sapiens cDNA clone 156161.5 similar to gb:M62726

DEFINITION IG HEAVY CHAIN V-III REGION (HUMAN);

ACCESSION R72787

NID 9846819

KEYWORDS EST.

SOURCE human clone=156161 library=Soares breast 2NBHst vector=pT73D

(Pharmacia) with a modified polylinker host=ph10B (ampicillin

resistant) primer=M13p1 Psite=Not I Psite2=Eco RI Adult female

1st strand cDNA was primed with a Not I - oligo(dT) primer (5'

TGTTACCAATCTGAAGTGGAGGGGGCGGCGTCTTTTTTTTTTTTTTTTTTTT

3').

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pT73 vector (Pharmacia). Library went through one round

of normalization to a Cot = 230. Library constructed by Bento

Soares and M. Fatima Bonaldo.

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 430)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Pifkin, L., Pohlman, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

TITLE

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL. Contact the
IMAGE Consortium (info@image.llnl.gov) for further information
Location/Qualifiers:

BASE COUNT	31 a	49 c	52 g	36 t	1 others
ORIGIN					
Query Match	12.1%	Score 45:	DB.4:	Length 159:	
Best Local Similarity	90.3%	Pred. No. 4.31e-41:			
Matches	55: Conservative	0: Mismatches	5: Indels	1: Gaps	1:

Db	108	ctgtgtcagctctggagctgatagaggaagctggg	-ctcagttgaaggtctcctgccaq	166
QY	1	CTCGAGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGCTCAGTGAAGGTCTCCTGCAAG		60
Db	167	gc 158		
QY	61	GC 62		
RESULT 12				
LOCUS	R8139	303 bp	mRNA	EST
DEFINITION	ypilg03.r1 Homo sapiens cDNA clone 18715c 5' similar to gb:M62726			
	IG HEAVY CHAIN V-II REGION (HUMAN);.			

FEATURES					
source					
Location/Qualifiers					
1...303					
/organism="Homo sapiens"					
/clone="187156"					
BASE COUNT					
ORIGIN					
62 a 65 c 91 g 76 t 9 others					
Query Match 11.6% Score 43; DB 51; Length 303;					

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Best Local Similarity 64.48: Pred. NO. 1.29e-37: 0.50s 0:
Matches 8: Conservative 6: Mismatches 48: Indels 0: Gaps 0:

Db 120 ctggaggaggtctggggaggagctggctccagccctgggagagatcccttagactctctgtaca 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1 ctctgacacatcttgaggagcttggagagcaagaaagctctggctctgacatctctgaaag 50
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 180 gacctctgattcacctctcattggattgggcaggagcactggagctccnccnccnccaggaag 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 gcttctgagagcacccttcagctgagctgagctgagctgagctgagctgagctgagctgag 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 240 gggctgggaattgggtg 254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 gggcttgagtgatg 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
LOCUS H43952 422 bp mRNA EST 21-JUL-1995
DEFINITION YC070965.1 Homo sapiens cDNA clone 183320.5 similar to gb:S55735
            IG ALPHA-1 CHAIN C REGION (HUMAN)..

```

[illegible]

BASE COUNT
ORIGIN

```

WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES             location/Qualifiers
source               1..223
                    /organism="Homo sapiens"
                    /clone="239074"
mRNA                 <1..>223
BASE COUNT          35 a   75 c   66 g   46 t   1 others
ORIGIN

Query Match      83%; Score 31; DB 89; Length 223;
Best Local Similarity 86.0%; Pred.No. 6.40e-18;
Matches 37; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

db    62 ctgcgacccctggggccagggaaccctggctcgcgtctcctca 104
      ||||| | | | | | | | | | | | | | | | | | | | |
cdy   330 ctgccagatggcgccacgcccacatttgcttcatcttcctca 372

```

[REDACTED]

Release 2.0 John F. Collins, BioComputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.

MParch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 15:25:49 1998; Maspar time 22.94 Seconds
Tabular output not generated.

Title: >US-08-844-215-24
Description: (1-372) from US08844215.seq
Perfect Score: 372
N A Sequence: 1 CTCGAGGAGTGTGGGGGTGA CCCTGGTCACGGTCTCTCA 372
Comp: GAGCTGCTCAGACCCGACT GGGACCACTGGCAGACGAT

Scoring table: TABLE default
Gap 6

Nmatch STD: Dbase 0; Query 0
Searched: 87531 seqs, 22996021 bases x 2
Post-processing: Minimum Match 88
Listing first 45 summaries

Database: n-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PT90 9:PT91
10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 7.726; Variance 4.117; scale 1.877

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					Pred No	
Result No	Score	Query Match	Length	Description	ID	
1	290	78.0	2287	Sequence 8, Applicati	Sequence 8, Applicati	2 820-205
2	238	64.0	812	Sequence 53, Applicati	Sequence 53, Applicati	4 766-164
3	238	64.0	812	Sequence 53, Applicati	Sequence 53, Applicati	4 766-164
4	238	64.0	813	Sequence 61, Applicati	Sequence 61, Applicati	4 766-164
5	238	64.0	813	Sequence 61, Applicati	Sequence 61, Applicati	4 766-164
6	223	59.9	441	Sequence 3, Applicati	Sequence 3, Applicati	3 346-152
7	218	58.6	687	Sequence 1, Applicati	Sequence 1, Applicati	2 936-148
8	218	58.6	687	Sequence 1, Applicati	Sequence 1, Applicati	2 936-148
9	218	58.6	687	Sequence 1, Applicati	Sequence 1, Applicati	2 936-148
10	195	52.7	363	Sequence 1, Applicati	Sequence 1, Applicati	5 976-131
11	156	41.9	360	Sequence 7, Applicati	Sequence 7, Applicati	1 116-99
12	148	39.8	3282	Sequence 154, Applicat	Sequence 154, Applicat	1 816-93
13	148	39.8	3282	Sequence 154, Applicat	Sequence 154, Applicat	1 816-93
14	148	39.8	3282	Sequence 154, Applicat	Sequence 154, Applicat	1 816-93
15	148	39.8	3282	Sequence 154, Applicat	Sequence 154, Applicat	1 816-93
16	148	39.8	13254	Sequence 156, Applicat	Sequence 156, Applicat	1 816-93
17	148	39.8	13254	Sequence 156, Applicat	Sequence 156, Applicat	1 816-93
18	148	39.8	13254	Sequence 156, Applicat	Sequence 156, Applicat	1 816-93
19	148	39.8	13254	Sequence 170, Applicat	Sequence 170, Applicat	1 816-93

20 139 37.4 451 11 PCI-US93-1 Sequence 11, Applicati 1 690-86
21 129 34.7 443 6 US-08-477 Sequence 9, Applicatio 8 776-79
22 129 34.7 443 7 US-08-487 Sequence 9, Applicatio 8 776-79
23 129 34.7 443 6 US-07-634 Sequence 9, Applicatio 8 776-79
24 129 34.7 443 7 US-08-474 Sequence 9, Applicatio 8 776-79
25 124 33.3 433 5 US-07-634 Sequence 18, Applicati 6 146-75
26 124 33.3 433 7 US-08-487 Sequence 18, Applicati 6 146-75
27 124 33.3 433 6 US-08-477 Sequence 18, Applicati 6 146-75
28 124 33.3 433 7 US-08-474 Sequence 18, Applicati 6 146-75
29 119 32.0 366 7 US-08-040 Sequence 5, Applicatio 4 206-71
30 119 32.0 366 5 US-08-236 Sequence 8, Applicatio 4 206-71
31 119 32.0 366 13 PCI-US95-0 Sequence 8, Applicatio 4 206-71
32 119 32.0 366 7 US-08-040 Sequence 7, Applicatio 4 206-71
33 118 31.7 357 7 US-08-467 Sequence 1, Applicatio 2 456-70
34 118 31.7 357 7 US-08-392 Sequence 1, Applicatio 2 456-70
35 117 31.5 351 6 US-08-236 Sequence 10, Applicati 1 436-69
36 117 31.5 351 13 PCI-US95-0 Sequence 10, Applicati 1 436-69
37 117 31.5 360 12 PCI-US94-0 Sequence 1, Applicatio 1 436-69
38 117 31.5 363 7 US-08-040 Sequence 4, Applicatio 1 436-69
39 117 31.5 363 7 US-08-040 Sequence 1, Applicatio 1 436-69
40 117 31.5 366 7 US-08-040 Sequence 2, Applicatio 1 436-69
41 117 31.5 366 7 US-08-040 Sequence 6, Applicatio 1 436-69
42 117 31.5 429 13 PCI-US95-0 Sequence 6, Applicatio 1 436-69
43 117 31.5 429 6 US-08-236 Sequence 6, Applicatio 1 436-69
44 117 31.5 1572 7 US-08-353 Sequence 23, Applicati 1 436-69
45 115 30.9 363 7 US-08-040 Sequence 3, Applicatio 4 836-68

ALIGNMENTS

RESULT 1
ID PCI-US96-10043-8 STANDARD; DNA; UNC; 2287 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 8, Application PC/TUS9610043
CC GENERAL INFORMATION:
CC APPLICANT: The General Hospital Corporation
CC TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02210-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1 0, Version #1 30
CC CURRENT APPLICATION NUMBER: PCI-US96-10043
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/000,213
CC FILING DATE: 14-JUN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lech, Karen F.
CC REGISTRATION NUMBER:
CC REFERENCE/POCKET NUMBER: 00786/24001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617/542-5070
CC TELEFAX: 617/542-5005
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2287 base pairs
CC TYPE: nucleic acid

```
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 2287 BP; 483 A; 752 C; 654 G; 398 T; 0 other;
Query Match 78.0%; Score 290; DB 14; Length 2287;
Best Local Similarity 89.0%; Pred. No. 2,82e-205;
Matches 331; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Db 82 CTGGTCAGTCTGGGCTCAGGTGAAGAGCCTGGTCTCGGTGAAGTCTCTCTGCAAG 141
QY 1 CTCGACAGTCTGGGCTCAGGTGAAGAGCCTGGTCTCTCTGCAAGTCTCTCTGCAAG 60
Db 142 GCTTCTGGAGGACCTTCAGCAGCTATCTATCAGTCTGGTCTGGAGAGGCTCTGCAAA 201
QY 61 GCTTCTGGAGGACCTTCAGCAGCTATCTATCAGTCTGGTCTGGAGAGGCTCTGCAAA 120
Db 202 GGCTTTGAGTGGATGGAGGATCATCCCTATCTTTTGTACAGCAAACTAGCCACAGAAG 261
QY 121 GGCTTTGAGTGGATGGAGGATCATCTTTTGTACAGCAAACTAGCCACAGAAG 180
Db 262 TTCAGGGCAGAGTACGATTACCGCGGACGAATCCAGGACACAGGCTATCATGGAGCTG 321
QY 181 TTCAGGGCAGAGTACGATTACCGCGGACGAATCCAGGACACAGGCTATCATGGAGCTG 240
Db 322 AGCAGCTGAGATCTCAGGACAGAGCCGCTGTATTACTGTGGAGAGATTAATGGAGCGTAT 381
QY 241 AGTAGCTGAGATCTCAGGACAGAGCCGCTGTATTACTGTGGAGAGATTAATGGAGCGTAT 300
Db 382 TGTAGTGGTGGTACTCTACTCTGGGCTGGTTCGACCCCTGGGCGAGGAACTCTGGTC 441
QY 301 TGTAGTGGTGGTACTCTACTCTGGGCTGGTTCGACCCCTGGGCGAGGAACTCTGGTC 360
Db 442 ACCGCTCTCTCA 453
QY 361 ACCGCTCTCTCA 372
RESULT 2
ID US-07-834-539A-53 STANDARD: DNA; UNC; 812 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 53, Application US/07834539A.
CC Sequence 53, Application US/07834539A
CC Patent No. 5633425
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 77
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/834,539A
CC FILING DATE: 19920205
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC
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CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 53:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 812 base pairs
CC TYPE: NUCLEIC ACID
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 241..335
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
CC FEATURE:
CC NAME/KEY: Exon
CC LOCATION: 372..677
CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
CC Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
Query Match 64.0%; Score 238; DB 7; Length 812;
Best Local Similarity 91.3%; Pred. No. 4.76e-164;
Matches 263; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Db 393 CTGTGTGAGTCTGGGCTGAGGTGAAGAGCCTGGTCTCGGTGAAGTCTCTCTGCAAG 452
QY 1 CTCGACAGTCTGGGCTGAGGTGAAGAGCCTGGTCTCTCTGCAAG 60
Db 453 GCTTCTGGAGGACCTTCAGCAGCTATCTATCAGTCTGGTCTGGAGAGGCTCTGCAAA 512
QY 61 GCTTCTGGAGGACCTTCAGCAGCTATCTATCAGTCTGGTCTGGAGAGGCTCTGCAAA 120
Db 513 GGCTTTGAGTGGATGGAGGATCATCCCTATCTTTTGTACAGCAAACTAGCCACAGAAG 572
QY 121 GGCTTTGAGTGGATGGAGGATCATCTTTTGTACAGCAAACTAGCCACAGAAG 180
Db 573 TTCAGGGCAGAGTACGATTACCGCGGACGAATCCAGGACACAGGCTATCATGGAGCTG 632
QY 181 TTCAGGGCAGAGTACGATTACCGCGGACGAATCCAGGACACAGGCTATCATGGAGCTG 240
Db 633 AGCAGCTGAGATCTCAGGACAGAGCCGCTGTATTACTGTGGAGAGAG 680
QY 241 AGTAGCTGAGATCTCAGGACAGAGCCGCTGTATTACTGTGGAGAGAG 288
RESULT 3
ID PCT-US92-06185-53 STANDARD: DNA; UNC; 812 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 53, Application PC/TUS9206185.
CC Sequence 53, Application PC/TUS9206185
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 75
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/06185
CC FILING DATE: 19910828
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC
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CC REGISTRATION NUMBER: 87654
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 53
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 812 base pairs
 CC TYPE: NUCLEIC ACID
 CC STRANDEDNESS: double
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: Exon
 CC LOCATION: 241..335
 CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
 CC NAME/KEY: Exon
 CC LOCATION: 372..677
 CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 55
 CC SEQUENCE 812 BP; 204 A; 188 C; 223 G; 197 T; 0 Other;

Query Match 54.0%, Score 238, DB 10, Length 812;
 Best Local Similarity 91.3%; Pred. No. 4.76e-164;
 Matches 263; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 393 CTGGTCAGCTGGGGCTGAGTGAAGAGCTGGGTCTGCTGAGGTCTCTTGAAG 452
 QY 1 CTCGAGCAGCTGGGGCTGAGGTGAAGAGCTGGGTCTCTTGAAGGTCTCTTGAAG 60
 Db 453 GCTTCGAGGACCTTCAGCAGCTATGATCAGCTGGGTGGGACAGAGCTTGAACAA 512
 QY 61 GCTTCGAGGACCTTCAGCAGCTATGATCAGCTGGGTGGGACAGAGCTTGAACAA 120
 Db 513 GGCCTTGAGTGAAGGAGATATCCTATCCTTGTGTATAGCAAACTAGCAGAGAG 572
 QY 121 GGCCTTGAGTGAAGGAGATATCCTTGTGTATAGCAAACTAGCAGAGAGAG 180
 Db 573 TTCCAGGGCAGAGTTCAGCATACCGGGGACAAATCCAGGACAGAGCTACATGGAGCTG 632
 QY 181 TTCCAGGGCAGAGTTCAGCATACCGGGGACAAATCCAGGACAGAGCTACATGGAGCTG 240
 Db 633 ACAGCCTTGAATCTGAGGACAGAGCTTGTATCTTGTATCTTGTGAGAGAG 680
 QY 241 AGTAGCCTGAGATCGGAGGACAGAGCTTGTATCTTGTGAGAGAG 288

RESULT 4
 ID PCT-US92-10983-61 STANDARD: DNA; UNC: 813 BP.

AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 61, Application PC/TUS9210983.
 CC Sequence 61, Application PC/TUS9210983
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals for
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 152
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC City: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/10983

CC FILING DATE: 19921217
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-2
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422

CC INFORMATION FOR SEQ ID NO: 61:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 813 base pairs
 CC TYPE: NUCLEIC ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 241..285
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 373..678

Query Match 64.0%, Score 238, DB 10, Length 813;
 Best Local Similarity 91.3%; Pred. No. 4.76e-164;
 Matches 263; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 394 CTGGTCAGCTGGGGCTGAGTGAAGAGCTGGGTCTGCTGAGGTCTCTTGAAG 453
 QY 1 CTCGAGCAGCTGGGGCTGAGGTGAAGAGCTGGGTCTCTTGAAGGTCTCTTGAAG 60
 Db 454 GCTTCGAGGACCTTCAGCAGCTATGATCAGCTGGGTGGGACAGAGCTTGAACAA 513
 QY 61 GCTTCGAGGACCTTCAGCAGCTATGATCAGCTGGGTGGGACAGAGCTTGAACAA 120
 Db 514 GGCCTTGAGTGAAGGAGATATCCTATCCTTGTGTATAGCAAACTAGCAGAGAG 573
 QY 121 GGCCTTGAGTGAAGGAGATATCCTTGTGTATAGCAAACTAGCAGAGAGAG 180
 Db 574 TTCCAGGGCAGAGTTCAGCATACCGGGGACAAATCCAGGACAGAGCTACATGGAGCTG 633
 QY 181 TTCCAGGGCAGAGTTCAGCATACCGGGGACAAATCCAGGACAGAGCTACATGGAGCTG 240
 Db 634 AGCAGCCTGAGATCTGAGGACAGAGCTTGTATCTTGTGAGAGAGAG 681
 QY 241 AGTAGCCTGAGATCGGAGGACAGAGCTTGTATCTTGTGAGAGAGAG 288

RESULT 5
 ID US-08-053-131-61 STANDARD: DNA; UNC: 813 BP.

AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 61, Application US/08053131.
 CC Sequence 61, Application US/08053131
 CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: One Market Plaza, Stewart Tower, Suite 200
 CC City: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/053,131
 CC FILING DATE: 26-APP-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/990,860
 CC FILING DATE: 16-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 61:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 813 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 241 285
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 373 678
 CC SQ Sequence 813 BP: 204 A; 189 C; 223 G; 197 T; 0 other;

Query Match 64.0%; Score 238; DB 7; Length 813;
 Best Local Similarity 91.3%; Pred. No. 4.76e-164;
 Matches 263; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 394 CTGGTGCAGCTGGGGCTGAGGTGAAGAAGCTGGGTCTCTCTGAGGTGAGGTCTCTCTGCAAG 453
 QY 1 CTCGAGCAGCTGGGGCTGAGGTGAAGAAGCTGGGTCTCTCTGAGGTGAGGTCTCTCTGCAAG 60
 Db 454 GCTTCTGGAGGCACCTTCAGCAGGTATCTATCAGCTGGGTGGCGACAGGCCCTTGACAA 513
 QY 61 GCTTCTGGAGGCACCTTCAGCGGCATGTTATCAGCTGGGTGGCGACAGGCCCTTGACAA 120
 Db 514 GGGCTTGAGTGGATGGGAGGATCATCCCTATCCTTGGTATAGCAAACTACGACACAGAG 573
 QY 121 GGGCTTGAGTGGATGGGAGGAGTATCTCTTTTGGCACATCAAACTCCGACACAGAG 180
 Db 574 TTCCAGGCGAGAGTACCATTCAGCGGACAAATCCAGAGCAGCAGCTACATGGAGCTG 633
 QY 181 TTCCAGGCGAGAGTCTCATTCAGCGGAGCAATCCGCGAGCAGCAGCTACATGGAGCTG 740
 Db 634 AGCAGCCTGAGATCTGAGCAGCAGCGCGGTGTATTACTGTGTGAGAGAC 681
 QY 241 AGTACGCTGAGATCGGAGGACACAGGCCCATCTATTACTGTGCGAAAGAC 288

RESULT 6
 ID US-08-217-918-3 STANDARD; DNA: UNC: 441 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 3, Application US/08217918.
 CC Sequence 3, Application US/08217918
 CC Patent No. 5506132
 CC GENERAL INFORMATION:
 CC APPLICANT: LAKE, PHILIP
 CC APPLICANT: OSTBERG, LARS
 CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
 CC TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS

CC NUMBER OF SEQUENCES: 4
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Khourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM: disk
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/217,918
 CC FILING DATE: 24-MAR-1994
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 3:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 441 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 1..441
 CC SQ Sequence 441 BP: 89 A; 125 C; 135 G; 92 T; 0 other;

Query Match 59.9%; Score 223; DB 6; Length 441;
 Best Local Similarity 89.4%; Pred. No. 3.34e-152;
 Matches 253; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 72 GCATCTGGGGCTGAGGTGAAGGCTGGGTCCTGGGTCGAGGTCCTGCAAGGCTTC 131
 QY 6 GCATCTGGGGCTGAGGTGAAGGCTGGGTCCTGGGTCGAGGTCCTGCAAGGCTTC 65
 Db 132 TGGAGGCACCTTCAGCAACTTTGCTATCAGCTGGGTGGCGACAGGCCCTTGGACAGGCT 191
 QY 66 TGGAGGCACCTTTAGCGGCCATGTTATCAGCTGGGTGGCGACAGGCCCTTGGACAGGCT 125
 Db 192 TGAGTGATGGGCGCATCATGCTCTCTTTTATATCTATCTACGACAGGCTTCCTCA 251
 QY 126 TGAGTGATGGGCGGAGTATCTCTTTTGGCATATCAAACTCCGACAGGCTTC 185
 Db 252 GGGCAGAGCTCAGATAGGCGGAGGCTCTCTAGGACAGGCTCAGAGGCTGAGGCTGAG 311
 QY 186 GGGCAGAGCTCAGATAGGCGGAGGCTCTCTAGGACAGGCTCAGAGGCTGAGGCTGAG 245
 Db 312 CCTGAGATCTGAGCAGAGCGGCCATGTATTACTGTGCGAGAGAC 354
 QY 246 CCTGAGATCTGAGCAGAGCGGCCATGTATTACTGTGCGAGAGAC 288

RESULT 7
 ID PCT-US95-11235-1 STANDARD; DNA: UNC: 687 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1, Application PC/TUS9511235.
 CC Sequence 1, Application PC/TUS9511235
 CC GENERAL INFORMATION:
 CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOCLONAL LIGHT CHAINS


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QY   181 TTCCAGGCGCAGATCTGGTGAIIAAGCGGACAAAGTCGGAGACACAGGTATTATCATGAGACTG 246
Db    250 ATCACTGTTAGATCTGAGAACACAGCGTGSTATTATTAATCTG 289
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QY   241 AGTAGCGTGAGATCGGAGGACAGCGGCATCTATTACTGTG 280

RESULT 12
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AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 154, Application PC/TUS9508743.
CC    Sequence 154, Application PC/TUS9508743.
CC    GENERAL INFORMATION:
CC    APPLICANT:
CC    TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC    TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC    NUMBER OF SEQUENCES: 170
CC    COMPUTER PEADABLE FORM:
CC    MEDIUM TYPE: Floppy disk
CC    COMPUTER: IBM PC compatible
CC    OPERATING SYSTEM: PC-DOS/MS-DOS
CC    SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: PCT/US95/08743
CC    FILING DATE: 11-JUL-1995
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: US 08/276,852
CC    FILING DATE: 18-JUL-1994
CC    INFORMATION FOR SEQ ID NO: 154:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 3282 base pairs
CC    TYPE: nucleic acid
CC    STRANDEDNESS: double
CC    TOPOLOGY: linear
CC    MOLECULE TYPE: DNA (genomic)
CC    FEATURE:
CC    NAME/KEY: CDS
CC    LOCATION: 15..452
CC    Sequence 3282 BP; 710 A; 1109 G; 864 C; 599 T; 0 other:

Query Match          39.8%; Score 148; DB 13; Length 3282;
Rest Local Similarity 76.4%; Pred No. 1,81e+93;
Matches 214; Conservative 0; Mismatches 66; Indels 0; Gaps

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QY    7 CASTCTGGGGGTGAGSSTGAAGAASCTGGGGGTTCAGTGAAGSSTTCTCTGACGGCTCT 66

Db    147 GGATACAGATTCAGTAACCTTTCTTATTTCATTCGTTGGGTCGCCAGCGCGCACAGAGTTT 206
QY    67 GGAGGTATCTTCAGTGGGGTCAATCTTACAGCGGAACAAGATTTTTAGGTCAAATTCGAG 126

Db    207 GAGTGGATGGATGATCAATCTCTTACAGCGGAACAAGATTTTTAGGTCAAATTCGAG 266
QY    127 GAGTGGATGGGAGGAGTATCTCTTTCTTTTGGCATCATCAACTTCGCGACAGAGTTCGAG 186

Db    267 GACAGAGTCAGCTTTTACCGGGGACATATCGGCACATCAAGCTATAATGATTGASAGAT 326
QY    187 GGTCAAGTCTTGATTATGAGAGGAATAATTCGGGAGTCAAGGTCAATGAGATGACAGATG 246

Db    327 CTCAGSSTCTGTAGACACAGGGTGTGTTAATATGTGGGAGAG 366
QY    247 CTGAGATGGGAGGAATGGGATCTATTACTTGGGSAANG 286

RESULT 13
ID    US-08-276-852-154 STANDARD; DNA: UNC; 3282 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 154, Application US/08276852.
CC    Sequence 154, Application US/08276852.
CC    Patent No. 5652138
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ZIP: 92037
COMPUTER READABLE FORM:

Sequence 3282 BP; 599 A; 864 C; 1109 G; 710 T; 0 other;

Best Local Similarity 75.4%; pred. NO. 1.81e-93;
Matches 214; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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CP 286 CTTCCGACACATTAATATGAGGAGGCTGCTCCGATATTCAGAGTACTTAGTCTCAGTCAAGG 227

3977 CTCTCTTCCCCCAATCTCTCTCCCTAAGCGTCACGCTCCCAAAATT 3036

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Cp 226 CTGTGCTGGCGGATTCGTCCGCGGTAATCGASACATCTGGGCGGAACTTCTGTGCGGAGT 167

Db 3037 CTTTGTTCCGTTGTAGGATTGATCCATCCCAATCCACCTCAAACTCTGTCCGGGGGGCT 3096

CP 166 TTGATGTGCCAAGAAAGACATACTGCGCGCCATCCACTCAAGCCCTTGTCCAGGGGCT 107

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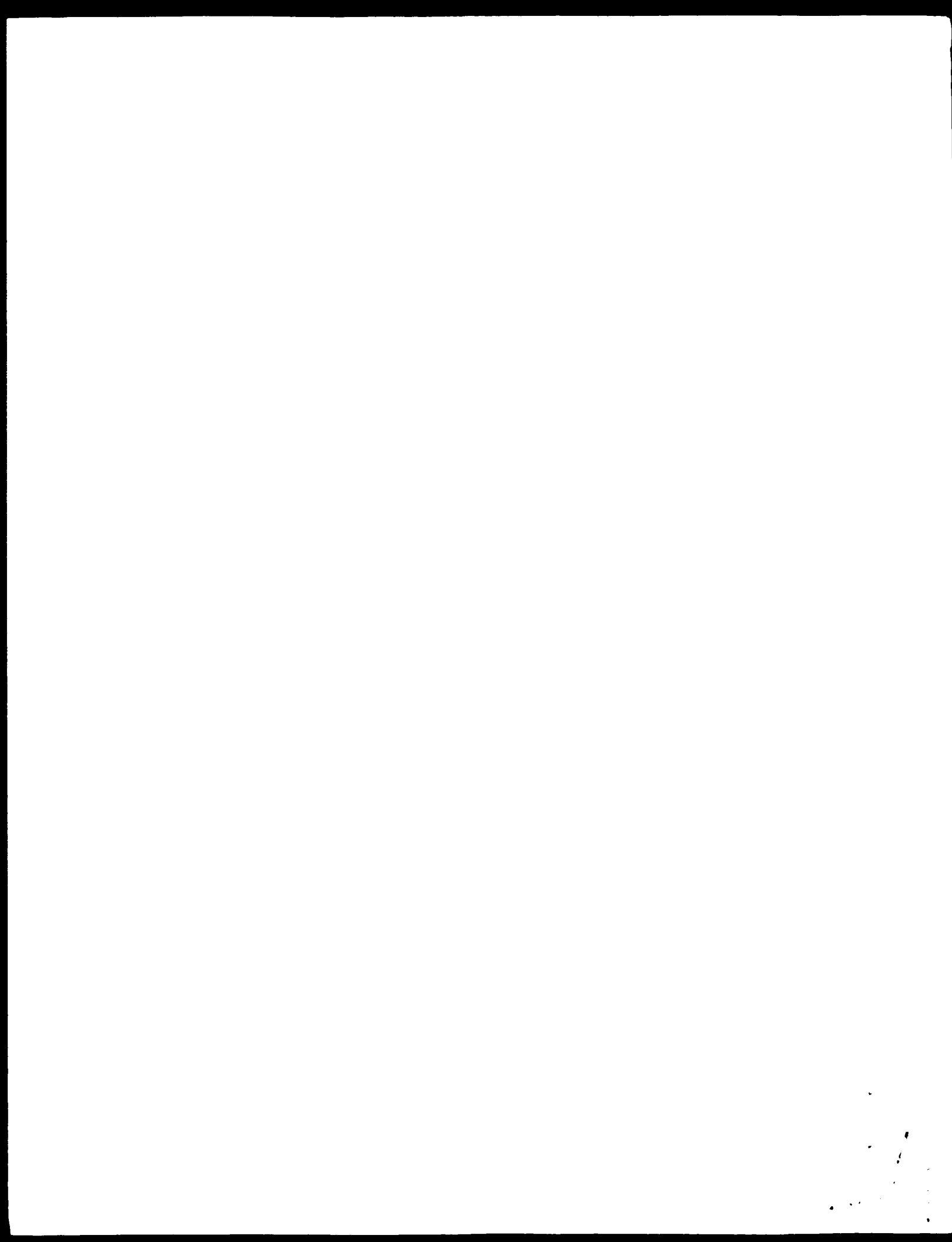
Ccp 106 GTGGACCCAGCTGATAACATGSGGGCTGAAGGGTGGTTCAGAAAGCCTTGCAGGAGACCT 47

db 3157 TCACTGAGGCCCCAGGCGTTCCTCACCTCAGCCCCGGA CTG 3196

45 TCACTGAGGACCCAGGGCTTCTTCACCTCAGCCCCAGACTG 7

Search completed: Tue Feb 24 15:26:44 1998

Job time : 55 secs.



WARNING

(TM)

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MPsrch_nh n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 10:09:25 1998: Maspar time 458.90 seconds
Tabular output not generated. 1151.231 Million cell updates/sec

Title: >US-08-844-215-24
Description: (-372) from US08844215.seq
Perfect Score: 372
N.A. Sequence: 1 CTCGAGGAGTCTGGCTGCA
Comp: GAGCTCTGACACCTCCACT

Scoring table: TABLE default
Gap 6
Nmatch STD: Phase 0: Query 0
Searched: 430261 seqs, 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1:ACT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HUM1
9:HUM2 10:HUM3 11:INV1 12:INV2 13:OP3 14:MAM 15:VET
16:PLN 17:PO1 18:PO2 19:PO3 20:SYN 21:UNC 22:VIP
genbankal01

Database: genbankal01
23:BO1 24:BO2 25:BO3 26:BO4 27:BO5 28:BO6 29:BO7
30:BO8 31:BO9 32:BO10 33:BO11 34:BO12 35:BO13
36:GEN1 37:GEN2 38:GEN3 39:GEN4 40:GEN5 41:GEN6 42:HTG1
43:HTG2 44:HTG3 45:HTG4 46:HTG5 47:INV1 48:INV2 49:INV3
50:INV4 51:INV5 52:INV6 53:INV7 54:INV8 55:INV9 56:INV10
57:INV11 58:INV12 59:MAM1 60:MAM2 61:MAM3 62:VET1
63:VET2 64:VET3 65:VET4 66:VET5 67:VET6 68:VET7 69:VET8
70:VET9 71:VET10 72:VET11 73:VET12 74:VET13 75:VET14 76:VET15
77:VET16 78:VET17 79:VET18 80:VET19 81:VET20 82:VET21 83:VET22
84:VET23 85:VET24 86:VET25 87:VET26 88:VET27 89:VET28
90:VET29 91:VET30 92:VET31 93:VET32 94:VET33 95:VET34
96:VET35 97:VET36 98:VET37 99:VET38 100:VET39 101:VET40
102:VET41 103:VET42 104:VET43 105:VET44 106:VET45 107:VET46
108:VET47 109:VET48 110:VET49 111:VET50 112:VET51 113:VET52
114:UNA
genbankb101

Database: genbankb101
115:VPL1 116:VPL2 117:VPL3 118:VPL4 119:VPL5 120:VPL6
121:VPL7 122:VPL8 123:VPL9 124:VPL10 125:VPL11
genbankc007
126:PO1 127:PO2 128:PO3 129:PO4 130:PO5 131:PO6 132:PO7
133:PO8 134:PO9 135:PO10 136:PO11 137:PO12
138:PO13 139:PO14 140:PO15 141:PO16 142:PO17 143:PO18
u-emb151_101
142:part1 143:part2

Statistics: Mean 10.010: Variance 4.434: scale 2.260
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
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2	254	68.3	534	99	HUMIGHDKN	Human Ig rearranged H	6.85e-207
3	253	68.0	507	87	HS201E5	H.sapiens mRNA for im	6.02e-204
4	253	68.0	507	87	HS201E2	H.sapiens mRNA for im	6.02e-204
5	253	68.0	507	87	HS201E4	H.sapiens mRNA for im	6.02e-204
6	253	68.0	507	87	HS201E6	H.sapiens mRNA for im	6.02e-204
7	252	67.7	534	99	HUMIGHDYN	Human Ig rearranged H	5.29e-203
8	251	67.5	522	87	HS201E8	H.sapiens mRNA for im	4.45e-203
9	249	66.9	480	87	HS201E3	H.sapiens mRNA for im	4.59e-203
10	249	66.9	483	87	HS201E5	H.sapiens mRNA for im	3.59e-200
11	249	66.9	510	87	HS201E9	H.sapiens mRNA for im	3.59e-200
12	249	66.9	510	87	HS201E6	H.sapiens mRNA for im	3.59e-200
13	249	66.9	510	87	HS201E7	H.sapiens mRNA for im	3.59e-200
14	249	66.9	510	87	HS201E2	H.sapiens mRNA for im	3.59e-200
15	249	66.9	522	87	HS201E3	H.sapiens mRNA for im	3.59e-200
16	249	66.9	525	87	HS201E1	H.sapiens mRNA for im	3.59e-200
17	249	66.9	525	87	HS201E4	H.sapiens mRNA for im	3.59e-200
18	248	66.7	360	96	HSVHGL18	H.sapiens germline f	3.15e-199
19	247	66.4	510	87	HS201E1	H.sapiens mRNA for im	2.77e-198
20	247	66.4	525	87	HS201E2	H.sapiens mRNA for im	2.77e-198
21	247	66.4	525	87	HS201E3	H.sapiens mRNA for im	2.77e-198
22	246	66.1	421	99	HUMIGHVAN	Human (fetal) Ig for	2.43e-197
23	246	66.1	872	99	HUMIGHREVA	Homo sapiens (1951) g	2.43e-197
24	245	65.9	357	102	UC0502	Human immunoglobulin	2.13e-196
25	245	65.9	392	91	HSIGVH11M	H.sapiens germline im	2.13e-196
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28	245	65.9	392	91	HSFVH1G	H.sapiens gene for im	2.13e-196
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30	245	65.9	392	91	HSIGVH1M	H.sapiens germline im	2.13e-196
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32	245	65.9	392	91	HSFVH1A	H.sapiens gene for im	2.13e-196
33	245	65.9	392	91	HSIGVH2M	H.sapiens germline im	2.13e-196
34	245	65.9	483	87	HS203M7	H.sapiens mRNA for im	2.13e-196
35	245	65.9	513	99	HUMIGHDKN	Human Ig rearranged H	2.13e-196
36	245	65.9	525	99	HUMIGHDKN	Human Ig rearranged H	2.13e-196
37	245	65.9	527	95	HSVH9582	Human clone HA immun	2.13e-196
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39	244	65.6	448	99	HSIGM201	Human mRNA for IgM M2	2.13e-196
40	244	65.6	474	87	HS201M2	Human Ig rearranged H	1.87e-195
41	244	65.6	501	87	HS201E8	H.sapiens mRNA for im	1.87e-195
42	244	65.6	501	87	HS201E6	H.sapiens mRNA for im	1.87e-195
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44	244	65.6	510	87	HS201E7	H.sapiens mRNA for im	1.87e-195
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DEFINITION		subgroup VH-1.				
ACCESSION		M65104				
NID		G1853344				
KEYWORDS		V-region; immunoglobulin heavy chain subgroup VH-1; rearranged DNA.				
SOURCE		Homo sapiens				
ORGANISM		Homo sapiens				
REFERENCE		1 (bases 1 to 528)				
AUTHORS		Kipps, T.J. and Duffy, S.F.				
TITLE		Relationship of the cDNAs B cell to human tonsillar lymphocytes that				
JOURNAL		express autoantibody-associated cross-reactive idiotypes				
MECLINE		J Clin Invest. 87 (5): 2087-2096 (1991)				
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DEFINITION	Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L7 subgroup VH-I.
ACCESSION	M65090


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NID      9619468
KEYWORDS immunoglobulin: variable region.
SOURCE   human.
ORGANISM Homo sapiens
REFERENCE Lebecque, S.
AUTHORS   Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
          Bancheureau, J. and Lebecque, S.
TITLE     Anti-CD40 plus interleukin-4-activated human naive B cell lines
          express unmutated immunoglobulin genes with intracolon heavy chain
          isotype variability
JOURNAL   Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE   95220422
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QY 361 ACCGTCCTCTCA 372

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DEFINITION H.sapiens mRNA for immunoglobulin variable region (clone 202-G9).
ACCESSION Z47261
NID 9619472
KEYWORDS immunoglobulin: variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Lebecque, S.
AUTHORS   Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
          Bancheureau, J. and Lebecque, S.
TITLE     Anti-CD40 plus interleukin-4-activated human naive B cell lines
          express unmutated immunoglobulin genes with intracolon heavy chain
          isotype variability
JOURNAL   Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE   95220422
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Best Local Similarity 86.0%; Pred. No. 6,02e-204;
Matches 320; Conservative 0; Mismatches 49; Indels 3; Gaps 2;

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Db 127 gctctgaggcacccttcagcagctatcctatcagctgggtggcagcagccctgggaca 186
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QY 361 ACCGTCCTCTCA 372

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ACCESSION M65094
NID g185324
KEYWORDS V-region; immunoglobulin heavy chain subgroup VH-1; rearranged DNA.
SOURCE Homo sapiens tonsil DNA.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa, Chordata;
          Vertebrata; Eutheria; Primates, Catarrhini, Hominoidea, Homo.
          1 (bases 1 to 534)
AUTHORS Kippes, R.J. and Duffy, S.F.
TITLE Relationship of the CD5 B cell to human tonsillar lymphocytes that
          express autoantibody-associated cross-reactive idiotypes
JOURNAL J. Clin. Invest. 87 (6), 2087-2096 (1991)
MEDLINE 91250563
FEATURES Location/Qualifiers

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QY 61 GCTTCTGGAGGCACCTTCAGCGGCCATGTTATCAGCTGGTGGCCACAGGCCCTTGGCAA 120
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QY 301 TGTAGTGTGTAACTGCTACTCCGGGGTTCCTCCAGAGATTCAGAGAGATTCAGAGAG 360
Db 523 accgtctctca 534
QY 361 ACCGTCCTCTCA 372
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LOCUS
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 202-G8).
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
SOURCE
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ORGANISM
Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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NID        g619471
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SOURCE     human.
ORGANISM   Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 522)
AUTHORS    Lebecque,S.
TITLE      Direct Submission
JOURNAL    Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE  2 (bases 1 to 522)
AUTHORS    Galibert,L., van Dooren,J., Durand,L., Rousset,F., Jefferis,R.,
Banchereau,J. and Lebecque,S.
TITLE      Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intracлонаl heavy chain
isotype variability
JOURNAL    Eur J Immunol. 25 (3), 733-737 (1995)
MEDLINE    95220422
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LOCUS
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 202-M3).
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
SOURCE     human
ORGANISM   Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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  REFERENCE 1 (bases 1 to 510)
  AUTHORS    Lebecque,S.
  TITLE      Direct Submission
  JOURNAL    Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
    Schering-Plough, Laboratory for Immunological Research, 27, Chemin
    des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
  REFERENCE 2 (bases 1 to 510)
  AUTHORS    Galibert,L., van Dooren,J., Durand,I., Pousset,F., Jefferis,P.,
    Bancheureau,J. and Lebecque,S.
  TITLE      Anti-CD40 plus interleukin-4-activated human naive B cell lines
    express unmutated immunoglobulin genes with intracell heavy chain
    isotype variability
  JOURNAL    Eur. J. Immunol. 25 (3), 733-737 (1995)
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    Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 510)
  AUTHORS    Lebecque,S.
  TITLE      Direct Submission
  JOURNAL    Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
    Schering-Plough, Laboratory for Immunological Research, 27, Chemin
    des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
  REFERENCE 2 (bases 1 to 510)
  AUTHORS    Galibert,L., van Dooren,J., Durand,I., Pousset,F., Jefferis,P.,
    Bancheureau,J. and Lebecque,S.
  TITLE      Anti-CD40 plus interleukin-4-activated human naive B cell lines
    express unmutated immunoglobulin genes with intracell heavy chain
    isotype variability
  JOURNAL    Eur. J. Immunol. 25 (3), 733-737 (1995)
  MEDLINE    95220422
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Qy 360 CACCGTCTCTCA 372

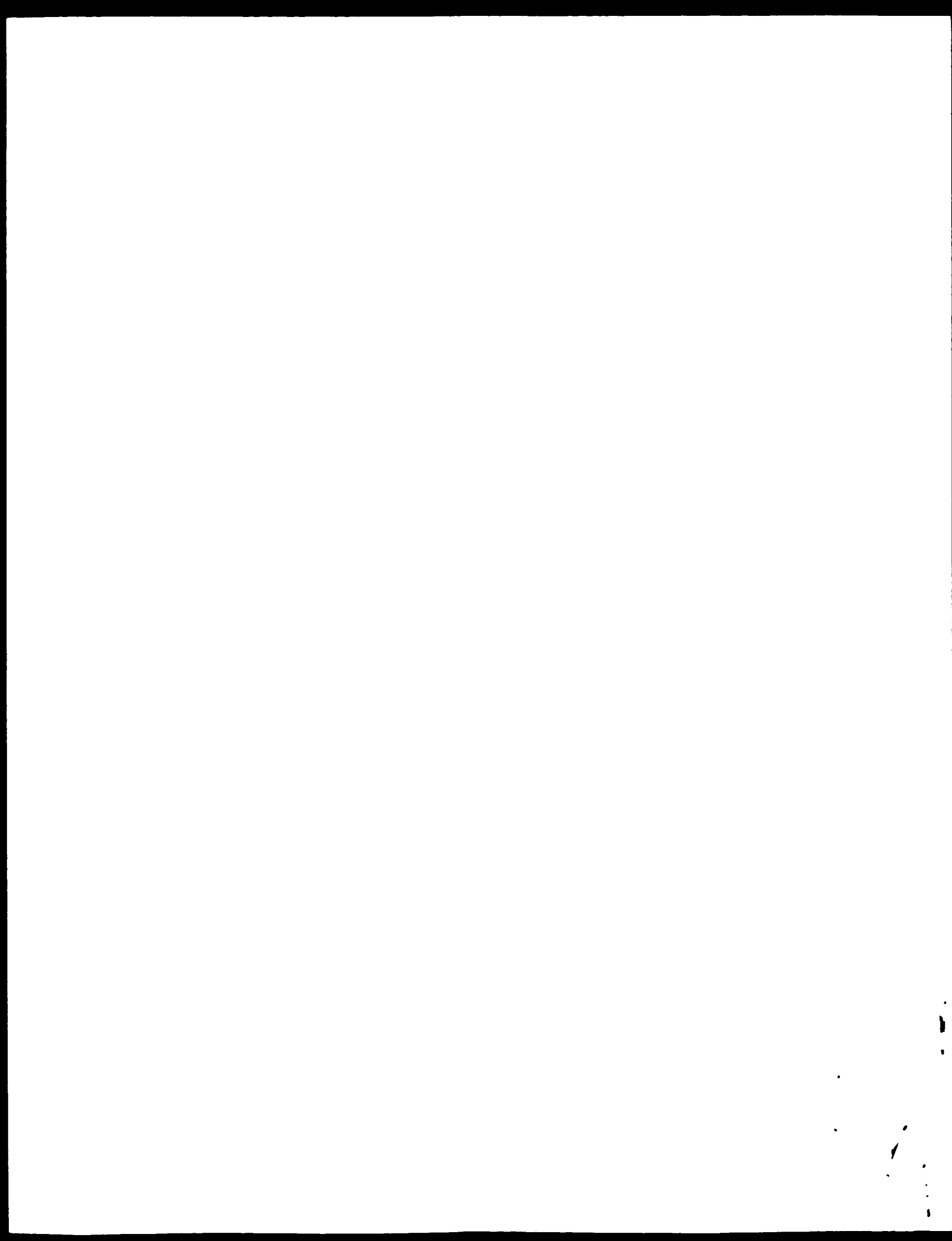
RESULT 15 HS202G3 522 bp RNA PRI 03-AUG-1995
LOCUS H sapiens mRNA for immunoglobulin variable region (clone 202-G3).
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 202-G3).
ACCESSION Z47259
NID 9619470
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 522)
AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE 2 (bases 1 to 522)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Pousset, F., Jefferis, R.,
Bancheau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
FEATURES
source Location/Qualifiers
1..522
/organism="Homo sapiens"
/clone="202-G3"
/tissue_type="blood"
/cell_type="B-lymphocyte"
BASE COUNT 99 a 142 c 177 g 104 t
ORIGIN
Query Match 56.9% Score 249; DB 87; Length 522;
Best Local Similarity 85.5% Pred No 3 59e-200;
Matches 318; Conservative 0; Mismatches 51; Indels 3; Gaps 2;

Db 67 ctggtgcactctgggctgagtgaggaagctggtggtggtctctggtgagggctctgag 126
Qy 1 CTGAGCACTCTGGGCTGAGTGAAGAAAGCTGGGTCTCAGTGAAGGTCTCTCTGCAAG 60
Db 127 gctctgagagcacccttcacacactatgctatcagctgagtgccagacagcccttgacaa 186
Qy 61 GCTTCTGGAGGCGACCTTCACGGCCATGTTATCAGCTGGGTGCGACAGGCCCTGGACAA 120
Db 187 gggcttgagtgagtgaggagatccctctattcttttggtacagcaaaactacgcacagaag 246
Qy 121 GGGCTTCAGTGGATGGGGGAGTATCTCTTCTTTGGGCAATCAAACTCGGCACAGAAG 180
Db 247 ttccagggagagtcacagattaccgcggagcaaaatccacagacagacctacatggagctg 306
Qy 181 TTCCAGGGCAGAGTCTCGATTACCGCGACCAATCCCGGAGCAGCAGAGCTACATGAGAGCTG 240
Db 307 agcagcctgagatctgagggacacgcgcgtgtattactgtgcgagagggggggttaagtc 366
Qy 241 AGTAGCCTGAGATCGGAGGACACGGCCATCTATTACTGTGCGAAGACCTTC-AAGATT 299
Db 367 gaattttgagtggttctc-atgggtactgtgtcagccctggggccagggaaacctggt 425
Qy 300 TTGTAGTGGTGGTAACCTGCTACCGGGGTCTTCCAGCAGTAGTGGGCGCAGGCCCTGGT 359
Db 426 caccgtctctca 438
Qy 360 CACCGTCTCTCA 372

RESULT 14 HS203E2 510 bp RNA PRI 03-AUG-1995
LOCUS H sapiens mRNA for immunoglobulin variable region (clone 203-E2).
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 203-E2).
ACCESSION Z47264
NID 9619475
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 510)
AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, Rhone, 69572, FRANCE
REFERENCE 2 (bases 1 to 510)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Pousset, F., Jefferis, R.,
Bancheau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
FEATURES
source Location/Qualifiers
1..510
/organism="Homo sapiens"
/clone="203-E2"
/tissue_type="blood"
/cell_type="B-lymphocyte"
BASE COUNT 105 a 142 c 155 g 104 t
ORIGIN
Query Match 66.9% Score 249; DB 87; Length 510;
Best Local Similarity 84.7% Pred No 3 59e-200;
Matches 316; Conservative 0; Mismatches 55; Indels 2; Gaps 2;

Db 67 ctggtgcactctgggctgagtgaggaagctggtctcctggttaaggtctctgcaag 126
Qy 1 CTGAGCACTCTGGGCTGAGTGAAGAAAGCTGGGTCTCAGTGAAGGTCTCTCTGCAAG 60
Db 127 gctctgagagcacccttcacacactatgctatcagctgagtgccagacagcccttgacaa 186
Qy 61 GCTTCTGGAGGCGACCTTCACGGCCATGTTATCAGCTGGGTGCGACAGGCCCTGGACAA 120

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[REDACTED]

(TM)

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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 10:33:12 1998. Maxpar time 54.71 Seconds
Tabular output not generated.
Title: >US-08-844-215-24
Description: (1-372) from US08844215.seq
Perfect Score: 372
N.A. Sequence: 1 CCGAGCAGCTGTGGGGCTGA
Comp: GAGCTGCTGACAGCCGAGCT
CCCTGGTCACCGTCTGCTCA 372
GGGACCGAGTGGCAGAGAGT

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 159651 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-geneseq30
1-part8 2-part2 3-part3 4-part4 5-part5 6-part6 7-part7
8-part8 9-part9 10-part10 11-part11 12-part12 13-part13
14-part14 15-part15 16-part16 17-part17 18-part18
19-part19 20-part20 21-part21 22-part22 23-part23
24-part24 25-part25 26-part26 27-part27 28-part28
29-part29 30-part30 31-part31 32-part32 33-part33

Statistics: Mean 8.112; Variance 4.715; scale 1.720
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result	No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	290	78.0	2287	4	Q25443	Sequence encoding ant	1 09e-186
2	290	78.0	2287	28	T60710	IgG1 gene	1 09e-186
3	243	55.3	204	14	Q80127	DP10 VH gene	1 46e-152
4	238	54.0	812	3	Q24119	Human heavy chain V r	6 08e-149
5	238	54.0	812	7	Q41185	Human heavy chain V r	6 08e-149
6	238	54.0	812	27	T37243	DNA fragment vh49.8,	9 09e-147
7	235	53.2	294	14	Q93128	HV152 VH gene	2 59e-145
8	233	52.6	1617	6	Q35099	Antibody D heavy chain	4 23e-138
9	223	59.9	441	14	Q82750	31kD anti-Vasiceella	6 20e-136
10	220	59.1	359	33	T72131	CEA-specific antibody	1 72e-134
11	218	58.6	687	22	T15262	PC3AP33 anti-tetanus	1 72e-134
12	218	58.6	4501	16	Q92546	PC3AP33 expression vec	9 05e-134
13	218	58.6	6166	16	Q92547	Expression vector, pp	1 72e-134
14	217	58.3	325	5	Q29767	Gene for Hv region of	2 11e-124
15	204	54.8	539	13	Q78956	Human immunoglobulin	

16 198 53.2 294 14 Q89329
17 196 52.7 363 19 T10938
18 194 52.2 438 31 T75422
19 192 51.6 564 13 Q78946
20 190 51.1 496 13 Q78941
21 188 50.5 512 13 Q78940
22 188 50.5 799 13 Q78984
23 187 50.3 372 9 Q55663
24 181 48.7 360 33 T72132
25 178 47.8 748 13 Q78983
26 176 47.3 529 13 Q78996
27 175 47.0 378 9 Q55662
28 171 46.0 585 33 T90022
29 170 45.7 324 6 Q85635
30 170 45.7 366 12 Q70085
31 168 45.2 500 14 Q79962
32 165 44.4 234 17 T04633
33 158 42.5 410 17 T15178
34 158 42.5 421 33 T73624
35 157 42.2 472 16 Q92540
36 154 41.4 372 16 Q92540
37 153 41.1 400 15 Q84539
38 153 41.1 400 23 T86653
39 153 41.1 822 23 T86662
40 153 41.1 822 15 Q94548
41 151 40.6 421 33 T73633
42 150 40.3 591 13 Q78955
43 149 40.1 421 33 T73636
44 148 39.8 3282 24 T40914
45 148 39.8 13254 24 T40915

ALIGNMENTS

RESULT 1
ID Q25443 standard; DNA: 2287 BP.
AC Q25443;
DE 02-JAN-1992 (first entry)
DI Sequence encoding antibody molecule IgG1.
KW Antibody; immunoglobulin G1; ds.
OS Homo sapiens.
FT exon 1..453 Location/Qualifiers
FT /tag= a 619..972
FT /tag= b 1361..1405
FT /tag= c 1524..1853
FT /tag= d 1950..2273
FT /tag= e
PN W09209293-A.
PD 11-JUN-1992. U08605.
PF 18-NOV-1991: US-618314.
PR 23-NOV-1991: GEN HOSPITAL CORP.
PA (GHEO) GEN HOSPITAL CORP.
PI Seed B, Walz G;
PI WPI: 92-036789/26
PI P-RSD8: R24442
PI Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PI - used in treating chronic inflammation, rheumatoid arthritis,
PI psoriasis, etc.
CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC inventors designed a molecule including several such sites for
CC attachment of sialyl-Lex side chains (see P24442). The
CC additional N-linked glycosylation sites are introduced at locations
CC which impair complement fixing and Fc receptor binding ability. They
CC are preferably located in the CH2 region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for
CC disrupting undesirable interactions between cells or proteins.
CC Disrupting this interaction has therapeutic applications, for

Db 130 ggccttgagtgatgagagagatcatccctatctttgtatagcaaacatagcacagag 189
 QY 121 GGCCTTGAGTGAATGAGGAGGAGATATCTCTTTCTTTGGTAAATCAATCAAAATGAGCAGAGAG 180
 Db 190 ttccaggagagatccagctattaccgagacgaatccagagacacagcctatagagctg 249
 QY 181 TTCAGGGCAGAGCTCTCGATTACCGGAGGAGGAAATCGGAGAGACAGACDCTATATGAGAGCTG 240
 Db 250 agcagcctatgattagagacacagcgccgtgtattactgtgca 292
 QY 241 AGTAGGCTGAGATCGGAGGACACGGGCATCTATTACTGTGCGA 283

RESULT 4

ID Q22419 standard; DNA: 812 BP.
 AC Q22419;
 DT 17-AUG-1992 (first entry)
 DE Human heavy chain V region gene VH49.8.
 KW Heavy chain; variable region; VH1 family; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT exon 1..286
 FT /tag= a
 FT /number= 1
 FT intron 287..373
 FT /tag= b
 FT /number= 1
 FT exon 373..812
 FT /tag= c
 FT /number= 1
 FT CDS 241..689
 FT /tag= d
 FT /number= 1
 FT misc_recomb 678..686
 FT /tag= e
 FT /number= 1
 FT /note= "recombination signal"
 FT misc_recomb 709..718
 FT /tag= f
 FT /number= 1
 FT /note= "recombination signal"
 PN W09203918-A.
 PD 19-MAR-1992.
 PF 28-AUG-1991; U06185.
 PR 29-AUG-1990; US-574748.
 PR 31-AUG-1990; US-575962.
 PA (GENP-) GENPHARM INT INC.
 PI Lonberg N, Kay R;
 DR WPI: 92-113952/14.
 DP P-PDB: P22358.
 PT Immunoglobulin transgenes - for prodn. of heterologous
 PT non-rearranged and/or rearranged lg chains
 PS Example 14; Page 87; 172pp; English.
 CC The human placental genomic DNA library cloned into the phage
 CC vector lambda FIX II was screened with the human VH1 family
 CC specific oligonucleotide (see Q22418). Phage clone lambda
 CC 49.8 was isolated and a 5.1 kb XbaI fragment containing the variable
 CC segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8
 CC An 800 bp region of this insert was sequenced. VH49.8 was found
 CC to have an open reading frame and intact splicing and recombination
 CC signals, thus indicating that the gene is functional.
 CC See also Q23419-49, Q22417-30.
 SQ Sequence 812 BP: 264 A: 189 C: 222 G: 197 T:

Query Match 64.0%, Score 238, DB 3, Length 812;
 Best Local Similarity 91.3%; Pred. No. 6,086-149;
 Matches 263, Conservative 0, Mismatches 25, Indels 0, Gaps 0;

Db 393 ctggttgagctctgggctagggaagagcctgggtctctctctggtgagagctccctctgag 402
 QY 1 CTGAGAGCAGTCTGAGGCTGAGTGAAAGAGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
 Db 453 gctcttgagagcctcttcagcaactatgctatagctgggtgcagagccctctggacaa 512
 QY 61 GCTTCTGGAGGCACTCTGAGGCTGAGTGAAAGAGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCT 120
 Db 513 ggccttgagtgatgagagagatcatccctatctctgtatagcaaacatagcacagag 572
 QY 121 GGCCTTGAGTGAATGAGGAGGAGATATCTCTTTCTTTGGTAAATCAATCAAAATGAGCAGAGAG 180

Db 573 ttccaggagagatccagctattaccgagacgaatccagagacacagcctatagagctg 632
 QY 181 TTCCAAGGAGAGATCTCGATTACCGGAGGAGGAAATCGGAGAGACAGACDCTATATGAGAGCTG 240
 Db 633 agcagcctatgattagagacacagcgccgtgtattactgtgca 680
 QY 241 AGTAGGCTGAGATCGGAGGACACGGGCATCTATTACTGTGCGA 288

RESULT 5

ID Q44185 standard; DNA: 812 BP.
 AC Q44185;
 DT 10-NOV-1993 (first entry)
 DE Human heavy chain V region gene VH49.8.
 KW Immunoglobulin; IgG; heavy chain; minilocus transgene;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT exon 1..286
 FT /tag= a
 FT /number= 1
 FT intron 287..372
 FT /tag= b
 FT /number= 1
 FT exon 373..812
 FT /tag= c
 FT /number= 2
 FT CDS 241..689
 FT /tag= d
 FT /number= 1
 FT /note= "CDS is interrupted by intron #1; the
 FT last three codons of the CDS are not
 FT translated in the amino acid sequence
 FT R38623."
 PN W09312227-A.
 PD 24-JUN-1993.
 PF 17-DEC-1992; U10983.
 PR 17-DEC-1991; US-810279.
 PR 18-MAR-1992; US-853408.
 PR 23-JUN-1992; US-904068.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Lonberg N;
 DR WPI: 93-214163/26.
 DP P-PDB: P38623.
 PT Transgenic non-human animals contg. immunoglobulin heavy chain
 PT trans gene - used to produce useful antibodies by isotype
 PT switching
 PS Example 12; Page 96; 196pp; English.
 CC A human placental genomic DNA library cloned into the phage vector
 CC lambda FIX II was screened with the human VH1 family specific
 CC oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a
 CC 5 kb XbaI fragment containing the variable segment VH49.8 was
 CC subcloned into pNN03 to generate plasmid pVH49.8. An 800bp
 CC region of this insert was sequenced (Q44185) and VH49.8 found to
 CC have an open reading frame and intact splicing and recombination
 CC signals, indicating that the gene is functional.
 SQ Sequence 812 BP: 264 A: 188 C: 223 G: 197 T:

Query Match 64.0%, Score 238, DB 7, Length 812;
 Best Local Similarity 91.3%; Pred. No. 6,086-149;
 Matches 263, Conservative 0, Mismatches 25, Indels 0, Gaps 0;

Db 393 ctggttgagctctgggctagggaagagcctgggtctctctctggtgagagctccctctgag 450
 QY 1 CTGAGAGCAGTCTGAGGCTGAGTGAAAGAGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
 Db 453 gctcttgagagcctcttcagcaactatgctatagctgggtgcagagccctctggacaa 512
 QY 61 GCTTCTGGAGGCACTCTGAGGCTGAGTGAAAGAGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCT 120
 Db 513 ggccttgagtgatgagagagatcatccctatctctgtatagcaaacatagcacagag 572
 QY 121 GGCCTTGAGTGAATGAGGAGGAGATATCTCTTTCTTTGGTAAATCAATCAAAATGAGCAGAGAG 180


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FT misc_RNA . 182...195
FT /tag= d
FT /label= CDR1
FT misc_RNA 197...238
FT /tag= e
FT /label= FR2
FT misc_RNA 239...289
FT /tag= f
FT /label= CDR2
FT misc_RNA 290...385
FT /tag= g
FT /label= FR3
FT misc_RNA 386...439
FT /tag= h
FT /label= CDR3
FT misc_RNA 440...472
FT /tag= i
FT /label= FR4
FT misc_RNA 473...763
FT /tag= j
FT /label= CH1
FT misc_RNA 764...811
FT /tag= k
FT /label= HINGE
FT misc_RNA 812...1141
FT /tag= l
FT /label= CH2
FT misc_RNA 1142...1462
FT /tag= m
FT /label= CH3
FT TATA_signal 1566...1571
FT /tag= n
PN EP-523949-A.
PD 20-JAN-1993
PF 14-JUL-1992; 306420
PR 15-JUL-1991; GR-015284.
PR 01-AUG-1991; GR-016594.
PR 23-MAP-1992; GR-006284.
PA (WELL ) WELLCOME FOUND LTD.
PI Crowe JS, Lewis AP;
DR WPI: 93-019551/03.
DR P-PSDB: R31024.
PT Prod'n. of recombinant prime antibodies - useful for treating
PT infections caused by hepatitis A, B and C, herpes,
PT cytomegalovirus, AIDS, AEC, also treat multiple sclerosis,
PT arthritis etc.
PS Disclosure: Fig 2; 35pp; English.
CC The sequences given in Q35099-100 encode the heavy and light chains
CC of Antibody D respectively. Antibody D is a monoclonal antibody which
CC was derived from peripheral blood lymphocytes from a hepatitis A virus
CC (HAV) sero positive patient. Antibody D is closely related in nature
CC to murine antibody 85B3. Total RNA was isolated from antibody D
CC expressing cells and polyadenylated RNA was extracted. These polyA
CC RNA's were used to prepare a cDNA library which was screened for human
CC kappa light (L) chains and two positive clones were detected.
CC Further heavy (H) chain clones were also isolated.
SQ Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;

Query Match 62.6%; Score 233; DB 6; Length 1617;
Best Local Similarity 81.7%; Pred No. 2 52e-145;
Matches 300; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 106 gaqctctggggctgaagtaaaagccctgggtctctcgatgacgtctctcgaagcattc 165
QY 6 GCAGTCTGGGGCTGAGGTGAAGCTTGGTCTCTCTGATGAGCTTCTCTCAAGGCTTC 65

Db 166 tgaagcaccctcagcaactagctatcagctgggtggcagagccctctgacaaagacct 225
QY 6 TGAGGACATCTTACGCGGTCATCTTATCAGCTGGGTGGTGAAGGCTCTGGACAAAGGCT 125

Db 226 tgaatgagtgaggagatcctcctctttttgtgtacacacactactacagaacttcca 285
QY 126 TGAATGATGAGGAGATCCTCCTCTTTTGTGTACACACACTACTACAGAACTTCCA 185

Query Match 59.9%; Score 223; DB 14; Length 441;
Best Local Similarity 89.4%; Pred. No. 4 23e-138;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 72 gcaqctctggggctgaggtgaagaagccctgggtctctcgatgacgtctctcgaagcattc 131
QY 6 GCAGTCTGGGGCTGAGGTGAAGCTTGGTCTCTCTGATGAGCTTCTCTCAAGGCTTC 65

Db 132 tgaagcaccctcagcaacttctgtatcagctgggtggcagagccctctgacaaagacct 191
QY 6 TGAGGACATCTTACGCGGTCATCTTATCAGCTGGGTGGTGAAGGCTCTGGACAAAGGCT 125

Db 192 tgaatgagtgaggagatcctcctctttttgtgtacacacactactacagaacttcca 251
QY 126 TGAATGATGAGGAGATCCTCCTCTTTTGTGTACACACACTACTACAGAACTTCCA 185

Db 252 gggcagagtcacgattagcgcgagcgcctctacagcacagcctacatgagcagagac 311
QY 186 GGGCAGAGTCACGATTAGCGCGAGCGCCTTACAGCACAGCCTACATGAGAACTTCCA 245

```

RESULT 9

ID Q82750 standard; cDNA: 441 BP.

AC Q82750:

DT 02-OCT-1995 (first entry)

DE 93KA9 anti-Varicella zoster virus antibody heavy chain variable.

DE region cDNA.

KW Varicella zoster virus; VZV; anti-VZV monoclonal antibody; 93KA9;

KW glycoprotein II subunit; vaccine; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 1..441

FT /*tag= a

FT PN WO9504080-A.

PD 09-FEB-1995.

PF 22-JUL-1994; US8241.

PR 28-JUL-1993; US-098479.

PR 24-MAP-1994; US-217918.

PA (SANO) SANDOZ PHARM CORP.

PI Lake P, Ostberg L;

DR WPI: 95-090612/12.

DR P-PSDB: R65019.

PT Human monoclonal antibodies specific for the glycoprotein II

PT subunit of varicella zoster virus - used in a therapy and

PT prophylaxis of infection

PS Claim 14; Fig 4B; 39pp; English.

CC A human anti-Varicella zoster virus monoclonal antibody was prepd.

CC using the trioma method of Ostberg et al. (1983) Hybridoma 2:361-367.

CC One resultant trioma neutralised VZV in the absence of complement.

CC This cell line, designated cell line TC93KA9, produced an antibody

CC designated 93KA9. cDNA for the light and heavy chain variable region

CC genes of the 93KA9 antibody were cloned using PCR. At least two

CC heavy chain (gamma-1) and two light chain (kappa) specific clones

CC were sequenced (see Q82749 & Q82750 respectively).

SQ Sequence 44; BF, 89 A, 125 C, 135 G, 92 T;

```

Db 312 cctgagatctgacgacagccatgtattactgtcggagac 354
QY 246 CCTGAGATCGGAGGACAGCGGCATCTATTAAGTCTGCGAAGAC 288

RESULT 10
ID T72131 standard: DNA; 369 BP.
AC T72131.
DT 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH gene.
KW Carcinoembryonic antigen; CEA: human; antibody; scFv.
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis; ss.
OS Homo sapiens.
PN WO9720932-A1.
PD 12-JUN-1997.
PF 09-DEC-1996: G03043.
PR 11-OCT-1996: GB-021395.
PR 07-DEC-1995: GB-025004.
PR 23-MAY-1996: GB-010824.
PA (CAB- ) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK;
DR WPI; 97-319779/29.
DR P-PSDB: W19881.
PT Specific binding members for human carcinoembryonic antigen - bind
PT to the A3-B3 extracellular domain of hCEA and are substantially
PT non-cross-reactive with human liver cells; used for diagnosing
PT cancer.
PS Example 1; Fig 1a; 128pp; English.
CC This nucleotide sequence codes for the heavy chain variable region
CC (VH) (W19881) of human carcinoembryonic antigen (hCEA)-specific
CC antibody CEA6 VH (T72126-32) and VL (T72133-35) gene sequences
CC that had been obtained by selection from a universal phage display
CC library. A claimed specific binding member (A) comprises an hCEA
CC specific antibody antigen binding domain that has a dissociation
CC constant for hCEA of less than 1 x 10-8 M, is non-cross-reactive
CC with human liver cells, and preferentially binds to the A3-B3
CC extracellular domain of hCEA and/or to cell-associated hCEA over
CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
CC VL sequences from CEA1-7, or their CDR sequences, as well as CEA6
CC VH and VL variants. (A) is used to detect cells expressing hCEA,
CC in vivo or in vitro, especially tumour cells for diagnosing cancer,
CC e.g. adenocarcinoma of the colon, lung or breast.
SQ Sequence 369 BP; 85 A; 101 C; 109 G; 74 T;

Query Match 59.1%; Score 220, DB 33; Length 369.
Best Local Similarity 89.9%; Pred. No. 6,20e-136;
Matches 248; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 16 cagctcggagctgaagtgaaagcctgggtcctcgtggaaggtctctgcaagcttct 75
QY 7 CAGCTCTGGGCGCTGAGTGGAAGAGGCTTGAGTCTGAGTGAAGGCTCTCTGCAAGGCTTCT 66

Db 76 ggagggcacccttcagcaactctctctatcaactggtgctgcaacagggccccggacaaggctt 135
QY 67 GGAGGACACCTTCAGCGGCCATGTTATCAGCTGGGCTGGGACAGGCCCCCTGGACAAAGGCTT 126

Db 136 gactgagtggaagatatacctcctccttcttggtacagcaaaactacgctcagaattccag 195
QY 127 GAGTGGATGAGGAGGAGTATCTTCTTCTTCTGACATCAAACTCTGACAGAGGCTTCAG 186

Db 196 ggagactcacattaccgagcaagaatccacgagcagcagcactacatggaagctgagcagc 255
QY 187 GCGAGAGTCTCGATTACCGGACCAATCCGCGAGCACAGGCTATATGGAGCTGAGTAGC 246

Db 256 ctgagatctggaagacacggccctgtattactgtgcg 291
QY 247 CTGAGATCGGAGGACAGCGGCCATCTATTACTGTGCG 282

*RESULT 11
ID T15202 standard: cDNA; 687 BP.
AC T15202.
DT 23-OCT-1996 (first entry)
DE PC3AP13 anti-tetanus toxoid Ig heavy chain variable domain cDNA.
KW Mutagenesis; Ig; immunoglobulin; Fv; framework region; variable; CDR;
KW complementarity determining region; light; heavy chain; PCR;
KW polymerase chain reaction; antibody library; diversity; affinity;
KW immunospecificity; ss.
OS Synthetic.
PN WO9607754-A1.
PD 14-MAR-1996.
PF 01-SEP-1995: U11235.
PR 02-SEP-1994: US-300386.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI; 96-171625/17.
PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
PT gene CDR - useful for prodn. of Ig heavy and light chain
PT combinatorial antibody libraries.
PS Example 1; Page 83; 125pp; English.
CC T15202 and T15203 are the heavy and light chain variable domains of
CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3
CC based expression vector. The heavy and light chain variable domains
CC are used in an example to demonstrate the prodn. of antibodies for
CC an antibody library using mutagenic primers. Mutagenic primers of the
CC invention have sequences at their 3' and 5' ends both capable of
CC binding different framework regions linked by a sequence 6 to 50
CC nucleotides long. Different immunoglobulins produced using the
CC primers may be used to produce antibody libraries having diverse and
CC novel immunospecificities and affinities. By using mutagenic ONS an
CC extremely large population of different randomised binding sites can
CC be created and use of the universal light chain increases the number
CC of combinations which yield functional heterodimeric antibodies.
SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T;

Query Match 58.6%; Score 219; DB 22; Length 687.
Best Local Similarity 88.1%; Pred. No. 1.72e-134;
Matches 252; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 1 ctcgagcagctgggttgaggtgaaagcctgggtcctcgtggaaggtctcctgcaag 60
QY 1 CTCGAGCAGCTGGGGCTGAGGCTGAAGAGCCCTGGGCTCTCAGTGAAGGCTCTCTGCAAG 60

Db 61 gctcttgagggcacccttcacaaattgcccattgagctcaagctgggtgagcagcccttgacaa 120
QY 61 GCTCTGAGGCGCACCTTCAGCGGCTATTTATCAGTGGTGGTGGTGGTGGTGGTGGTGGT 120

Db 121 gggcttgagtggtggagggggtctcctcctcctcctcctcctcctcctcctcctcctc 180
QY 121 GGGCTTGAGTGGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 180

Db 181 ttcagagcagagtracacattaccgagcagcagcagcagcagcagcagcagcagcagcag 240
QY 181 TTCAGAGCAGAGTCTGATTATTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240

Db 241 agcagcctgagatctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 286
QY 241 AGTATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 286

RESULT 12
ID Q9546 standard: DNA; 4691 BP.
AC Q9546.
DT 11-MAR-1996 (first entry)
DE PComb3 expression vector.
KW PComb3; phagemid expression vector; bacteriophage; coat protein 3;
KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;
KW bacterial membrane, periplasm. E. coli, human, Fab. HIV; gp120;
KW combinatorial Fab library; cassette; Fd/cp3; lacZ promoter/operator;
KW ribosome binding site; PRS; PelP leader; spacer; tether sequence;
KW MT4; pMT4-3, antibody, ss, cyclic.
OS Synthetic.
PN WO9511317-A1.
PD 27-APR-1995.

```

PF 19-OCT-1994: 211907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PI (Scripps) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immunotherapy of
 HIV-induced disease
 PS Example 1: Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, cpIII (cp3), which is expressed
 CC prior to extrusion in the phage assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, FD/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC pEB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a pEB leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the M4 Fab display phagemid expression vector, pM4-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 SQ Sequence 4591 BP: 1170 A: 1171 C: 1232 G: 1118 T:

Query Match 58.5% Score 218: DB 16: Length 4631.
 Best Local Similarity 88.1%: Pred No 1 72e-134.
 Matches 232: Conservative 0: Mismatches 34: Indels 0: Gaps 0:
 Db 3424 ctcaagcagctctgggctgagtgaaagcctgggctctcgtgaggtctctcctcagc 3483
 QY 1 CTCGAGCAGCTCGGCTGAGTGTAAGAGCGCTGGCTCTCACTGTAAGCTCTCTCAAG 60
 Db 3484 gctctggaggaaccttcacaaattatgacatcagctgggtgcgacagccctcgacaa 3543
 QY 61 GCTTCTGGAGGACACCTTCACGCGGCTATGATCATGCTGGGTGTAAGAGCGCTCTCA 120
 Db 3544 gggcttaagtgatgggagggatcttcccttctgtaatacagcaagtagcagcaaac 3603
 QY 121 GGGCTTGAAGTGGATGGGAGGAGATATCTCTTCTTGGGACATCAAACTCCGACAC 180
 Db 3604 ttccagggcagagtcacacattacgcgggagcaatccacggggcagacccctacatggagctg 3663
 QY 181 TTCCAGGGGACACATCTGATTACCGGAGAGCAATCCGGAGGACACAGCTACATGGAGCTG 240
 Db 3664 aacagctgaatctgaggaacagcccatattatttctcagag 3709
 QY 241 AATAAGCTTGAATGAGAGGACACCGGAGATCTATATATCTCTCTCAAG 286

RESULT 13
 ID Q92547 standard: DNA: 6166 BP.
 AC Q92547:
 DT 11-MAR-1996 (first entry)
 DE Expression vector, pPho-IT.
 KW Human: Fab: variable chain: heavy, light, region, VH, VL, HIV, gp120.
 KW 3b1: 3b3: 3b4: 3b9: M4: humanised; monoclonal antibody; MAb;
 KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
 KW alkaline phosphatase; phoA: ss; cyclic.

OS Synthetic.
 PN W09511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994: 211907.
 PR 19-OCT-1993: US-139409.
 PR 26-APR-1994: US-233619.
 PR 19-SEP-1994: US-308841.
 PI (Scripps) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA.
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immunotherapy of
 HIV-induced disease
 PS Example 2: Page 193-197; 249pp; English.
 CC This sequence represents the expression vector, pPho-IT which is a
 CC modified version of the phagemid expression vector, pComb3 given in
 CC Q92546. pPho-IT provides for the expression of soluble Fabs which are
 CC secreted into the periplasmic space which is regulated from the alkaline
 CC phosphatase (phoA) promoter. This plasmid was used within the scope of
 CC the invention to express various mutagenised human Fab's which comprise
 CC heavy and light variable regions which bind to HIV gp120. pPho-IT
 CC consists of a DNA molecule having two cassettes to express two soluble
 CC proteins a heavy chain and a light chain. The vector comprises,
 CC operatively linked 5' to 3', a first cassette consisting of the phoA
 CC promoter/operator sequences, an EcoRI restriction site, a ribosome
 CC binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
 CC region, a cloning region bordered by 5' SacI and 3' XbaI restriction
 CC sites, an NcoI restriction site between the two cassettes, and a second
 CC cassette consisting of an expression control RBS, a pEB leader, a human
 CC consensus amino terminus spacer region comprising the sequence EVQLLE,
 CC a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
 CC followed by a SfiI site, expression control stop sequences and a NotI
 CC restriction site. The pPho-IT expression vector contains a light
 CC chain stuffer that is 1200 bp in length and a heavy chain stuffer that
 CC is 300 bp in length. The nucleotide sequences of the heavy and light
 CC chain stuffers encode the heavy and light chain variable domains of a
 CC tetanus toxin-specific Fab.
 SQ Sequence 6166 BP: 1416 A: 1706 C: 1629 G: 1415 T:

Query Match 58.5% Score 218: DB 16: Length 6166.
 Best Local Similarity 88.1%: Pred No 1 72e-134.
 Matches 252: Conservative 0: Mismatches 34: Indels 0: Gaps 0:
 Db 5354 ctcaagcagctctgggctgagtgaaagcctgggctctcgtgaggtctctcctcagc 5413
 QY 1 CTCGAGCAGCTCGGCTGAGTGTAAGAGCGCTGGCTCTCACTGTAAGCTCTCTCAAG 60
 Db 5414 gctctggaggaaccttcacaaattatgacatcagctgggtgcgacagccctcgacaa 5473
 QY 61 GCTTCTGGAGGACACCTTCACGCGGCTATGATCATGCTGGGTGTAAGAGCGCTCTCA 120
 Db 5474 gggcttaagtgatgggagggatcttcccttctgtaatacagcaagtagcagcaaac 5533
 QY 121 GGGCTTGAAGTGGATGGGAGGAGATATCTCTTCTTGGGACATCAAACTCCGACAC 180
 Db 5534 ttccagggcagagtcacacattacgcgggagcaatccacggggcagacccctacatggagctg 5593
 QY 181 TTCCAGGGGACACATCTGATTACCGGAGAGCAATCCGGAGGACACAGCTACATGGAGCTG 240
 Db 5594 aacagctgaatctgaggaacagcccatattatttctcagag 5639
 QY 241 AATAAGCTTGAATGAGAGGACACCGGAGATCTATATATCTCTCTCAAG 286

RESULT 14
 ID Q9767 standard: CDNA: 325 BP.
 AC Q9767:
 DT 18-MAR-1993 (first entry)
 DE Gene for Hv region of human rheumatoid factor antibody.
 KW Heavy chain; variable region; YES8C; arthritis; ss.
 KW Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 20..325

```

RESULT 15
ID Q78956 standard; DNA; 539 BP.
AC Q78956;
DI 02-AUG-1995 (first entry)
DE Human immunoglobulin Vh gene #18.
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
OS Homo sapiens.
FH Key
FH Key Location/Qualifiers
CDS 47..481
FT
FT /*tag= a
FT /product= human immunoglobulin variable heavy chain
FT intron 93..176
FT /*tag= b
FT /*tag=
FT misc_signal 482..484
FT /*tag= C
FT /*tag=
FT /note= "miscellaneous signal, does not conform to
FT terminator or splice site sequence"
FT

```

WIRECARD (TM)

Release 2.10 John F. Collins, BioComputing Research Unit
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MPsrch_nn n a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 10:51 37 1998 MasPar: time 1:5 24 Seconds
910.343 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-24
Description: (1-372) from US08844215 seq
Perfect Score: 372
N.A. Sequence: 1 CTCGAGCAGTCTGGGCTCA
Comp: GAGCTGCTCAGACCGGAGCT

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0: Query 0
Searched: 37346 seqs, 141010104 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-C
1:EST197 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202
7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208
13:EST209 14:EST210 15:EST211 16:EST212 17:EST213
18:EST214 19:EST215 20:EST216 21:EST217 22:EST218
23:EST219 24:EST220 25:EST221 26:EST222 27:EST223
28:EST224 29:EST225 30:EST226 31:EST227 32:EST228
33:EST229 34:EST230 35:EST231 36:EST232 37:EST233
38:EST234 39:EST235 40:EST236 41:EST237 42:EST238
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48:EST244 49:EST245 50:EST246 51:EST247 52:EST248
53:EST249 54:EST250 55:EST251 56:EST252 57:EST253
58:EST254 59:EST255 60:EST256 61:EST257 62:EST258
63:EST259 64:EST260 65:EST261 66:EST262 67:EST263
68:EST264 69:EST265 70:EST266 71:EST267 72:EST268
73:EST269 74:EST270 75:EST271 76:EST272 77:EST273
78:EST274 79:EST275 80:EST276 81:EST277 82:EST278
83:EST279 84:EST280 85:EST281 86:EST282 87:EST283
88:EST284 89:EST285 90:EST286 91:EST287 92:EST288
93:EST289 94:EST290 95:EST291 96:EST292 97:EST293
98:EST294

Database: EST-D
99:EST295 100:EST296 101:EST297 102:EST298 103:EST299
104:EST300 105:EST301 106:EST302 107:EST303 108:EST304
109:EST305 110:EST306 111:EST307 112:EST308 113:EST309
114:EST310 115:EST311 116:EST312 117:EST313 118:EST314
119:EST315

Statistics: Mean 9.411 Variance 1.920 scale 5.163
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Prod. No.
1	148	39.8	379.99	AA291381	2144502.r1 Soares ova	8.55e-247
2	119	32.0	279.26	AA300571	EST13661 Testis tumor	1.65e-186
3	109	29.3	291.58	AA377074	EST89603 Small Intest	5.42e-145
4	100	26.9	265.58	AA377129	EST89650 Small Intest	1.10e-147
5	83	22.3	266.80	AA402547	2047007.r1 Soares ova	1.30e-113
6	64	17.2	266.64	AA383972	EST97425 Thymus II Ho	1.18e-76
7	42	11.3	273.26	AA300982	EST13889 Testis tumor	1.86e-36
8	42	11.3	241.25	AA395793	EST100902 Pancreas tu	1.86e-36
9	36	9.7	280.37	AA326855	EST10457 Colon I Homo	2.83e-26
10	35	9.4	230.85	AA428970	2048002.r1 Soares ova	1.95e-24
11	35	9.4	240.52	AA260289	EST69410 Lymph node	1.95e-24
12	35	9.4	366.59	AA378112	EST91017 Synovial sar	1.05e-24
13	30	8.1	256.26	AA300605	EST13453 Testis tumor	7.96e-17
14	29	7.8	326.37	AA327241	EST10532 Colon I Homo	2.58e-15
15	28	7.5	268.52	AA360195	EST69374 Lymph node	7.94e-14
16	27	7.3	304.26	AA300945	EST13823 Testis tumor	2.27e-12
17	26	7.0	364.16	AA098196	mn86005.r1 Stratagene	6.09e-11
18	26	7.0	371.37	AA327565	EST30921 Colon I Homo	6.09e-11
19	25	6.7	294.31	AA314630	EST18648 Lung Homo sa	1.52e-09
20	23	6.2	420.1	AA175689	ms94002.r1 Soares mu	7.44e-07
21	22	5.9	278.60	AA381086	EST94138 Activated T	1.45e-05
22	21	5.6	243.37	AA326372	EST30287 Colon I Homo	2.55e-04
23	21	5.6	267.52	AA360197	EST59376 Lymph node I	2.55e-04
24	21	5.6	295.37	AA328574	EST32070 Embryo, 12 w	2.55e-04
25	21	5.6	307.58	AA377311	EST89959 Small Intest	2.55e-04
26	21	5.6	455.22	AA146478	mr05007.r1 Soares mu	2.55e-04
27	21	5.6	551.82	AA418907	2013002.r1 Soares mu	2.55e-04
28	20	5.4	170.79	AA400764	2111005.r1 Soares tes	4.01e-03
29	20	5.4	255.76	AA352433	EST60427 Activated T	4.01e-03
30	20	5.4	263.14	AA247551	cs44510.seq.F Human I	4.01e-03
31	20	5.4	281.35	AA321321	EST24509 Corbellum I	4.01e-03
32	20	5.4	318.113	AA448258	2083011.r1 Soares tes	4.01e-03
33	20	5.4	331.78	AA393400	EST11003 Testis tumor	4.01e-03
34	20	5.4	334.26	AA399325	EST11003 Testis tumor	4.01e-03
35	20	5.4	371.16	AA089308	mc95005.r1 Stratagene	4.01e-03
36	20	5.4	387.15	AA501114	mx79007.r1 Soares mu	4.01e-03
37	20	5.4	400.113	AA472709	2047112.r1 Soares tes	4.01e-03
38	20	5.4	425.112	AA443899	EST46002.r1 Soares ova	4.01e-03
39	20	5.4	435.88	AA55774	2111009.r1 Stratagene	4.01e-03
40	20	5.4	469.12	AA409922	2046009.r1 Soares mu	4.01e-03
41	20	5.4	482.30	AA316361	EST18109 Jurkat T cell	4.01e-03
42	20	5.4	480.47	AA371016	2046002.r1 Soares mu	4.01e-03
43	20	5.4	516.14	AA346435	LE05332.Frigo LD GFA	4.01e-02
44	19	5.1	337.118	CEIK018AXP	C. elegans CGNA clone	5.60e-02
45	19	5.1	431.11	AA336855	2501003.r1 Soares mu	5.60e-02

ALIGNMENTS

RESULT 1	AA291381	379 bp	EST	16-MAY-1997
LOCUS	2144502.r1 Soares ova	tumor	NCBI	EST
DEFINITION	5' similar to gb M:851175 HEAVY CHAIN PPTINSEPR V I REGION (HUMAN)			
ACCESSION	AA291381			
NID	g1939359			
KEYWORDS	EST			
SOURCE	human			
ORGANISM	Homo sapiens			
	Eukaryotes; mitochondrial eukaryotes, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 379)			
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, R., Post, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, K., Wylier, T., Waterston, R., and Wilson, R.			
TITLE	WASHU-Merck EST Project 1997			

ORGANISM	Homo sapiens	similar to immunoglobulin heavy chain, VDJ region.
REFERENCE	AA377128	
AUTHORS	Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata; Vertebrata: Mammalia; Eutheria: Primates; Catarrhini: Hominoidea; Homo.	
1 (bases 1 to 291)	Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C., Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F., Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olson, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.	
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	
JOURNAL	Nature 377 (6547 Suppl.), 3-174 (1995)	
MEDLINE	96026280	
COMMENT	Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tldb/hgi/hgi.html) Seq primer: M13 Reverse.	
FEATURES	Location/Qualifiers	
source	1..291	
organism	"Homo sapiens"	
note	"Organ: small intestine; Vector: pBluescript SK-"	
site	1: EcoRI; Site 2: XhoI	
clone_lib	"Small intestine 1"	
dev_stage	"adult"	
BASE COUNT	67 a 73 c 89 g 51 t 1 others	
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Query Match	29.3%; Score 109; DB 58; Length 291;	
Best Local Similarity	75.7%; Pred. No. 5.42e-166;	
Mismatches	159; Conservative 0; Mismatches 51; Indels 0; Gaps 0;	
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QY	1 CTCGAGCAGCTGTGGGCTCTAGGTGGAAGAAAGCTGTGGGCTCTAGGAGGCTCTGCAAG 60	
Db	141 gctattggatcacaccttccactgattatcactcaactgggtgcgacagccctggacag 200	
QY	61 GCTTCTGGAGGACCTTCAAGCGGCAIGTATCACTGTGGGCTCTGCAAGGCTCTGCAAC 120	
Db	201 gaacttgatgagatgagatgagatgagacccagcaaatgagagctgcgactgtgcacagaag 260	
QY	121 GAGCTTCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180	
Db	261 ttccgagagagatcacctcctgacccagcagc 290	
QY	181 TTCCATGAGAGAGCTCTGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 210	
RESULT	4	
LOCUS	AA377128 265 bp mRNA	EST 21-APR-1997
DEFINITION	EST89660 Small intestine 1 Homo sapiens cDNA 5' end similar to	
BASE COUNT	57 a 69 c 79 g 58 t 2 others	
ORIGIN		
Query Match	26.9%; Score 100; DB 58; Length 265;	
Best Local Similarity	84.5%; Pred. No. 1.18e-147;	
Mismatches	120; Conservative 0; Mismatches 22; Indels 0; Gaps 0;	
Db	104 ctgtgcaactctggagtgaggtgaagaaagcctgagcctcactgaagctcctcgaag 163	
QY	1 CTCGAGCAGCTCTGGGGCTGAGGTGAGGAGGCTGTGGGCTCTGCAAGGCTCTGCAAG 60	
Db	164 anttctggttacacctttaccacatacaggtatcacctgggtgcacacagccctcggacaa 223	
QY	61 GCTTCTGGAGGAGCTCTGAGCGGCAIGTATCACTGTGGGCTCTGCAAGGCTCTGCAAG 120	
Db	224 gggctcgaactgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 245	
QY	121 GGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 142	
RESULT	5	
LOCUS	AA402547 266 bp mRNA	EST 15-MAY-1997


```

10
RESULT 10
LOCUS
DEFINITION
AA428870 230 bp mRNA EST 20-MAY-1997
cva3b2.r1 Soares ovar; tumor N6HOT Homo sapiens cDNA clone 75694c
5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN) :.
ACCESSION
AA428970
NID
g2110596
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryote, mitochondrial, eukaryotes, Metazoa, Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
1 (bases 1 to 230)
REFERENCE
1 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Kucaba, T., Lucy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, P.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through INL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28ml3 rev2 Er from AmerSham.
Location/Qualifiers
1..230
FEATURES
source

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TGTTACCAATCTCAAGTCGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
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/sex="Female"

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RESULT	11				EST	21-APR-1997
LOCUS		AA360289	240 bp	mRNA		
DEFINITION		EST649410 Lymph node, subtracted Homo sapiens cDNA 5' end similar to similar to immunoglobulin gamma heavy chain, V(III) region (GB:U03894).				
ACCESSION		AA360289				
NID		g2012607				
KEYWORDS		EST.				
SOURCE		human.				

REFERENCE
AUTHORS
1 (bases 1 to 326)
Adams,J.D., Kerlavags,A.P., Fleischmann,P.D., Fuldner,P.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,C.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Frichman,I.L., Geoghagen,N.S.,
Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,S.Jr.,
Keller,J.M., Kelley,C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,
Moreno-Palaoques,P.F., McDonald,L.A., Nguyen,D.T., Pellierino,S.M.,
Phillips,C.A., Pyder,S.F., Scott,J.L., Saudke,D.W., Shirley,P.

Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,B.F., Fortie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Raymond,L., Fanon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

Other ESTs: TH0169513
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the tigr Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

Location/Qualifiers
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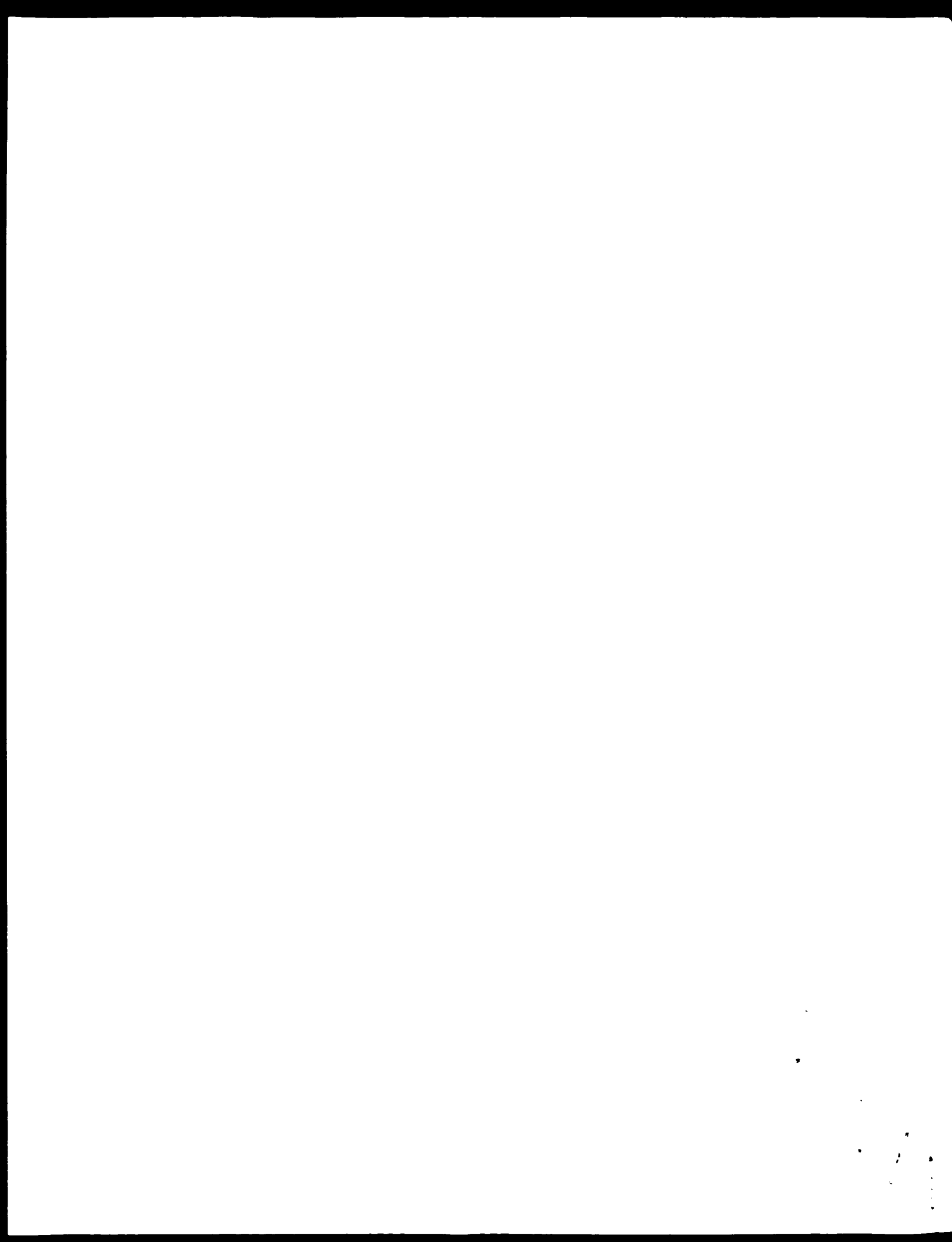
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EST 21-APP-1997
EST mpNA
EST560195 258 bp Lymph node I. Homo sapiens cDNA 5' end similar to
immunoglobulin heavy chain, VDJ regions (CB:X67306).
EST560195
92012573
EST.
human.

Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 258)
Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A., Buit,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gorayne,I.H., White,C., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,D.W., Fitzhugh,W.M., Fritchman,T.L., Geordadev,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Li,J., Li,I., Marmaro,S.M., Merrick,J.M., Moreno-Palancas,P.F., McDonald,I.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Pyder,S.E., Scott,T.L., Saudet,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,B.F., Fortie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Raymond,L., Fanon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,

Search completed: Tue Feb 24 11:00:26 1998
Job time : 529 secs.



and is derived by analysis of the total error distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
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2	217	58.8		372	102	HUMIGHDXN	Human Ig rearranged H	2, 540-1774
3	217	58.8		534	99	HUMIGHCKN	Human Ig rearranged H	2, 540-1779
4	216	58.5		421	99	HUMIGHBHT	Human (fetal) Ig rear	2, 476-1778
5	215	58.3		448	99	HUMIGHBHT	Human Ig rearranged H	2, 396-1777
6	215	58.3		483	87	HS203M5	H.sapiens mRNA for im	2, 396-1777
7	215	58.3		510	87	HS203P9	H.sapiens mRNA for im	2, 396-1777
8	215	58.3		510	87	HS203P6	H.sapiens mRNA for im	2, 396-1777
9	215	58.3		510	87	HS203B7	H.sapiens mRNA for im	2, 396-1777
10	215	58.3		510	87	HS203B2	H.sapiens mRNA for im	2, 396-1777
11	215	58.3		525	87	HS203G4	H.sapiens mRNA for im	2, 396-1777
12	215	58.3		525	87	HS203G1	H.sapiens mRNA for im	2, 396-1777
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14	214	58.0		366	96	HSVHP53	H.sapiens mRNA for im	2, 320-1776
15	214	58.0		392	91	HSVPHG3	H.sapiens gene for im	2, 320-1776
16	214	58.0		392	91	HSVGH2M	H.sapiens germline im	2, 320-1776
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18	214	58.0		392	91	HSVPH1A	H.sapiens gene for im	2, 320-1776
19	214	58.0		392	91	HSVPH1A	H.sapiens gene for im	2, 320-1776
20	214	58.0		392	91	HSVGH1M	H.sapiens germline im	2, 320-1776
21	214	58.0		392	91	HSVPH1M	H.sapiens gene for im	2, 320-1776
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28	214	58.0		474	96	HSVPH1B2	H.sapiens mRNA for im	2, 320-1776
29	214	58.0		474	97	HSVPH1B	H.sapiens mRNA for im	2, 320-1776
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36	214	58.0		510	99	HUMIGH2N	Human Ig rearranged H	2, 320-1776
37	214	58.0		513	99	HUMIGH2N	Human Ig rearranged H	2, 320-1776
38	214	58.0		516	87	HS201B2	H.sapiens mRNA for im	2, 320-1776
39	214	58.0		516	87	HS201B7	H.sapiens mRNA for im	2, 320-1776
40	214	58.0		516	87	HS201B6	H.sapiens mRNA for im	2, 320-1776
41	214	58.0		525	99	HUMIGH2N	Human Ig rearranged H	2, 320-1776
42	214	58.0		534	99	HUMIGH2N	Human Ig rearranged H	2, 320-1776
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ALIGNMENT

RESULT	1
Locus	HRM1341YN 538 bp DNA
DEFINITION	Human Ig rearranged H chain gene V-region (V-D-J) hybridoma 142, subgroup VH-1.
ACCESSION	M65104
NID	g185344
KEYWORDS	V-region, immunoglobulin heavy chain subgroup VH-1; rearranged DNA
SOURCE	Homo sapiens tonsil DNA.
ORGANISM	Homo sapiens
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; vertebrata; Eutheria; Plimates; Catarrhini; Hominoidea; Homo.
PREFERENCE	1 (bases 1 to 528)
AUTHORS	Kipps, T.J., and Duffy, S.F.
TITLE	Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes
JOURNAL	J. Clin. Invest. 87 (5): 2087-2094 (1991)
MOLECULE	91250563

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Matches 304; Conservative 0; Mismatches 62; Indels 3; Gaps 2.		
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Db	223	gctctgagagacaccttcagcagctatgctatcagctgaggtgagagagagagagagaa 282
Qy	61	GTITTTGGAGACACTTCAGAGATACACTATTTCAGTGTGTGGACAGGCTGGACAA 120
Db	283	gggcttgagtgagtgagggatcatccctatcttttgtagcaaaactacgcacagaaag 342
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Qy	181	TTTCAGGGCAGACTCTCGATAACCGCCAGCATTCCACGAGCAGACAGCTACATGGAAC 240
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Qy	241	ACTAGCCTCAGATCTGAGGACACGCGCGTCTATTTCGTGCGAGAGTCTGTAATACCAAT 300
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NID	9392691				
KEYWORDS	human.				
SOURCE	Human sapiens				
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REFERENCE	1 (bases 1 to 372)				
AUTHORS	Huang, C. and Stollar, B.D.				
TITLE	A majority of immunoglobulin H chain cDNA of normal human adult blood lymphocytes resembles cDNA for fetal Ig and natural autoantibodies				
JOURNAL	J. Immunol. 151, 5290-5300 (1993)				
MEDLINE	94044753				
REFERENCE	2 (bases 1 to 372)				
AUTHORS	Stollar, B.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-APR-1993) Stollar B.D., Tufts University, Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA				
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Db	310	gcaat--gggtg--g-tactagagc-cttgactgactgagggcaggggacccctggtcacc 363			
Qy	301	GCAATCCGCGACACGATGGGATATTACTTTCGACTACTGGGGCCAGGGAACCTGGTCACC 360			
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QY 241 ATATGCTTCAGATCTCAGATACAGGCGGTATTTCTGTCGACAGCTGTAATACCAAA 300
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RESULT 7 HS203E9 510 bp RNA PRI 03-AUG-1995
LOCUS H.sapiens mRNA for immunoglobulin variable region (clone 203-E9).
DEFINITION
ACCESSION Z47257
NID G619478
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 510)
AUTHORS Lebecque,S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, France, 69572, FRANCE
REFERENCE 2 (bases 1 to 510)
AUTHORS Galibert,L., van Dooren,J., Durand,I., Pousset,F., Jefferis,R.,
Banchereau,J. and Lebecque,S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intraclonal heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
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QY 181 TTTCAGGCGAGACTCTCGAATACCGCGAGATTCCTCAAGACAGCTACATGGAAC 240
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QY 358 ACGGTCCTCTCA 369
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RESULT 8 HS203E6 510 bp RNA PRI 03-AUG-1995
LOCUS H.sapiens mRNA for immunoglobulin variable region (clone 203-E6).
DEFINITION
ACCESSION Z47265
NID G619476
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 510)
AUTHORS Lebecque,S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P.11 CEDEX, Dardilly, France, 69572, FRANCE
REFERENCE 2 (bases 1 to 510)
AUTHORS Galibert,L., van Dooren,J., Durand,I., Pousset,F., Jefferis,R.,
Banchereau,J. and Lebecque,S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intraclonal heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
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/clone="203-E6"
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BASE COUNT 105 a 142 c 155 g 108 t
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Best Local Similarity 80.9%; Pred. No. 2,39e-177.
Matches 301; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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QY 301 GCAATCCGGCACACGATG---GGATATTACTTTGACTACTGGGCCAGGAAACCTGGTC 357
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DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 203-E7).
ACCESSION 247266
NID 9619477
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 510)
AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P. 11 CEDEX, Dardilly, Phone, 69572, FRANCE
REFERENCE 2 (bases 1 to 510)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
Banchereau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 105 a 142 c 155 g 108 t
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Query Match 58.3%; Score 215; DB 87; Length 510;
Best Local Similarity 80.9%; Pred. No. 2.39e-177;
Matches 301; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

Db 67 ctggtcagctctgggctgagtggaagcctgggtctcctcgtggaagctctcctcgaag 126
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QY 301 GCAATCCGGCACACGATG---GGATATTACTTTGACTACTGGGCCAGGAAACCTGGTC 357
Db 427 accgtctctca 438
QY 358 ACCGTCCTCTCA 369

RESULT 11
LOCUS HS203G4 525 bp RNA PRI 03-AUG-1995
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 203-G4).
ACCESSION 247271
NID 9619482
KEYWORDS immunoglobulin; variable region.

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RESULT 10
LOCUS HS203E2 510 bp RNA PRI 03-AUG-1995
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 203-E2).
ACCESSION 247264
NID 9619475
KEYWORDS immunoglobulin; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 510)
AUTHORS Lebecque, S.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1994) Serge Lebecque, Molecular Biology,
Schering-Plough, Laboratory for Immunological Research, 27, Chemin
des Peupliers, B.P. 11 CEDEX, Dardilly, Phone, 69572, FRANCE
REFERENCE 2 (bases 1 to 510)
AUTHORS Galibert, L., van Dooren, J., Durand, I., Rousset, F., Jefferis, R.,
Banchereau, J., and Lebecque, S.
TITLE Anti-CD40 plus interleukin-4-activated human naive B cell lines
express unmutated immunoglobulin genes with intrachain heavy chain
isotype variability
JOURNAL Eur. J. Immunol. 25 (3), 733-737 (1995)
MEDLINE 95220422
FEATURES Location/Qualifiers
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Query Match 58.3%; Score 215; DB 87; Length 510;
Best Local Similarity 80.9%; Pred. No. 2.39e-177;
Matches 301; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

Db 67 ctggtcagctctgggctgagtggaagcctgggtctcctcgtggaagctctcctcgaag 126
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Db 127 gctctggagccacttcagcagctatgctatcagctgggtggcagagccctggagaa 186
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QY 241 AGTAGCCTCAGATCTGAGGACACGGCCGCTATTCTTGTGGAGAGTCGTAATACCAAA 300
Db 367 gaatttttgagtggttcagtgactggttcacccctgggacaggaacccctggctc 426
QY 301 GCAATCCGGCACACGATG---GGATATTACTTTGACTACTGGGCCAGGAAACCTGGTC 357
Db 427 accgtctctca 438
QY 358 ACCGTCCTCTCA 369

RESULT 11
LOCUS HS203G4 525 bp RNA PRI 03-AUG-1995
DEFINITION H sapiens mRNA for immunoglobulin variable region (clone 203-G4).
ACCESSION 247271
NID 9619482
KEYWORDS immunoglobulin; variable region.

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Direct Submission
Submitted (10-AUG-1993) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
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BASE COUNT 81 a 92 c 112 g 72 t

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Db 70 gcttcgagggcacctcagcagctatgctcagctgggtgcgacagccctggacaa 129
QY 61 GTTTTGGAGACACCTTCAGCAGATACACTATTCACTTCGTCGACAGCCCTGGACAA 120

Db 130 gggcttgagtgatgggggatacctcctattcttggtacagcaaacactacgcacagaag 189
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Db 190 ttccagggcagagtcacagattaccgcggagcgaattccacagcacagcctacatggagctg 249
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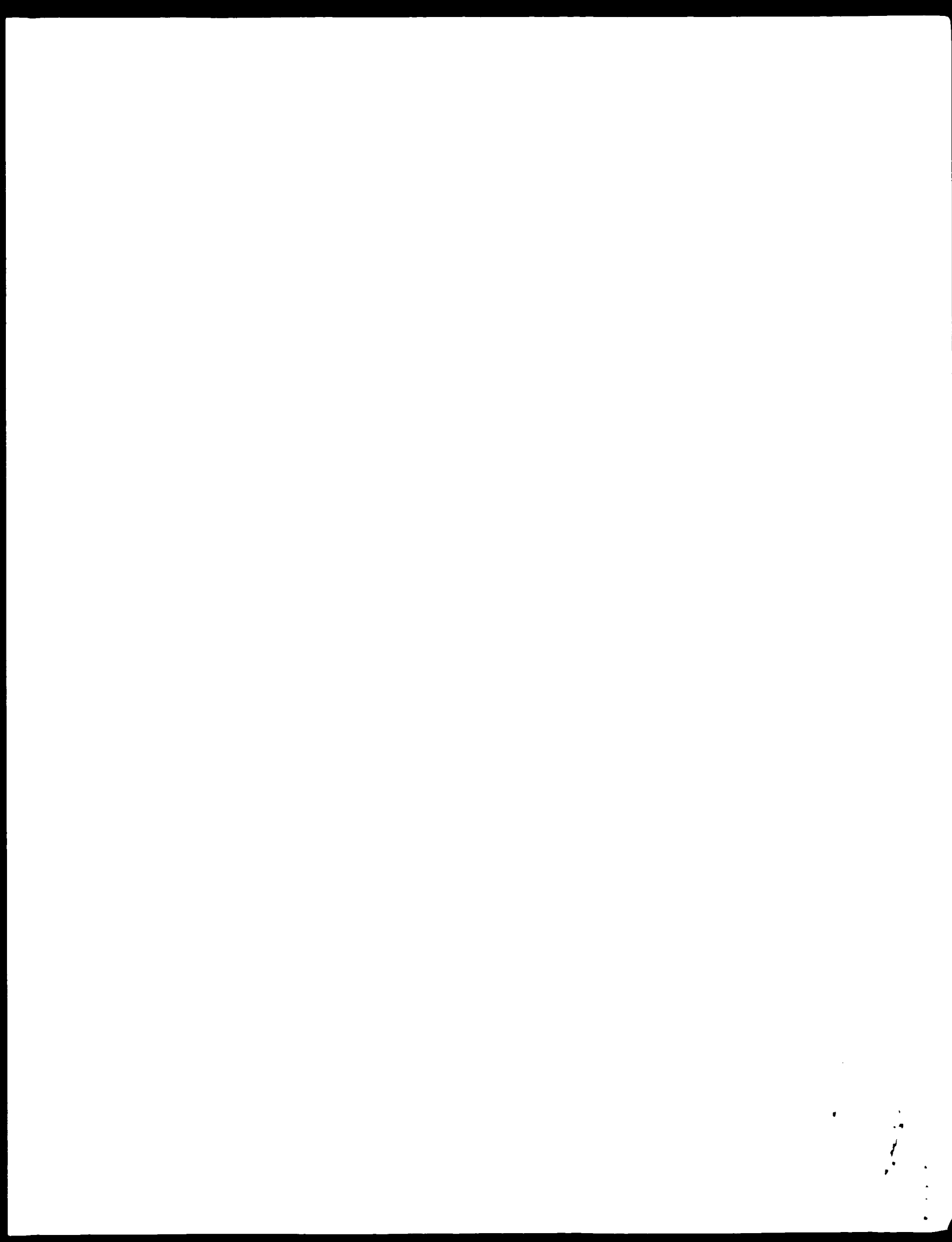
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RESULT 14
LOCUS HSVHP53 366 bp RNA PRI 01-JUN-1993
DEFINITION H.sapiens mRNA for Ig heavy chain variable region.
ACCESSION X64329
KEYWORDS g37829
Ig heavy chain; immunoglobulin; immunoglobulin heavy chain variable region; VH region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates, Catarrhini, Hominoidea, Homo
REFERENCE 1 (bases 1 to 366)
AUTHORS Ebeling,S.
DIRECT SUBMISSION
TITLE Ebeling,S.
JOURNAL Submitted (23-DEC-1991) S. Ebeling, Dept clinical Immunology,
University Hospital Utrecht, Heidelberglaan, 3584 CX Utrecht, THE NETHERLANDS
REFERENCE 2 (bases 1 to 366)
AUTHORS Ebeling,S.B., Schutte,M.E., Akkermans-Koolhaas,K.E., Bloem,A.C., Gmelig-Meyling,F.H. and Logtenberg,F.
TITLE Expression of members of the immunoglobulin VH3 gene families is not restricted at the level of individual genes in human chronic lymphocytic leukemia
JOURNAL Int. Immunol. 4 (3), 313-320 (1992)
55LINE 92232604
See also X64234-43 & X64147

BASE COUNT 88 a 97 c 122 g 85 t
ORIGIN

Query Match 58.0% Score 214 DB 91 Length 392
Best Local Similarity 87.4% Pred. No. 2.32e-176
Matches 250: Conservative 0: Mismatches 36: Indels 0: Gaps 0:
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QY 1 CTCAGACATCTGGGCTTGAAGTGAAGAAAGCCGAGGCTCTGGGTCGAAGGTCGTCAG 60
Db 166 qctctggagggcccttcagagctatgctatcagctgggtccacacagccctcagacaa 225
QY 61 GTTTTGGAGACACTTTCAGAGATACACATATTCAGTGGTTCAGTGGTTCAGTGG 120
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Db 286 ttccaggcagagatcagattaccgggagcgaatccacagacacacagccctacatggagctg 345
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Search completed: Tue Feb 24 09:57:27 1998
Job time : 492 secs.



WHEEL (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsearch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 15:17:02 1998. Maxbar time 22.64 Seconds
Tabular output not generated. 749.495 Million cell updates/sec

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Description: (1-369) from US08844215.seq
Perfect Score: 369
N.A. Sequence: 1 CTCGACGACGTCGGGTGACCCTGGTCACCGTCCTCTCA 369
Comp: GAGCTGTGACACCGGACTGGGACGACGACGAGAGT

Scoring table: TABLE default
Gap 5
Nmatch STD: Dbase 0; Query 0
Searched: 87531 seqs, 22996021 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:back1 2.51 3.52 4.53 5.54 6.55 7.56 8 PCT90 9 PCT91
10:PCT92 11:PCT93 12:PCT94 13 PCT95 14 PCT96
Statistics: Mean 7.662; Variance 3.815; scale 2.002

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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21 125 33.9 443 6 US-08-477- Sequence 9, Applicatio 2 380-81
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23 125 33.9 443 5 US-07-634- Sequence 9, Applicatio 2 380-81
24 125 33.9 443 7 US-08-474- Sequence 9, Applicatio 2 380-81
25 124 33.6 433 6 US-07-634- Sequence 18, Applicati 1 590-80
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27 124 33.6 433 6 US-08-477- Sequence 18, Applicati 1 580-80
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31 118 32.0 366 13 PCT-US95-0 Sequence 8, Applicatio 1 330-75
32 117 31.7 351 6 US-08-236- Sequence 10, Applicati 8 770-75
33 117 31.7 351 13 PCT-US95-0 Sequence 10, Applicati 8 770-75
34 117 31.7 363 7 US-08-040- Sequence 1, Applicatio 8 770-75
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39 115 31.2 363 7 US-08-040- Sequence 3, Applicatio 3 810-73
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41 113 30.6 363 7 US-08-040- Sequence 2, Applicatio 1 640-71
42 113 30.6 366 7 US-08-040- Sequence 6, Applicatio 1 640-71
43 113 30.6 732 6 US-08-230- Sequence 1, Applicatio 1 640-71
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ALIGNMENTS

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DT 01-JAN-1900
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CC Sequence 8, Application PC/TUS9610043
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CC APPLICANT: The General Hospital Corporation
CC TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
CC TITLE OF INVENTION: AND METHODS
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02210-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/10043
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/009,213
CC FILING DATE: 14-JUN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lech, Karen F.
CC REGISTRATION NUMBER:
CC REFERENCE/INCKET NUMBER: 00785/244001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617/542-5070
CC TELEFAX: 617/542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2287 base pairs
CC TYPE: nucleic acid

CC REGISTRATION NUMBER: 87654
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 53:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 812 base pairs
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 CC TOPOLOGY: linear
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 CC LOCATION: 241..335
 CC OTHER INFORMATION: Codes for peptide of SEQ ID NO 54
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 CC LOCATION: 372..677
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 CC Sequence 61, Application PC/TUS9210983.
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 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals for
 CC PRODUCTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 152
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/10983

CC FILING DATE: 19921217
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-2
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 61:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 813 base pairs
 CC TYPE: NUCLEIC ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: 241..285
 CC NAME/KEY: CDS
 CC LOCATION: 373..678
 CC Sequence 813 BP: 204 A: 199 C: 223 G: 197 T: 0 Other:

Query Match: 56.9%, Score 210, DB 10, Length 813
 Best Local Similarity: 86.7%, Pred. No. 2,96e-152,
 Matches 248: Conservative 0; Mismatches 38; Indels 0; Gaps 0;

DB 344 CTGCTGCTGAGTCTGGGGTTCATGAGTGAAGAGGCTGGGTTCTGCTGAGCTCTGAGG 453
 QY 1 CTGAGAGAGTCTGGGGTTCATGAGTGAAGAGGCTGGGTTCTGCTGAGCTCTGAGG 60
 DB 454 GCTTCTGGAGGCACTTCAGAGGATCTGATCAGTGGGTTGGGACAGAGGCTGGGACAA 513
 QY 61 GTTTTTCAGACACACTTCAGAGGATCTGATCAGTGGGTTGGGACAGAGGCTGGGACAA 120
 DB 514 GGGCTTTGAGTGAAGAGGATCAACCTGATCTGATGATGATGATGATGATGATGATGATG 573
 QY 121 GGGCTTTGAGTGAAGAGGATCAACCTGATCTGATGATGATGATGATGATGATGATGATG 180
 DB 574 TTCAGAGGCACTTCAGAGGATCTGATCAGTGGGTTGGGACAGAGGCTGGGACAA 513
 QY 181 TTTTTCAGACACACTTCAGAGGATCTGATCAGTGGGTTGGGACAGAGGCTGGGACAA 240
 DB 613 AGTACCTTCAGATCTGAGGACAGAGGCTGGGTTCTGATCTGATCTGATCTGATCTGATCTG 678
 QY 241 AGTACCTTCAGATCTGAGGACAGAGGCTGGGTTCTGATCTGATCTGATCTGATCTGATCTG 286

RESULT 5

ID US-08-053-131-61 STANDARD: DNA; UNC: 813 BP.

AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 61, Application US/08053131.
 CC Sequence 61, Application US/08053131.
 CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals for
 CC PRODUCTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: One Market Plaza, Stewart Tower, Suite 200
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 61:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 813 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 241..285
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 373..678
CC Sequence 813 BP: 204 A; 189 C; 223 G; 197 T; 0 other;
Query Match 56.9%; Score 210; DB 7; Length 813;
Best Local Similarity 86.7%; Pred. No. 2.96e-152;
Matches 248; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
Db 394 CTGGTGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGTCTCTGGTGAAGTCTCTCTCAAG 453
QY 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGTCTCTGGTGAAGTCTCTCTCAAG 60
Db 454 GCTTCGAGGACCGCTTCAGCAGGTATGCTATCATCTGCTGGTGGGACAGCCCTGGACAA 513
QY 61 GTTTTTCGAGACCGCTTCAGCAGGTATGCTATCATCTGCTGGTGGGACAGCCCTGGACAA 120
Db 514 GGGCTTGAGTGGTGGGAGGATCATCTCTCTGCTATGCTATGCTATGCTATGCTATGCTATG 573
QY 121 GGGCTTGAGTGGTGGGAGGATCATCTCTCTGCTATGCTATGCTATGCTATGCTATGCTATG 180
Db 574 TTCCAGGGCAGGTACGATTACCGGCGGACAAATCCACGAGCAGCAGCTACATGGAGCTG 633
QY 181 TTTCAGGGCAGGTACGATTACCGGCGGACAAATCCACGAGCAGCAGCTACATGGAGCTG 240
Db 634 AGCAGCCTGAGATCTGAGGACACCGGCTGTGTATTTACTTGTGCGAGAG 679
QY 241 AGTACCTCTGAGATCTGAGGACACCGGCTGTGTATTTACTTGTGCGAGAG 286
RESULT 6
ID PCT-US94-01258-1 STANDARD: DNA; UNC: 687 BP
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9401258.
CC Sequence 1, Application PC/TUS9401258
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OF RANDOMIZED IMMUNOGLOBULIN LIGHT
CC CHAINS
CC NUMBER OF SEQUENCES: 61

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01258
CC FILING DATE: 02-FEB-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 687 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC Sequence 687 BP: 155 A; 211 C; 195 G; 126 T; 0 other;
Query Match 52.6%; Score 194; DB 12; Length 687;
Best Local Similarity 83.4%; Pred. No. 8.57e-139;
Matches 240; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
Db 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGTCTCTGGTGAAGTCTCTCTCAAG 50
QY 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCGCTGGGTCTCTGGTGAAGTCTCTCTCAAG 60
Db 61 GCTTCGAGGACCGCTTCAGCAGGTATGCTATCATCTGCTGGTGGGACAGCCCTGGACAA 120
QY 61 GTTTTTCGAGACCGCTTCAGCAGGTATGCTATCATCTGCTGGTGGGACAGCCCTGGACAA 120
Db 121 GGGCTTGAGTGGTGGGAGGATCATCTCTCTGCTATGCTATGCTATGCTATGCTATGCTATG 180
QY 121 GGGCTTGAGTGGTGGGAGGATCATCTCTCTGCTATGCTATGCTATGCTATGCTATGCTATG 180
Db 181 TTCAGGGCAGGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 240
QY 181 TTCAGGGCAGGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 240
Db 241 AGCAGCCTGAGATCTGAGGACACCGGCTGTGTATTTACTTGTGCGAGAG 286
QY 241 AGTACCTCTGAGATCTGAGGACACCGGCTGTGTATTTACTTGTGCGAGAG 286
RESULT 7
ID US-08-300-386A-1 STANDARD: DNA; UNC: 687 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08300386A.
CC Sequence 1, Application US/08300386A
CC Patent No. 5667988
CC GENERAL INFORMATION:
CC APPLICANT: Barbas, Carlos F, III
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OF RANDOMIZED IMMUNOGLOBULIN LIGHT
CC CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10666 No. 5667988th Torrey Pines Road, IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/300.386A
 CC FILING DATE: 02-SEP-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/826,623
 CC FILING DATE: 27-JAN-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 687 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC Sequence 687 BP: 155 A: 211 C: 195 G: 126 T: 0 other:
 CC
 CC Query Match 52.6%, Score 194, DB 7: Length 687:
 CC Best Local Similarity 83.9%, Pred No. 8.57e-139,
 CC Matches 240: Conservative 0: Mismatches 46: Indels 0: Gaps 0:
 CC
 Db 1 CTCGAGCAGCTCGGGGCTGAGTGAAGGCTGGGTCTCGGTGAGGCTCTCTGAGG 60
 QY 1 CTCGAGCAGCTCGGGGCTGAGTGAAGGCTGGGTCTCGGTGAGGCTCTCTGAGG 60
 Db 61 GTTCTCGAGGAGCCTTCAACAAATTATGCCATCAGCTGGGTGGACAGGCGCTGGACAA 120
 QY 61 GTTCTCGAGGAGCCTTCAACAAATTATGCCATCAGCTGGGTGGACAGGCGCTGGACAA 120
 Db 121 GGCTTTGATGTAAGTGAAGGAGGAGTCTGCTTTTGGTAAATAGCAAGTACGACAAAC 180
 QY 121 GGCTTTGATGTAAGTGAAGGAGGAGTCTGCTTTTGGTAAATAGCAAGTACGACAAAC 180
 Db 181 TTCCAGGCGTGAAGTACCAATACCGGAGCAATACCGGAGCAAGTATATGAGGCTG 240
 QY 181 TTTCAGGCGTGAAGTACCAATACCGGAGCAATACCGGAGCAAGTATATGAGGCTG 240
 Db 241 AGCAGGCTGAGATCTGAGGAGCAAGGCGCTATATATTGCGGAGAG 286
 QY 241 AGTAGGCTGAGATCTGAGGAGCAAGGCGCTATATATTGCGGAGAG 286
 CC
 CC RESULT 8
 CC ID PCT-US95-11235-1 STANDARD: DNA: UNC: 687 BP.
 CC AC xxxxxx
 CC DT 01-JAN-1900
 CC DE Sequence 1, Application PCT/US9511235
 CC CC Sequence 1, Application PCT/US9511235
 CC CC GENERAL INFORMATION:
 CC CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
 CC CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT

CHAINS
 CC NUMBER OF SEQUENCES: 70
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute
 CC STREET: 10666 North Torrey Pines Road, IPC8
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/11235
 CC FILING DATE: 01-SEP-1995
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/300,386
 CC FILING DATE: 02-SEP-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/826,623
 CC FILING DATE: 27-JAN-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1 (PC)
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 687 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC Sequence 687 BP: 155 A: 211 C: 195 G: 126 T: 0 other:
 CC
 CC Query Match 52.6%, Score 194, DB 13: Length 687:
 CC Best Local Similarity 83.9%, Pred No. 8.57e-139,
 CC Matches 240: Conservative 0: Mismatches 46: Indels 0: Gaps 0:
 CC
 Db 1 CTCGAGCAGCTCGGGGCTGAGTGAAGGCTGGGTCTCGGTGAGGCTCTCTGAGG 60
 QY 1 CTCGAGCAGCTCGGGGCTGAGTGAAGGCTGGGTCTCGGTGAGGCTCTCTGAGG 60
 Db 61 GTTCTCGAGGAGCCTTCAACAAATTATGCCATCAGCTGGGTGGACAGGCGCTGGACAA 120
 QY 61 GTTCTCGAGGAGCCTTCAACAAATTATGCCATCAGCTGGGTGGACAGGCGCTGGACAA 120
 Db 121 GGCTTTGATGTAAGTGAAGGAGGAGTCTGCTTTTGGTAAATAGCAAGTACGACAAAC 180
 QY 121 GGCTTTGATGTAAGTGAAGGAGGAGTCTGCTTTTGGTAAATAGCAAGTACGACAAAC 180
 Db 181 TTCCAGGCGTGAAGTACCAATACCGGAGCAATACCGGAGCAAGTATATGAGGCTG 240
 QY 181 TTTCAGGCGTGAAGTACCAATACCGGAGCAATACCGGAGCAAGTATATGAGGCTG 240
 Db 241 AGCAGGCTGAGATCTGAGGAGCAAGGCGCTATATATTGCGGAGAG 286
 QY 241 AGTAGGCTGAGATCTGAGGAGCAAGGCGCTATATATTGCGGAGAG 286

QY 241 ACTAGCTCAGATCTGAGGACACGGCCCTGCTATTCTTGCGGAGAG 286

RESULT 9

ID US-08-217-918-3 STANDARD; DNA: UNC: 441 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 3, Application US/08217918.
CC Sequence 3, Application US/08217918
CC Patent No. 5506132
CC GENERAL INFORMATION:
CC APPLICANT: LAKE, PHILIP
CC APPLICANT: GTEBPS, LAPS
CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
CC TITLE OF INVENTION: VAPICELLA-ZOSTER VIRUS
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/217,918
CC FILING DATE: 24-MAR-1994
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO. 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 441 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHEetical: NO
CC ANTI-SENSE: NO
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..441
CC Sequence 441 BP; 89 A; 125 C; 135 G; 92 T; 0 other;

Query Match 52.0%, Score 192; DB 6, Length 441;
Best Local Similarity 82.9%; Pred. No. 4,10e-137;
Matches 242; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 72 GCATCTGGGGCTGAGTGAAGAGCGCTGGCTCGGTGGAAGTCTCTCTCAAGGCTTC 131
QY 6 GCAGCTGGGGCTGAGTGAAGAGCGCTGGCTCGGTGGAAGTCTCTCTCAAGTTC 65
Db 132 TGGAGGCACTCTCAGCAACTTTGCTATCAGCTGGGTGGGAGAGGCGCTGACAGGCT 191
QY 66 TGGAGACACCTCTCAGCAGATACACTATTTCAGTGGTGGGAGAGGCGCTGGAGGCGC 125
Db 192 TGAGTGGAGGGGCAATGATGCTCTCTCTTCTTACGTCACCTACGACACAGAGTTCGA 251
QY 126 TGAGTGGAGGGAATATCATCTCTCTCTATATACACCAACTACGCGGAGAGTTCGA 185
Db 252 GGGCAGAGTCACTAGGAGGAGAGCGCTCTTACGAGCAGAGCGCTACATGGAGCTGAGAG 311
QY 186 GGGCAGAGTCTGATACACCGCCGACCATTCACGAGCAGAGCGCTACATGGAGTGA 245
Db 312 CCTGAGATCTGAGCAGACAGGCGCATATCTACTGTGGAGAGACATAAGAGCA 363

QY 246 CCTCAGATCTGAGGACACGGCCGCTATTCTTGCGGAGAGTGTAAATATCA 297

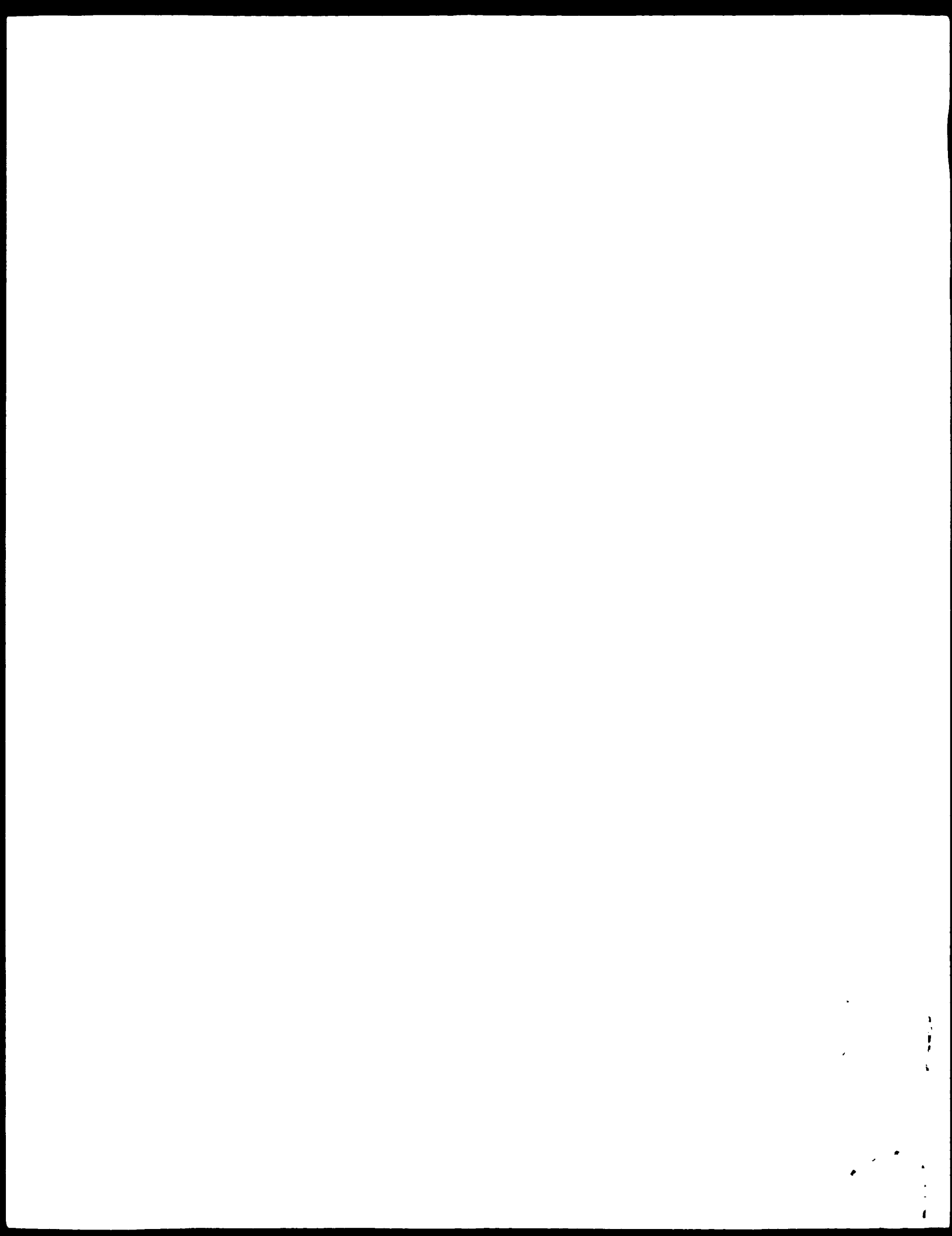
RESULT 10

ID US-08-264-093-1 STANDARD; DNA: UNC: 363 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application US/08264093.
CC Sequence 1, Application US/08264093
CC Patent No. 5639863
CC GENERAL INFORMATION:
CC APPLICANT: Michael D. Dan
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CC TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
CC TITLE OF INVENTION: ANTIGEN
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ridout & Maybee
CC STREET: 2300 Richmond-Adelaide Centre
CC CITY: Toronto
CC STATE: Ontario
CC COUNTRY: Canada
CC ZIP: M5H 2J7
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: MS-DOS 6.00
CC SOFTWARE: ASCII Editor
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/264,093
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA: No 5639863 applicable
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lake, James P
CC REGISTRATION NUMBER: 31081
CC REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (416) 868-1482
CC TELEFAX: (416) 362-0823
CC INFORMATION FOR SEQ ID NO. 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 363 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single stranded
CC TOPOLOGY: linear
CC Sequence 363 BP; 84 A; 97 C; 108 G; 74 T; 0 other;

Query Match 47.4%, Score 175; DB 7; Length 363;
Best Local Similarity 80.3%; Pred. No. 7,28e-123;
Matches 232; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 19 CTGGTGCAAGTGTGAGTGAAGAGCGCTGGCTCGGTGGAAGTCTCTCTCAAG 69
QY 1 CTGAGCACTGTGAGGCTTGAGGCTGAAGAGCGCTGGCTCGGTGGAAGTCTCTCTCAAG 60
Db 70 GCTTCTGCTTACACTTACACCTATGCTGCTAGTGGGTGGAGACAGGCGCTGGACAA 129
QY 61 GTTTTGGAGACACCTTCCAGCATACACTATTTCAGTGGTGGTGGAGAGGCGCTGACAA 120
Db 130 GGGCTTGGAGTGGGATGGATGATCAGCGGCTGACAACTAACACAACTCTGACAGAG 189
QY 121 GGGCTTGGAGTGGGAAATATATCTCTCTATATACACCAACTACGCGGAGAG 180
Db 190 TTCCAGGCGAGAGTCTGATGACACAGACACATCTGATGAGCACTATATAGGAGGTC 249
QY 181 TTTCAGGCGAGAGTCTGATGACACAGAGAGTCTGATGAGCACTATATAGGAGGTC 240
Db 250 AGGAGGCTGATCTGAGCAGACAGGCGGCTGATATCTAGTGGTGGGAGCTGG 298
QY 241 AGTAGCTTCAGATCTGAGGAGACACGGCGCTATATTCTGTGGAGAGTTC 289

ADDRESS-- The Scripps Research Institute, Office of
 ADDRESSEE: Patent Counsel
 STREET: 10550 N. Torrey Pines Road, Suite 220,
 STREET: Mail Drop 1P08
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/276,852
 FILING DATE: 18-JUN-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/178,302
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SCPI452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 169:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 382 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 Sequence 3282 BP: 599 A; 864 C; 1109 G; 710 T; 0 other;



WORLD

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_rng n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 09:57:46 1998: MasPar time 61.22 Seconds
Tabular output not generated. 695.503 Million cell updates/sec

Title: >US-08-844-215-23
Description: (1-369) from US08844215 seq1
Perfect Score: 369
N.A. Sequence: 1 CTGACGACGACTCTGCGGCTCA 369
Comp: GAGCTGCTGACGACCGGACT CCGACGACGAGGAGGAGT

Scoring table: TABLE default
Cap 6

Nmatch STD : Dbase 0; Query 0
Searched: 159551 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq30
1:part4 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.032; Variance 4.357; scale 1.843
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result		Query		Match		Length		DB		ID		Description		Pred. No.	
1	217	59.8	2387	4	Q25443	2387	4	Q25443	2387	4	Q25443	Sequence encoding ant	1 01e-143	1	01e-143
2	217	59.8	2387	28	T60739	2387	28	T60739	2387	28	T60739	IGL gene	1 01e-143	2	01e-143
3	213	57.7	294	14	Q89327	294	14	Q89327	294	14	Q89327	DF10 VH gene	1 25e-140	3	01e-143
4	210	56.9	812	3	Q24419	812	3	Q24419	812	3	Q24419	Human heavy chain V r	2 59e-138	4	01e-143
5	210	56.9	812	7	Q44185	812	7	Q44185	812	7	Q44185	Human heavy chain V r	2 59e-138	5	01e-143
6	209	56.9	812	27	T37243	812	27	T37243	812	27	T37243	DNA fragment v49.8	2 59e-137	6	01e-143
7	209	56.5	294	14	Q89329	294	14	Q89329	294	14	Q89329	HV1263 VH gene	1 53e-137	7	01e-143
8	209	56.5	369	33	T372131	369	33	T372131	369	33	T372131	CEA-specific antibody	1 53e-137	8	01e-143
9	198	53.7	1617	6	Q35099	1617	6	Q35099	1617	6	Q35099	Antibody D heavy chain	4 66e-129	9	01e-143
10	194	52.4	467	22	T15202	467	22	T15202	467	22	T15202	PCAP13 anti-tetanus	5 60e-126	10	01e-143
11	194	52.4	467	16	Q25443	467	16	Q25443	467	16	Q25443	pComb3 expression vec	5 60e-126	11	01e-143
12	194	52.6	1616	15	Q92547	1616	15	Q92547	1616	15	Q92547	Expression vector, pc	5 60e-126	12	01e-143
13	192	52.0	441	14	Q82750	441	14	Q82750	441	14	Q82750	gkA9 anti-Variocella	1 94e-124	13	01e-143
14	189	51.2	325	5	Q29767	325	5	Q29767	325	5	Q29767	Gene for H ₂ region of	3 94e-122	14	01e-143
15	187	50.7	378	9	Q35662	378	9	Q35662	378	9	Q35662	Monoclonal antibody G	1 35e-120	15	01e-143

16	184	49.9	799	13	Q78984	799	13	Q78984	799	13	Q78984	Human immunoglobulin	2 74e-118
17	178	48.2	294	14	Q89329	294	14	Q89329	294	14	Q89329	CPH1.2 VH-1 H chain	1 10e-113
18	178	48.2	438	31	T75422	438	31	T75422	438	31	T75422	Human anti-tumour ant	1 10e-113
19	178	48.2	512	13	Q78940	512	13	Q78940	512	13	Q78940	Human immunoglobulin	1 10e-113
20	176	47.7	539	13	Q78956	539	13	Q78956	539	13	Q78956	Human immunoglobulin	3 77e-112
21	175	47.4	363	19	T10938	363	19	T10938	363	19	T10938	VHmu coding sequence	2 20e-111
22	173	46.9	372	9	Q55663	372	9	Q55663	372	9	Q55663	Monoclonal antibody G	7 51e-110
23	172	46.6	564	13	Q78946	564	13	Q78946	564	13	Q78946	Human immunoglobulin	4 38e-109
24	168	45.5	495	13	Q78941	495	13	Q78941	495	13	Q78941	Human immunoglobulin	5 05e-106
25	165	44.7	585	33	T90022	585	33	T90022	585	33	T90022	DNA encoding heavy ch	9 93e-104
26	160	43.4	600	13	Q78962	600	13	Q78962	600	13	Q78962	Human immunoglobulin	6 55e-100
27	158	42.8	294	6	Q26335	294	6	Q26335	294	6	Q26335	SP2 Ig3 heavy chain c	2 20e-98
28	158	42.8	360	33	T72132	360	33	T72132	360	33	T72132	CEA-specific antibody	2 20e-98
29	158	42.8	369	12	Q70985	369	12	Q70985	369	12	Q70985	DNA encoding MAb bear	2 20e-98
30	158	42.8	629	13	Q78996	629	13	Q78996	629	13	Q78996	Human immunoglobulin	2 20e-98
31	157	42.5	421	33	T73524	421	33	T73524	421	33	T73524	cDNA for humanised he	1 27e-97
32	157	42.5	591	13	Q78955	591	13	Q78955	591	13	Q78955	Human immunoglobulin	1 27e-97
33	157	42.5	748	13	Q78983	748	13	Q78983	748	13	Q78983	Human immunoglobulin	1 27e-97
34	155	42.0	421	33	T73633	421	33	T73633	421	33	T73633	cDNA for humanised he	4 26e-96
35	153	41.5	421	33	T73636	421	33	T73636	421	33	T73636	cDNA for humanised he	1 42e-94
36	143	38.8	360	9	Q55616	360	9	Q55616	360	9	Q55616	Humanised heavy chain	5 69e-87
37	143	38.8	372	15	Q32540	372	15	Q32540	372	15	Q32540	Encodes VH Fab M74 wh	5 69e-87
38	142	38.5	409	15	Q44539	409	15	Q44539	409	15	Q44539	Human/murine chimeric	3 26e-86
39	142	38.5	409	23	T38653	409	23	T38653	409	23	T38653	Chimeric human/murin	3 26e-86
40	142	38.5	822	23	T38662	822	23	T38662	822	23	T38662	Chimeric human/murin	3 26e-86
41	142	38.5	822	15	Q94548	822	15	Q94548	822	15	Q94548	Plasmid pSCFV7 hwt1	3 26e-86
42	141	38.2	421	33	T73640	421	33	T73640	421	33	T73640	cDNA for humanised he	1 87e-85
43	138	37.4	410	17	T16178	410	17	T16178	410	17	T16178	Hu1308 VH encoding se	3 51e-83
44	137	37.4	410	14	Q67193	410	14	Q67193	410	14	Q67193	Humanized 1308F VH DN	3 51e-83
45	137	37.1	3282	24	T40914	3282	24	T40914	3282	24	T40914	DNA encoding VH regio	2 01e-82

ALIGNMENTS

RESULT 1 standard: DNA: 2287 BP.
ID Q25443;
AC Q25443;
DE Sequence encoding antibody molecule IgG1.
DT 02-JAN-1992 (first entry)
KW Antibody; immunoglobulin G1; ds.
OS Homo sapiens. Location/Qualifiers
FH Key 1..453
FT exon a
FT /tag= 612..972
FT exon b
FT /tag= 1361..1405
FT exon c
FT /tag= 1524..1853
FT exon d
FT /tag= 1950..2273
FT exon e
FT /tag= 1950..2273
PN WO9209293-A.
PD 11-JUN-1992.
PF 18-NOV-1991: U08605.
PR 23-NOV-1990: US-619314.
PA (GEO) GEN HOSPITAL CORP.
PI Seed B, Walz G;
DR WPI: 92-216789/26.
DP P-250P, R2442.
DT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PS - used in treating chronic inflammation, rheumatoid arthritis,
PSoriasis, etc.
CC Disclosure: Fig 1: 46pp; English.
CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC inventors designed a molecule including several such sites for
CC attachment of sialyl-Lex side chains (see R2442, FI). The
CC additional N-linked glycosylation sites are introduced at locations
CC which impair complement fixing and Fc receptor binding activity. They
CC are preferably located in the CH2 region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for
CC disrupting undesirable interactions between cells or proteins
CC Disrupting this interaction has therapeutic applications, for

QY 246 CCTCAGATCTGAGACACGGCGCTCTATTTCTGTGGCAGAG-TGTAATACCAATGCAG 304
 Db 406 ttttaccggccgggtgtgctggttcgacccctggggccagggccacccctggtcaccgt 465
 QY 305 TCCGGCACACCAT-GGGATAT-TACTTTGACTACTGTGGCCAGGAACCTGTGTACCGT 362
 Db 466 ctctctca 472
 QY 363 CTCCTCA 369

RESULT 10

ID T15202 standard; cDNA; 687 BP.
 AC T15202:
 DT 23-OCT-1996 (first entry)
 DE pC3AP313 anti-tetanus toxoid Ig heavy chain variable domain cDNA.
 KW Mutagenesis; Ig; immunoglobulin; FR; framework region; variable; CDR;
 KW complementarity determining region; light; heavy chain; PCR;
 KW polymerase chain reaction; antibody library; diversity; affinity;
 KW immunospecificity; ss.
 OS Synthetic.
 PN WO9607754-A1.
 PD 14-MAR-1996.
 PF 01-SEP-1995; U11235.
 PR 02-SEP-1994; US-300386.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-171625/17.
 PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PS Example 1: Page 83; 125pp; English.
 CC T15202 and T15203 are the heavy and light chain variable domains of
 CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3
 CC based expression vector. The heavy and light chain variable domains
 CC are used in an example to demonstrate the prodn. of antibodies for
 CC an antibody library using mutagenic primers. Mutagenic primers of the
 CC invention have sequences at their 3' and 5' ends both capable of
 CC binding different framework regions linked by a sequence 6 to 50
 CC nucleotides long. Different immunoglobulins produced using the
 CC primers may be used to produce antibody libraries having diverse and
 CC novel immunospecificities and affinities. By using mutagenic ONS an
 CC extremely large population of different randomised binding sites can
 CC be created and use of the universal light chain increases the number
 CC of combinations which yield functional heterodimeric antibodies.
 SQ Sequence 687 BP; 155 A; 211 C; 195 G; 126 T;

Query Match 52.6%; Score 194; DB 22; Length 687;
 Best Local Similarity 83.9%; Pred No. 5.60e-126;
 Matches 240; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 1 ctgcagcagctctggggtgaggtgaagaagcctgggtcctcggtgaggtcctctgcagg 60
 QY 1 CTCGAGCAGTCTGGGCTGAGTGAAGAGCCTGGGTCTCGGTGAGGTCTCTGTGAG 60
 Db 61 gcttcggagcacccttcaacaattatgccatcagctgggtgcgacagcccttgacaa 120
 QY 61 GTTTTGGAGACACCTTCAGCAGATACACTATTTCAGTGTGGCAGCGCCCTGGACAA 120
 Db 121 gggcttgagtgagtgagggatctccctttccgtaataacacaaagtacgacaaac 180
 QY 121 GGGCTTGAGTGGTGAATATATCTCTGTCTATTAATACCAACATACGCGCAGAG 180
 Db 181 ttccagggcagagtcaccattaccggcggaagaatccacggcgacagccctacatggagctg 240
 QY 181 TTTCAGGCGACACTCTCGATAACCGCGGAGTTCACGAGCAGACGCTACATGGAAGT 240
 Db 241 agcagccttgcagtgagacacggccatattattgttcgagag 286
 QY 241 AGTAGCCTCAGATCTGAGGACACGCGGCTCTATTCTGTGCGAGAG 286

RESULT 11

ID Q92546 standard; DNA; 4691 BP.
 AC Q92546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;
 KW bacterial membrane, periplasm; E. coli; human; Fab; HIV; gp120;
 KW combinatorial Fab library; cassette; fd/cp3; lacZ promoter/operator;
 KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;
 KW M14; pM14-3; antibody; ss; cyclic.
 OS Synthetic.
 PN WO9511317-A1.
 PD 27-APR-1995.
 PF 19-OCT-1994; U11907.
 PR 19-OCT-1993; US-139409.
 PR 26-APR-1994; US-233619.
 PR 19-SEP-1994; US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of
 PT HIV-induced disease
 PS Example 1: Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phage encodes
 CC the 406 residue minor phage coat protein, cpIII (cp3), which is expressed
 CC prior to extrusion in the phage assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector was designed for the cloning
 CC of combinatorial Fab libraries. pComb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC PelB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a PelB leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the M14 Fab display phagemid expression vector, pM14-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 SQ Sequence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T;

Query Match 52.6%; Score 194; DB 16; Length 4691;
 Best Local Similarity 83.9%; Pred. No. 5.60e-126;
 Matches 240; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 3424 ctgcagcagctctggggtgaggtgaagaagcctgggtcctcggtgaggtcctctgcagg 3483
 QY 1 CTCGAGCAGTCTGGGCTGAGGTGAAGAGCCTGGGTCTCGGTGAAGTCTCTGTGAG 60
 Db 3484 gcttcggagcacccttcaacaattatgccatcagctgggtgcgacagcccttgacaa 3543
 QY 61 GTTTTGGAGACACCTTCAGCAGATACACTATTTCAGTGTGGCAGCGCCCTGGACAA 120
 Db 3544 gggcttgagtgagtgagggatctccctttccgtaataacagaaagtacgacaaar 3603
 QY 121 GGGCTTGAGTGGTGAATATATCTCTGTCTATTAATACCAACATACGCGCAGAG 180
 Db 3604 ttccagggcagagtcaccattaccggcggaagaatccacggcgacagccctacatggagctg 3663
 QY 181 TTTTCAGGCGACACTCTCGATAACCGCGGAGTTCATTAACAGTACAGCTTACAACTG 240
 Db 3664 agcagcctgcagctctgcagacagcgccatattattgtgcgagag 3709

WATERMAN

(TM)

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MParch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm:
Run on: Tue Feb 24 10:06:36 1998. Maspar time 133.85 Seconds
Tabular output not generated.
695,522 Million cell updates/sec

Title: >US-08-844-215-23
Description: (1-369) from US08844215.seq
Perfect Score: 369
N.A. Sequence: 1 CCGAGAGAGACTGGGCGGCA.....CCCTGGTCACTGCTGCTCA 369
Comp: GAGTGTGTCAGAGAGACT.....GGGACCTAGTGGTGGAGAGAGT

Scoring table:
Gap 6
TABLE default
Nmatch STD : Dbase 0: Query 0
Searched: 333433 seqs, 126143548 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
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9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19
20:STS20 21:STS21 22:STS22 23:STS23 24:STS24
25:STS25 26:STS26 27:STS27 28:STS28 29:STS29
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85:STS85 86:STS86 87:STS87 88:STS88 89:STS89
90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96

Statistics: Mean 9.810; Variance 1.755; scale 5.589
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Query	Description	Pred. No.
No	Score	Match Length DB	ID
1	75	20 3	256 54
2	36	9 9	230 57

3	36	9.8	238 69	HS1300451	aa63q01.r1	NCI_CGAP_E	3.24e-24
4	36	9.8	238 35	AA505044	aa63q01.r1	NCI_CGAP_E	3.24e-24
5	30	8.1	511 63	HS1259634	zx8th07.r1	Soares ova	6.99e-19
6	30	8.1	511 17	AA464794	zx8th07.r1	Soares ova	6.99e-19
7	29	7.9	507 24	AA472093	zhigaoe.r1	Soares ova	3.06e-17
8	29	7.9	597 83	MM1264658	zhigaoe.r1	Soares ova	3.06e-17
9	23	6.2	259 30	AA488043	zh12f07.r1	Stratagene	4.90e-08
10	23	6.2	259 56	HS1281117	zh12f07.r1	Stratagene	4.90e-08
11	22	6.0	314 1	DM7805T	D. melanogaster	STS d	1.24e-06
12	22	6.0	435 80	HSAA7475	zh76c05.s1	NCI_CGAP_B	1.24e-06
13	22	6.0	435 40	AA507475	zh76c05.s1	NCI_CGAP_B	1.24e-06
14	21	5.7	155 1	DM3607S	D. melanogaster	STS d	2.80e-05
15	21	5.7	420 39	AA515152	na68c12.s1	NCI_CGAP_L	2.80e-05
16	21	5.7	420 71	HS1308760	na68c12.s1	NCI_CGAP_L	2.80e-05
17	21	5.7	451 75	HSAA40659	zo10h03.s1	Stratagene	2.80e-05
18	20	5.4	37 81	MM1242806	zof02f.r1	Soares ova	5.65e-04
19	20	5.4	170 80	HSAA7641	zt71b05.s1	Soares tes	5.65e-04
20	20	5.4	252 48	HS0774	NT5402	Normalised	5.65e-04
21	20	5.4	312 80	HS2254903	EST56674	Infant brain	5.65e-04
22	20	5.4	318 51	HS1248261	zx83e11.s1	Soares tes	5.65e-04
23	20	5.4	323 8	GA5518	human STS	EST282031	5.65e-04
24	20	5.4	330 9	GA29728	human STS	SHGC-45108	5.65e-04
25	20	5.4	345 23	AA471693	MBAPCX5E05T3	Brugia m	5.65e-04
26	20	5.4	345 46	BMAA71693	MBAPCX5E05T3	Brugia m	5.65e-04
27	20	5.4	404 5	G18085	human STS	SPAC-7277 c	5.65e-04
28	20	5.4	423 16	AA464355	zx81b01.r1	Soares ova	5.65e-04
29	20	5.4	423 67	HS1258135	zx81b01.r1	Soares ova	5.65e-04
30	20	5.4	425 77	HSAA38999	zx45d08.s1	Soares ova	5.65e-04
31	20	5.4	455 89	MMAA27173	ve83c01.r1	Soares mou	5.65e-04
32	20	5.4	473 33	AA498291	vh38g11.r1	Barstead m	5.65e-04
33	20	5.4	473 85	MM1294742	vh38g11.r1	Barstead m	5.65e-04
34	20	5.4	481 58	HS1336238	zx8b11.s1	Soares ova	5.65e-04
35	20	5.4	487 72	HS137412	ni61q10.s1	NCI_CGAP_2	5.65e-04
36	20	5.4	487 43	AA525938	ni61q10.s1	NCI_CGAP_2	5.65e-04
37	19	5.1	303 91	T09272	EST07155	Homo sapiens	1.00e-02
38	19	5.1	367 80	HS2254401	EST55954	Infant brain	1.00e-02
39	19	5.1	409 35	AA505056	vq40c06.r1	Soares mou	1.00e-02
40	19	5.1	431 46	BMAA6792	MRAPC24G01T3	Brugia m	1.00e-02
41	19	5.1	439 88	MM1312457	vi03h09.r1	Barstead m	1.00e-02
42	19	5.1	439 40	AA518911	vi03h09.r1	Barstead m	1.00e-02
43	19	5.1	466 64	HS1271305	zx76g12.s1	Soares NIH	1.00e-02
44	19	5.1	517 58	HS1241170	zx76f09.r1	Soares tes	1.00e-02
45	19	5.1	538 39	AA516910	vh47q01.r1	Barstead m	1.00e-02

ALIGNMENTS

RESULT 1
ID HS1202138 standard, RNA; EST, 266 BP.
AC AA402547,
NI 92056386
DI 01-MAY-1997 (Rel. 51, Created)
DT 22-MAY-1997 (Rel. 55, Last updated, Version 2)
DE 7047h07 r1 Soares ovari tumor N80T Homo sapiens cDNA clone 71111
DE 5' similar to gb:U8779 IG GAMMA-1 CHAIN C REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhina; Hominoidea; Homo.
RN [1]
RP 1-266

RA Hillier L, Allen M, Bowles L, Dubuque T, Geisel G, Jost S,
RA Kucaba T, Lacy M, Le N, Lennon G, Marra M, Martin J,
RA Moore B, Schellenberg K, Steptoe M, Tan F, Theising B,
RA White V, Wyllie T, Waterston R, Wilson R;
RI "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Willson PK WashU-Merck EST Project, Washington University
CC School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63104 Tel. 314 286 1900 Fax. 314 286 1910 Email:
CC estwason.wustl.edu This clone is available royalty-free through
CC LNCB. Contact the LNCB Consortium (lncb@lncb.gov) for
CC further information. Seq primer: 28a13 rev2 Et from AmerSham.


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FT mRNA /lab_host="DH10B"
SQ Sequence 238 BP: 57 A; 69 C; 66 G; 46 T; 0 other:

Query Match 9.8% Score 46; DP 69; Length 238;
Best Local Similarity 64.3%; Pred. No. 3,246-29;
Matches 81; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 8 gaggttaaaacccggaggatctctgagatctctctgagattctgatacagcttt 67
QY 19 GAGGTGAAGAGCCCTGGGTCCTCGTGAAGGTCTCTCTGAGGTTTGGAGACACCTTC 78

Db 68 accagcagctgattccactgggtgcgcagatgccgggaaagaactctagtgtatagg 127
QY 79 AGCAGATACACTTTCAGTGGTTCGACAGGCCCTGGACAGGCCCTGAGTGGATGGGA 138

Db 128 agcatc 133
QY 139 AATATC 144

RESULT 4
LOCUS AA0505044 238 bp mRNA EST 02-JUL-1997
DEFINITION aa63q01.r1 NC1-CGAP-GCB1 Homo sapiens cDNA clone 825648 5' similar
to SW:HV05_MOUSE P01749 IG HEAVY CHAIN PRECURSOR V REGION ;.
ACCESSION AA0505044
NID 92241204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata:
Vertebrata: Mammalia: Euthera: Primates: Catarrhini: Homiidae;
Homo.
REFERENCE 1 (bases 1 to 238)
AUTHORS NC1-CGAP.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NC1-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..238
/organism="Homo sapiens"
/clone="825648"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I, Site 2: Eco RI; 1st
strand cDNA was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD+),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTGAAGTGGAGCGCGGCTCATTTTTTTTTTTTTTTT-
3'. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/clone="825648"
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/tissue_type="germinal center B cell"
/lab_host="DH10B"
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57 a 69 c 66 g 46 t
MRNA
BASE COUNT
ORIGIN

Query Match 9.8% Score 36; DP 35; Length 238;
Best Local Similarity 64.3%; Pred. No. 3,246-29;
Matches 81; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 8 gaggttaaaacccggaggatctctgagatctctctgagattctgatacagcttt 67
QY 19 GAGGTGAAGAGCCCTGGGTCCTCGTGAAGGTCTCTCTGAGGTTTGGAGACACCTTC 78

Db 68 accagcagctgattccactgggtgcgcagatgccgggaaagaactctagtgtatagg 127
QY 79 AGCAGATACACTTTCAGTGGTTCGACAGGCCCTGGACAGGCCCTGAGTGGATGGGA 138

Db 128 agcatc 133
QY 139 AATATC 144

RESULT 5
ID HS1258634 standard; RNA: EST: 511 BP.
AC AA646794;
NI 92189678;
DT 13-JUN-1997 (Rel. 52, Created)
DE z83h07.r1 Soares ovary tumor NBH0T Homo sapiens cDNA clone R10397
DE 5' similar to gb:L21964 IG HEAVY CHAIN V-II REGION (HUMAN)..
KW EST.
OS Homo sapiens (human)
OC Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata:
OC Vertebrata: Euthera: Primates: Catarrhini: Homiidae; Homo.
RN [1]
RP 1-511
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White F., Wyllie T., Waterston R., Wilson R.;
PT "Washington University EST Project 1997";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
est@wustl.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham High
CC quality sequence stop: 414.
FH Key
FH Location/Qualifiers
FT source
FT 1..511
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TGTTACCAATCTGAAGTGGAGCGCGGCTCATTTTTTTTTTTTTTTT-3'].
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/clone="810397"
/clone_lib="Soares ovary tumor NBH0T"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>511
MRNA
SQ Sequence 511 BP: 105 A; 169 C; 124 G; 112 T; 0 other;

Query Match 8.1% Score 30; DP 63; Length 511;
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RESULT 13
LOCUS      Ar507475      435 bp      mPNA      EST      15-JUL-1997
DEFINITION n076095.s1 NCI-CCAP-Fri 1 Homo sapiens cDNA clone 964424 similar to
            q0.X14584 IG HEAVY CHAIN PFCUPSP V-III REGION (HUMAN);
ACCESSION  Ar507475
            Ar50475
            q2243914
            NID
            EST.
SOURCE      human..
ORGANISM   Homo sapiens
            Eukaryota; Eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE  1 (bases 1 to 435)
AUTHORS   NCI-CCAP.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I M A G E Consortium/LLNL at:
            www-bio.llnl.gov/bbr/image/image.html

```

